



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 174153

TO: Nita M Minnifield
Location: rem/3C01/3C18
Art Unit: 1645
Monday, December 19, 2005

Case Serial Number: 09/970076

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Minnifield,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

*Reviewed
12/05
mm*

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STIC-Biotech/ChemLib

174153

mg

From: Chan, Christina
Sent: Tuesday, December 13, 2005 6:38 PM
To: Minnifield, Nita; STIC-Biotech/ChemLib
Subject: RE: rush interference sequence search

Please ~~rush~~ Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Minnifield, Nita
Sent: Tuesday, December 13, 2005 1:27 PM
To: Chan, Christina
Subject: rush interference sequence search

Christina, please approve, AF amdt.

STIC

09/970076

Please do an interference sequence search on the following sequences found in the above application.

Please search against both aa and nt databases.

SEQ ID NO: 1
nt 104-1207 of SEQ ID NO: 1
SEQ ID NO: 2
aa 27-321 of SEQ ID NO: 2
aa 28-320 of SEQ ID NO: 2
aa 41-227 of SEQ ID NO: 2
aa 44-216 of SEQ ID NO: 2
aa 42-222 of SEQ ID NO: 2

Please provide a paper copy of all results.

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: 12/14/05
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search _____
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

reverse to AA
B + C - reverse to NA

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; SEQ ID NO 8
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (309)..(1202)
US-09-620-312D-8

Alignment Scores:
Pred. No.: 2,528-108 Length: 1609
Score: 899.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-09-620-312D-8 (1-1609)

OY 1 AapLeuTYrPheIleLeuAapLySerGIySerValLeuHISHTPrAsnGluIleTYr 20
DB 438 GACCTGTACTTCAATTTGGACAAATCAGAAAGTGTGCTGCACACTGGAAATGAATCTAT 497
OY 21 TyrPheValGluGlnLeuAlaHisLyPheIleSerProGlnLeuArgMetSerPheIle 40
DB 498 TACTTGTGGAAACAGTTGGCTCACAATTCATCAGCCACAGTTGAGAAATGCTTTATTT 557
OY 41 ValPheSerThrArgGlyThrThrLeuMetLyLeuThrGluAsnArgGluGlnIleArg 60
DB 558 GTTTCCTCCAGCCGAGAAACAACCTTAATGAACATGACAGAAAGACAGAAACAATCCGT 617
OY 61 GlnGlyLeuGluGlnLeuGlnLyValLeuProGlyGlyAapThrTYrMetHisGluGly 80
DB 618 CAAAGCCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACATTAATGATGAAGA 677
OY 81 PheGluArgAlaSerGlnGlnIleTYrTYrGluAsnArgGlnGlyTYrArgThrAlaSer 100
DB 678 TTTGAAAGGGCCAGAGAGATTTATTTATGAAGAACAGACAGAGGTACAGACAGCCAGC 737
OY 101 ValIleIleAlaLeuThrAapGlyGluLeuHisGluAapLeuPhePheTYrSerGluArg 120
DB 738 GTCAATCATTTGCTTTCATGATGAGAACTCCATGAAGATCTTTTTCATTCAGAGAGG 797
OY 121 GluAlaAsnArgSerArgAapLeuGlyAlaIleValTYrCYeValGlyValLyAsnPhe 140
DB 798 GAGGCTAATAGCTCTCGAGATCTTGCTGCAATGTTTACTGTGGTGTGAAGATTTTC 857
OY 141 AengIuThrGlnLeuAlaArgIleAlaAspSerLyAsnHisValPheProValAsnAap 160
DB 858 AATGAGACACAGCTGGCCGAGATTCGGGACAGTAAGATCATGTGTTCCCGTGAATGAC 917
OY 161 GlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu 173
DB 918 GGCCTTCAGGCTCTGCAGAGCATCATCACTCAATTTTG 956

RESULT 2
US-10-104-047-669
; Sequence 669, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cdna
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10104,047
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 669
; LENGTH: 2234
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-10-104-047-669

Alignment Scores:
Pred. No.: 4,498-58 Length: 2234
Score: 519.00 Matches: 103
Percent Similarity: 79.19% Conservative: 34
Best Local Similarity: 59.54% Mismatches: 34
Query Match: 57.73% Indels: 2
DB: 3 Gaps: 1

US-09-970-076-2_COPY_44_216 (1-173) x US-10-104-047-669 (1-2234)

OY 1 AapLeuTYrPheIleLeuAapLySerGIySerValLeuHISHTPrAsnGluIleTYr 20
DB 658 GATCTCACTTCGCTCTGACAAAGTGTGGAGTGGCAAAATTAATGAAATTTAT 717
OY 21 TyrPheValGluGlnLeuAlaHisLyPheIleSerProGlnLeuArgMetSerPheIle 40
DB 718 AATTCGTACAGCAACTTGGCGAGAGATTTGTAGCCTCGAAATGAGATTTCTTTCATT 777
OY 41 ValPheSerThrArgGlyThrThrLeuMetLyLeuThrGluAsnArgGluGlnIleArg 60
DB 778 GTGTTTCTTCTCAAGCAACTATATTTTGCATTTAATGAGACAGAGCAAAATCAGT 837
OY 61 GlnGlyLeuGluGlnLeuGlnLyValLeuProGlyGlyAapThrTYrMetHisGluGly 80
DB 838 AAGGCTTGGAGATTTTAAACGTGTAGTCCAGTGAAGAGACATATATCATCAAGAGA 897
OY 81 PheGluArgAlaSerGlnGlnIleTYrTYrGluAsnArgGlnGlyTYrArgThrAlaSer 100
DB 898 CTAAAGCTAGCAATGAACAAATTT-----CAGAAAGCAGAGGCTTAAAACTCCAGT 951
OY 101 ValIleIleAlaLeuThrAapGlyGluLeuHisGluAapLeuPhePheTYrSerGluArg 120
DB 952 ATCATTAATTTGCTGACAGATGGAAGTGAACGGTCTGTGCCATCATATGACAGAGAA 1011
OY 121 GluAlaAsnArgSerArgAapLeuGlyAlaIleValTYrCYeValGlyValLyAsnPhe 140
DB 1012 GAGCGAAAGATATCATGAGTCACTTGGGCTGTGTATTTGTGTGGTGTCTGATATTTT 1071
OY 141 AengIuThrGlnLeuAlaArgIleAlaAspSerLyAsnHisValPheProValAsnAap 160
DB 1072 GAAACAAGCAGCTTGAAGAAATGCTGATTTCCANAGAGCAAGTTTCCCTGTCAAGGT 1131
OY 161 GlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu 173
DB 1132 GGAATTCAGGCTCTTAAAGAAATATTAATCTATACTA 1170

RESULT 3
US-09-774-528-297
; Sequence 297, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyao
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/774,528
; NUMBER OF SEQ ID NOS: 441
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:01:37, Search time 121.458 Seconds

(without alignments)
3531.884 Million cell updates/sec

Title: US-09-970-076-2_COPY_44_216
Perfect score: 899
Sequence: 1 DLYFLDKSSVLHMHMEIY.....HYFVNDFOALGSIHSIL 173

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Xgapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

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3: /cgn2_6/ptodata/1/ina/65.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCrus.COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP.COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE.COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	899	100.0	1609	3	US-09-620-312D-8
2	519	57.7	2234	3	US-10-104-047-669
3	461	51.3	1492	3	US-09-774-528-297
4	461	51.3	1492	3	US-10-120-988-297
5	138.5	15.4	3528	2	US-08-286-889-36
6	138.5	15.4	3528	2	US-08-485-618-36
7	138.5	15.4	3528	2	US-08-362-652-36
8	138.5	15.4	3528	2	US-08-605-672-36
9	138.5	15.4	3528	2	US-08-482-293A-36

10	138.5	15.4	3528	2	US-08-943-363-36	Sequence 36, App1
11	138.5	15.4	3528	3	US-09-193-043-36	Sequence 36, App1
12	138.5	15.4	3528	3	US-09-688-307A-36	Sequence 36, App1
13	138.5	15.4	3528	3	US-09-350-259-36	Sequence 36, App1
14	138.5	15.4	3597	2	US-08-485-618-54	Sequence 54, App1
15	138.5	15.4	3597	2	US-08-362-652-54	Sequence 54, App1
16	138.5	15.4	3597	2	US-08-605-672-54	Sequence 54, App1
17	138.5	15.4	3597	2	US-08-482-293A-54	Sequence 54, App1
18	138.5	15.4	3597	2	US-08-943-363-54	Sequence 54, App1
19	138.5	15.4	3597	3	US-09-193-043-54	Sequence 54, App1
20	138.5	15.4	3597	3	US-09-688-307A-54	Sequence 54, App1
21	138.5	15.4	3597	2	US-08-485-618-54	Sequence 45, App1
22	134.5	15.0	3519	2	US-08-286-889-45	Sequence 45, App1
23	134.5	15.0	3519	2	US-08-485-618-45	Sequence 45, App1
24	134.5	15.0	3519	2	US-08-362-652-45	Sequence 45, App1
25	134.5	15.0	3519	2	US-08-605-672-45	Sequence 45, App1
26	134.5	15.0	3519	2	US-08-482-293A-45	Sequence 45, App1
27	134.5	15.0	3519	2	US-08-943-363-45	Sequence 45, App1
28	134.5	15.0	3519	3	US-09-193-043-45	Sequence 45, App1
29	134.5	15.0	3519	3	US-09-688-307A-45	Sequence 45, App1
30	134.5	15.0	3519	3	US-09-350-259-45	Sequence 45, App1
31	134.5	15.0	3803	2	US-08-485-618-52	Sequence 52, App1
32	134.5	15.0	3803	2	US-08-362-652-52	Sequence 52, App1
33	134.5	15.0	3803	2	US-08-605-672-52	Sequence 52, App1
34	134.5	15.0	3803	2	US-08-482-293A-52	Sequence 52, App1
35	134.5	15.0	3803	2	US-08-943-363-52	Sequence 52, App1
36	134.5	15.0	3803	3	US-09-193-043-52	Sequence 52, App1
37	134.5	15.0	3803	3	US-09-688-307A-52	Sequence 52, App1
38	134.5	15.0	3533	2	US-09-350-259-52	Sequence 52, App1
39	128.5	14.3	3533	3	US-08-476-062A-40	Sequence 40, App1
40	128.5	14.3	3533	6	PCT-US96-01314-40	Patent No. 5424399
41	128.5	14.3	3533	3	US-09-023-655-1147	Sequence 1147, Ap
42	128.5	14.3	3533	3	US-09-809-517A-37	Sequence 37, App1
43	128.5	14.3	4154	3	US-09-023-655-1178	Sequence 1178, Ap
44	128.5	14.3	4154	3	US-09-023-655-1178	Sequence 1178, Ap
45	128.5	14.3	4740	3	US-09-902-481B-2	Sequence 2, App1

ALIGNMENTS

RESULT 1
US-09-620-312D-8
Sequence 8, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Aundt, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehman, Tom
APPLICANT: Xue, Aiding J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungang
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_files Version 1.0

[illegible][illegible]


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OY 40 ILevalPheSerThrArgGlyThrThreumetySLeuThrglu----- 54
DB 544 ATGCAATCTGACACATCTGTAAGACCCATTTTACCTTCATGAAATTCAGAAACATCTGG 603
OY 55 AApArgGluGlnIleArgGlnIleuGluGlnIleValLeuProGlyGlyAsp 74
DB 604 GACCTTCAGAGCTGTGGATCCCATTTCTCCAGCTGCACA-----GGCCTG 648
OY 75 ThrTyMetHisGluGlyPheGluArgIleAspSerGluGlnIleTyThrGluAsnArgGln 94
DB 649 ACCTACACAGCCACAGGATCCGACAGATGAGAGAGCTTTCATTCATGACAGATGG 708
OY 95 GlyTyArgThrAla---SerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp 113
DB 709 TCCCGTAAAGTCCAGAGAGATCTCTCTTCATCAGAGATGGGACAGAAATACAGAGAC 768
OY 114 LeuPhePheTySerGlu-----ArgGluAlaAsnArgSerArgAspLeuGlyAlaIle 131
DB 769 CCCCTGAGATATAGTATGTCTCATTCGCCGCGACAGCAAGCT-----GGCATCAT 819
OY 132 ValTyCyValGlyValIleAsp---PheAsnGlu---ThrGlnLeuAlaArgIle--- 148
DB 820 CGTATGCTATTTGGGTGGAGATGCTTCCAGAGCCCATCTGCCCTGAGAGAGCTGAAC 879
OY 149 -----AlaAspSerLyAspHisValPheProValAsnAspGlyPheGlnAla 164
DB 880 ACCATTGGCTCAGCTCCCCACAGACACACGCTTCAAGTATGAGAAC---TTTCACACA 936
OY 165 LeuGlnGlyIle 168
DB 937 CTTCGACAGATC 948

RESULT 7
US-08-362-652-36
Sequence 36, Application US/08362652
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
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SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3456
US-08-362-652-36

Alignment Scores:
Pred. No.: 1.13e-07 Length: 3528
Score: 138.50 Matches: 52
Percent Similarity: 47.83% Conserved: 36
Best Local Similarity: 28.26% Mismatches: 71
Query Match: 15.41% Indels: 25
Gaps: 2

US-09-970-076-2_COPY_44_216 (1-173) x US-08-362-652-36 (1-3528)

OY 1 AApLeuTyPheIleLeuAspLySerGlySerVal---LeuHisIleTrpAsnGluIle 19
DB 424 GACATGCTTTCATGATGATGCTTCCGACATTAACCAAGGACTTTGCCAGATG 483
OY 20 TyTyPheValGluGlnLeuAlaHisLyAspHeIleSerProGlnLeuArgMetSerPhe 39
DB 484 AAGACCTTTGCAAGCTTTGATGGAGAGTTTGGACACACAGACACTTGTCTCCCTG 543
OY 40 ILevalPheSerThrArgGlyThrThreumetySLeuThrglu----- 54
DB 544 ATGCAATCTGACACATCTGTAAGACCCATTTTACCTTCATGAAATTCAGAAACATCTGG 603
OY 55 AApArgGluGlnIleArgGlnIleuGluGlnIleValLeuProGlyGlyAsp 74
DB 544 ATGCAATCTGACACATCTGTAAGACCCATTTTACCTTCATGAAATTCAGAAACATCTGG 603
OY 604 GACCTTCAGAGCTGTGGATCCCATTTCTCCAGCTGCACA-----GGCCTG 648
OY 75 ThrTyMetHisGluGlyPheGluArgIleAspSerGluGlnIleTyThrGluAsnArgGln 94
DB 649 ACCTACACAGCCACAGGATCCGACAGATGAGAGAGCTTTCATTCATGACAGATGG 708
OY 95 GlyTyArgThrAla---SerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp 113
DB 709 TCCCGTAAAGTCCAGAGAGATCTCTCTTCATCAGAGATGGGACAGAAATACAGAGAC 768
OY 114 LeuPhePheTySerGlu-----ArgGluAlaAsnArgSerArgAspLeuGlyAlaIle 131
DB 769 CCCCTGAGATATAGTATGTCTCATTCGCCGCGACAGCAAGCT-----GGCATCAT 819
OY 132 ValTyCyValGlyValIleAsp---PheAsnGlu---ThrGlnLeuAlaArgIle--- 148
DB 820 CGTATGCTATTTGGGTGGAGATGCTTCCAGAGCCCATCTGCCCTGAGAGAGCTGAAC 879
OY 149 -----AlaAspSerLyAspHisValPheProValAsnAspGlyPheGlnAla 164
DB 880 ACCATTGGCTCAGCTCCCCACAGACACACGCTTCAAGTATGAGAAC---TTTCACACA 936
OY 165 LeuGlnGlyIle 168
DB 937 CTTCGACAGATC 948

RESULT 8
US-08-605-672-36
Sequence 36, Application US/08605672
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
```

CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3456
US-08-605-672-36
US-08-605-672-36
Alignment Scores:
Pred. No.: 1.13e-07 Length: 3528
Score: 138.50 Matches: 52
Percent Similarity: 47.83% Conservative: 36
Best Local Similarity: 28.26% Mismatches: 71
Query Match: 15.41% Indels: 25
DB: Gaps: 10
US-09-970-076-2_COPY_44_216 (1-173) x US-08-605-672-36 (1-3528)
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DB 424 GACATTGCTTCTTCGATGATGGTTCGACGACATTACCAAGGACCTTGCCCATG 43
QY 20 TyTyTyPhVaIgluInleuAlahIeIyPheIleSerProglInleuAArgMetSerPhe 39
DB 484 AAGGACTTGTCAAGCTTGAAGGGAGAGTTTCCGACGACGACGACCTGTTCTCCCTG 543
QY 40 lleValPheSerThArGlyThrThrLeuMetUylSleuThglu----- 54
DB 544 ATGCATACCTGCAACATCCTGAGAGACCATTTACCTTCACTGATTCAGAAATCAGAAATCCTG 603
QY 55 AapArgGluInIleatrgInglYleuGluInleuGluInyValIeuProglYglYasp 74
DB 604 GACCTCAGAGCTCGTGATGCCATTGTCCAGCTGCA-----GGCTG 648
QY 75 ThTyTmechIsgluIlyPhegluArgAlSserGluInIleTyTyrgluAenArgGln 94
DB 649 ACCTACACAGCCACAGCATCCGACAGTGTGAGAGAGCTATTTCATAGCAAGATGGG 708
QY 95 GlTyTyArGthrAla---SerValIleIleAlaIeuThArSpglyGluIleuHIsGluAap 113

DB 709 TCCCTTAAGTCCCAAGAAATCTCTTGTGCATCAGATGGCGACGAATAACAGAGAC 768
QY 114 leuPhePheTyRserGlu-----ArgGluAlaAenArgSerArgAapleuGlyAlaIle 131
DB 769 CCCCTGAGATGATGATGATCATTCGCCCGCAGACAAAGCT-----GGCATCATT 819
QY 132 ValTyRcySvalGlyValIyAap---PheAenglu---ThrGlnleuAlaArgIle--- 148
DB 820 CGTATGCTATTGGGAGATGCTTCCAGAGACCCACATGCTCCCTGAAGAGCTGAAC 879
QY 149 -----AlaaspSerlySaphIsValPheProValaAenAapGlyPheGlnAla 164
DB 880 ACCATTGGCTACGCTCCCCCAGACAGACACGCTTCAAGTACGAGCAAC---TTTGACAGCA 936
QY 165 leuGlnGlyIle 168
DB 937 CTTGCGAGCATC 948
RESULT 9
US-08-482-293A-36
Sequence 36, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshhall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3456
US-08-482-293A-36

Alignment Scores:
 Pred. No.: 1,13e-07 Length: 3528
 Score: 138.50 Matches: 52
 Percent Similarity: 47.83% Conservative: 36
 Best Local Similarity: 28.26% Mismatches: 71
 Query Match: 15.41% Indels: 25
 DB: 2 Gaps: 10

US-09-970-076-2_COPY_44_216 (1-173) x US-08-482-293A-36 (1-3528)

```

QY 1 AspleuYrPheIleuAaplySerGlySerVal---LeuHshIstrpAangluile 19
DB 424 GACATTCGCTTCTGATGATGTTCTGGCAGCATTAACCAAGGAGCTTGGCCAGATG 483
QY 20 TyrTyrcyValGluInLeuAlaHleYvPheIleSerProGluInLeuAArgMetSerPhe 39
DB 484 AAGGACTTGTCAAGCTTGTATGGAGAGTTTGGAGCAGACCACTTGTCTCCCTG 543
QY 40 IleValPheSerThrArgGlyThrThleuMetLysLeuThrglu----- 54
DB 544 ATGCATATACCTGACATCTCGAAGCCCATTTTACCTTCACCTGAATTCAGAACATCTCG 603
QY 55 AspArgGluGlnIleArgGlnGlyLeuGluInLeuGlnYvAlaLeuProGlyGlyAsp 74
DB 604 GACCTCAGAGCTGGTGAGATCCCATTTGTCAGCTGCA-----GGCCTG 648
QY 75 ThrTyrcMetHshGluGlyPheGluArgAlaSerGluGlnIleTyrcGluAAsnArgGln 94
DB 649 ACCTACACAGCCACAGGATCCGAGCATGTGAAGCATTTCTATGCAAGAAATACAGAGAC 708
QY 95 GlyTyrcArgThrAla---SerValIleIleAlaLeuThrAspGlyGluLeuHshGluAsp 113
DB 709 TCCCGTAAAGTGCACAGAGATCTCTCTGTCTACAGATGGGCAAAATACAGAGAC 768
QY 114 LeuPheHshTyrcSerGlu-----ArgGluAlaAsnArgSerArgAspLeuGlyAlaIle 131
DB 769 CCCCTGAGTATGATGATGTCATTCGCCGCCAGACAAAGCT-----GGCATCATTT 819
QY 132 ValTyrcyValGlyValIleYvAsp---PheAsnGlu---ThrgInLeuAlaArgIle--- 148
DB 820 CGTTATGCTATTGGGGTGGAGATCCCTTCAGAGACCCCACTGCCCTGAAGAGACTGAC 879
QY 149 -----AlaAspSerLysAspHshValPheProValaAsnArgGlyPheGluAla 164
DB 880 ACCATTCGCTCAGCTCCCCACAGAGACCGTGTCAAGTAGAGCAAC---TTGCAGCA 936
QY 165 LeuGlnGlyIle 168
DB 937 CTTGCGAGCATC 948

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RESULT 10

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US-08-943-363-36
Sequence 36, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seair Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943.363

```

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FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3456
US-08-943-363-36

```

Alignment Scores:
 Pred. No.: 1,13e-07 Length: 3528
 Score: 138.50 Matches: 52
 Percent Similarity: 47.83% Conservative: 36
 Best Local Similarity: 28.26% Mismatches: 71
 Query Match: 15.41% Indels: 25
 DB: 2 Gaps: 10

US-09-970-076-2_COPY_44_216 (1-173) x US-08-943-363-36 (1-3528)

```

QY 1 AspleuYrPheIleuAaplySerGlySerVal---LeuHshIstrpAangluile 19
DB 424 GACATTCGCTTCTGATGATGTTCTGGCAGCATTAACCAAGGAGCTTGGCCAGATG 483
QY 20 TyrTyrcyValGluInLeuAlaHleYvPheIleSerProGluInLeuAArgMetSerPhe 39
DB 484 AAGGACTTGTCAAGCTTGTATGGAGAGTTTGGAGCAGACCACTTGTCTCCCTG 543
QY 40 IleValPheSerThrArgGlyThrThleuMetLysLeuThrglu----- 54
DB 544 ATGCATATACCTGACATCTCGAAGCCCATTTTACCTTCACCTGAATTCAGAACATCTCG 603
QY 55 AspArgGluGlnIleArgGlnGlyLeuGluInLeuGlnYvAlaLeuProGlyGlyAsp 74
DB 604 GACCTCAGAGCTGGTGAGATCCCATTTGTCAGCTGCA-----GGCCTG 648
QY 75 ThrTyrcMetHshGluGlyPheGluArgAlaSerGluGlnIleTyrcGluAAsnArgGln 94
DB 649 ACCTACACAGCCACAGGATCCGAGCATGTGAAGCATTTTCTATGCAAGAAATACAGAGAC 708
QY 95 GlyTyrcArgThrAla---SerValIleIleAlaLeuThrAspGlyGluLeuHshGluAsp 113
DB 709 TCCCGTAAAGTGCACAGAGATCTCTGTCTACAGATGGGCAAAATACAGAGAC 768
QY 114 LeuPheHshTyrcSerGlu-----ArgGluAlaAsnArgSerArgAspLeuGlyAlaIle 131
DB 769 CCCCTGAGTATGATGATGTCATTCGCCGCCAGACAAAGCT-----GGCATCATTT 819
QY 132 ValTyrcyValGlyValIleYvAsp---PheAsnGlu---ThrgInLeuAlaArgIle--- 148
DB 820 CGTTATGCTATTGGGGTGGAGATCCCTTCAGAGACCCCACTGCCCTGAAGAGACTGAC 879

```

OY 149 -----AlaAspSerIySaPhisValPheProValIAsnaSPGIyPheGlnIla 164
DB 880 ACCATTGGCTGACGCTCCCCACAGACGCGTTCAGAGTACGCAAC---TTTCACACA 936
OY 165 LeuGlnGlyIle 168
DB 937 CTCGCGACGATC 948

RESULT 11
US-09-193-043-36
Sequence 36, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36
LENGTH: 3528
TYPE: DNA
ORGANISM: Rattus rattus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(3453)
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-193-043-36

Alignment Scores:
Pred. No.: 1.13e-07 Length: 3528
Score: 138.50 Matches: 52
Percent Similarity: 47.83% Conservative: 36
Best Local Similarity: 28.26% Mismatches: 71
Query Match: 15.41% Indels: 25
DB: 3 Gaps: 10

US-09-970-076-2_COPY_44_216 (1-173) x US-09-193-043-36 (1-3528)

OY 1 AAPLeuTyRPhelIleuNaSPlySergIyServal---LeuNHistIRPaNGluIle 19
DB 424 GACATTGCTTCTCGTGTATGATGTTGGCAGCATTAACCAAGGACCTTGGCCCGAGATG 483
OY 20 TyTyRPhValGluGlnIleuValHisIySPheIleSergProGlnIleuArgMetSerphe 39
DB 484 AAGGACTTTGTCAAACTTGTATGGAGAGTTGGCAGACGCAAGCCTTGTCTCCG 543
OY 40 ILeValPheSerThrArgIyThrThrLeuMetLysLeuThrGlu----- 54
DB 544 ATGCATTAATCTCGAACTCTGAAAGACCATTTTACCTCACTGAATTTCAAGACATCTCG 603
OY 55 AAPArgGluGlnIleArgGlnIyLeuGluGlnIleuGlnIleValLeuProGlyIyAap 74
DB 604 GACCTCAGAGCCTGGTGTATCCCATGTCACCTGCA-----GGCCTG 648
OY 75 ThrTyRMetHisGluGlyPheGluArgAlaSerGluGlnIleTyTyRgluAenArgGln 94
DB 649 ACCTTACACAGCCACAGCATCCGACAGCATGAGAGAGCTATTTCATGCAAGATGGG 708
OY 95 GLyTyArgThrAla---ServalIleIleAlaLeuThraSPGIyGluLeuNHistGluAap 113
DB 709 TCCCGTAAAGTCCCAAGAAATCTCTCTGTGCATCAGATGGGACAAATACAGAGAC 768

OY 114 LeuPheThyYsGrgIu-----ArgGluIlaSnaArgSerArgSPleuGlyAlaIle 131
DB 769 CCCCTGAGTATGATGATGATTCATTCGCCGCCACAGCAAAAGT-----GGCATCATTT 819
OY 132 ValTyRcysValGlyValIyAsp---PheANGlu---ThrGlnIleuAlaArgIle--- 148
DB 820 CGTATGCTATTGGAGTGGAGATGCTTCCAGAGAGCCCATGCGCTTAAGAGACTGAAAC 879
OY 149 -----AlaAspSerIySaPhisValPheProValIAsnaSPGIyPheGlnIla 164
DB 880 ACCATTGGCTGACGCTCCCCACAGACGCGTTCAGAGTACGCAAC---TTTCACACA 936
OY 165 LeuGlnGlyIle 168
DB 937 CTCGCGACGATC 948

RESULT 12
US-09-688-307A-36
Sequence 36, Application US/09688307A
Patent No. 6432404
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 6432404el Human Beta-2
FILE REFERENCE: 27866/36646
CURRENT APPLICATION NUMBER: US/09/688,307A
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 08/605,672
PRIOR FILING DATE: 1996-02-22
PRIOR APPLICATION NUMBER: 08/173,497
PRIOR FILING DATE: 1993-12-23
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR FILING DATE: 1994-08-05
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR FILING DATE: 1994-12-21
PRIOR APPLICATION NUMBER: 08/943,363
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36
LENGTH: 3528
TYPE: DNA
ORGANISM: Rattus rattus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(3453)
OTHER INFORMATION: Description of Artificial Sequence: primer
NAME/KEY: misc_feature
LOCATION: 361
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 464
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 486
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 506
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 1117
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 1118
OTHER INFORMATION: Xaa = any or unknown amino acid
US-09-688-307A-36

Alignment Scores:
Pred. No.: 1.13e-07 Length: 3528
Score: 138.50 Matches: 52

```
Percent Similarity: 47.83% Conservative: 36
Best Local Similarity: 28.26% Mismatches: 71
Query Match: 15.41% Identities: 25
DB: 3 Gaps: 10
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US-09-970-076-2_COPY_44_216 (1-173) X US-09-688-307A-36 (1-3528)

```

Oy      1  AarvLeuTherHeiLeuShaerLyuSerGluYseVal---LeuNiNiNiETpDAaNgLuLe 19
         |||:::|||||
Db      424  GACATCTCTTCTCGATTGATGGTTCTGGACAGCATTAACCAAGGAACTTTGGCCAGATG 48
Oy      20  TATpTyrPheValGluInLeuAlaNiVlyrPheLeSerProGlnLeuAlaGMeSerPhe 39
         |||:::|||||
Db      484  AAGGACTTTGTCAAGCTTTGATGGAGAGATTGGTTCGAGACACAGACACCTGTGTCTCC 54
Oy      40  ILeValPheSerThrArgGlyThrThrLeuMetLyuLeuThiGlu-----54
         :::::|||||
Db      544  ATGCAAAATCTCGAAACATCTCGAAAGCCCAATTTTACCTTCACTGAATTCAGAAATCTCTG 60
Oy      55  AArpArgGluGlnIleArgGlnGlyLeuGluGluGlnLyuValLeuProGlyGlyAAsr 74
         |||:::|||||
Db      604  GACCCCTCAGACCTGGTGGATGCCCATTTGCTGCACCTGCA-----GGCCTG 64
Oy      75  ThrTyrMetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGlyAlaArgGln 94
         |||:::|||||
Db      649  ACCCAACACAGCCACAGGACATCCGAGACAGTATGCAAGACCTTTTCAATGCAAGATGGG 70
Oy      95  GLyTyrArgThrAla---SerValIleIleAlaLeuThrAAsrGlyLyuLeuNiGluAAsr 113
         |||:::|||||
Db      709  TCCCGTAAAGATGCGCAAGAAAGATCTCTGTGATCATCAAGATGGGCGAAATACAGAAC 76
Oy      114  LeuPhePheTyrSerGlu-----ArgGluAlaAAsrSerArgAAsrLeuGlyAlaIle 131
         |||:::|||||
Db      769  CCCCTGAGATATGATGATGATCATCTCCGCGCGGACAAAGCT-----GGCATCATTT 81
Oy      132  ValTyrGlyValGlyValLyuAAsr---PheAlaGlu---ThiGlnLeuAlaArgIle--- 148
         |||:::|||||
Db      820  CGTTATGCTATTTGGGGGGAGATGCTCTTCCAGAGCCCAACCTGACGCTTAAAGAGCTGAAC 87
Oy      149  -----AlaAAsrSerLyuAAsrHisValPheProValAAsrAspGlyPheGlnAla 164
         |||:::|||||
Db      880  ACCATTGGCTCAGCTCCCGCCACAGACAGACAGTGTTCAGGTGAGAAC---TTTGACGCA 93
Oy      165  LeuGlnGlyIle 168
         |||:::|||||
Db      937  CTTCGACAGCATC 948

RESULT 13
US-09-350-259--36
Sequence 36, Application US/09350259
Patent No. 6620915
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Monica
TITLE OF INVENTION: No. 6620915el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
EARLIER FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36
LENGTH: 3528
TYPE: DNA

```

```

: ORGANISM: Rattus rattus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(3453)
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: primer
: OS-09-350-259-36

```

Alignment Scores:	
Pred. No.:	1.13e-07
Score:	138.50
Percent Similarity:	47.8%
Best Local Similarity:	28.26
Query Match:	15.4%
DB:	3
Length:	352
Matches:	52
Conservative:	36
Mismatches:	71
Indels:	25
Gaps:	10

US-09-970-076-2_COPY_4_216 (1-173) x US-09-350-259-36 (1-3528)

```

0Y      1 AepLeuTYrPhelieleuAaBrLySeRgiSeVal--LeuNhiNtSTraNgnIle 13
Db      424 GACATGGCTTTCTGTATGATGTTCTGGACAGATTAACAAAGGACTTGGCCCAAGTGG
0Y      20 TyTYrPhVaIgluNleuAaIahIeLySPhelieSeRProGInleuAArgMeSeRPh 39
Db      484 AAGACTTTGTCAAACTTTGATGGGAAGAGTTTGGACACACAGACACTTGTCTCCCTG
0Y      40 IleValPheSeRThraRgiLyThrThrLeuMetLybLeuThrgIu----- 54
Db      544 ATCAATACSTCGAAACATCTCTGAAGACCCATTTTACCTTCACTGAATTCAGAACATCTCG
0Y      55 AaRArggluNleIaRgInleuNgiIyueNgiIyVaIleuProGlyIaAaR 74
Db      604 GACCTCTCAAGGCTGTGGATGCCATGTCTCCAGCTGCA-----GGCCTG 64
0Y      75 ThrTYrMetNtSeIuNgiPheNgiuAaIaSeRgiuNleIyTYrTYrGluAaRgIn 94
Db      649 ACCTACACAGCCACAGGACATCCGACAGATGAAGAGATTTTCACTTACACAAATGGG 70
0Y      95 GlyTYrArgThraIa---SeRValIleIleAlaIeThraRgiIyGluNhiNtGluAaR 11
Db      709 TCCCGTAAAGTCCCAAGAAAGATCTCTGTGCATCAACAGATGGGCAAAATACAGAAC 76
0Y      114 LeuPhePheTYSeRgiu----ArgIuIlaAaNaRSeRArgAaRleuGlyIaIle 131
Db      769 CCCCCTGAGATTAAGATGATCTATTCGCCGCCAGACAAAGCT-----GGCATCATTT 81
0Y      132 ValTYrCyVaIglYValIyAaR--PheAeNgiu--ThrgInleuAaIaRgIle-- 148
Db      820 CGTTATGATATTGGGGTGGAGATCCCTTCCACAGAGCCCACTGCCCTGTAGAGACCTAAC 87
0Y      149 -----AlaAspSeRlyAaRhiIaVaIaPheProVaIaAaNaRgiIyPheGluAa 164
Db      880 ACCATTGGCTCAAGCTCCCCACAGACACACGATGTTCAAGTAAGGCAC--TTTGCAGCA 93
0Y      165 leuNgiIyIle 168
Db      937 CTTCGACGACATC 948

RESULT 14
US-08-485-618-54
/ Sequence 54, Application US/08485618
/ Patent No. 5728533
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States

```

```

? ZIP: 60606-6402
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/485,618
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/173,497
? FILING DATE: 23-DEC-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/286,889
? FILING DATE: 5-AUG-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/362,652
? FILING DATE: 21-DEC-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Williams Jr., Joseph A.
? REGISTRATION NUMBER: 38,659
? REFERENCE/DOCKET NUMBER: 27866/32797
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-474-6300
? TELEFAX: 312-474-0448
? TELEK: 25-3856
? INFORMATION FOR SEQ ID NO: 54:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 3597 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: CDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 40..3525
? US-08-485-618-54

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Alignment Scores:		
Pred. No.:	1.16e-07	Length: 3587
Score:	138.50	Matches: 52
Percent Similarity:	47.83%	Conservative: 36
Best Local Similarity:	28.26%	Mismatches: 71
Query Match:	15.41%	Indels: 25
DB:	2	Gaps: 10

```

Oy      1  AepLeuTyrrPhaIleuAaerLySerGlySeVal---LeuHishIerPhaengIuIle 19
Db      493  GACATTCCTCTTCTCGATGATGGATCTTGGACAGATTAAACCAAGGACCTTGGCCCAAGATG 552
Oy      20  TyrrTyrrPhaValGluInLeuAaIshLySphaIleSerProGluInLeuAaGmetSerPhe 39
Db      553  AAGGACTTTGTCAAAAGCCTTGAATGGAGAGATTGGACAGACACAGACACTTGTCTCCCTG 612
Oy      40  ILevalPheSerThrArgIyThrThrIleuMeLyLeuThrGlu----- 54
Db      613  ATGCAAATACTCGAACATCTCGAAGACCCATTTTAACTTCAGCTAAATTCAAAGACATCTCG 672
Oy      55  AepArvgIuGlnIleArvgInGlyLeuGluInLeuGlnLySValLeuProGlyGlyAep 74
Db      673  GACCTTCAGAGCCTGGTGGATCCCATTCGCACCTCCAA-----GGCCTG 717
Oy      75  ThrTyrrMeaHisGluIyPheGluArvgIaIaSerGluGlnIleTyrrTyrrGluAaArvgIn 94
Db      718  ACCTACACACGCCACAGGCAATCCGGACAGTGAAGAGCATTTATTCATATAGCAAGAAATGGG 777
Oy      95  GlTyrrArvgThrAla---SerValIleIleAlaLeuThrAepGlyGluHisGlyAep 113
Db      778  TCCCCGTAAGAAGTGGCAAGAGATCTCTCTGTGCATCAACATGGGCGAAGATTCACAGAGAC 837

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QY      114  LeuDehheHeYseargiu-----ArguilaAsnargsearigaDeuLeuGLYAlIle 131
Db      838  CCCCTGGAGTATGTGATGTGCATTCCTCCGCGCGACAAAGCT-----GGATCATTT 888
QY      132  ValTYrCyseValgiVallyeAeP---PheasnGlu---ThrgInleuAlaArgIle--- 148
Db      889  CGTTATCTCTATGGGGGTGGAGATGCTTCCAGAGCCCACTGCGCTGAAAGAACTGCAAC 948
QY      149  -----AlaAePseTlyeAeAphIleValPheToValAenAePgiYrPheGluAla 164
Db      949  ACCATTGGCTCAGGTCTCCCCACAGACAGACAGCTGTTCAGGTAGGAAC--TTTGCAGCA 1005
QY      165  IeuGInglYIle 168
Db      1006  CTTCGACGATC 1017

```

RESULT 15
US-08-362-652-54
Sequence 54, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362 653

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1      /
2      / FILING DATE: 435
3      / CLASSIFICATION: 435
4      / PRIOR APPLICATION DATA:
5      / PRIOR APPLICATION NUMBER: US 08/173,497
6      / APPLICATION NUMBER: 23-DEC-1993
7      / FILING DATE: 23-DEC-1993
8      / PRIOR APPLICATION DATA:
9      / APPLICATION NUMBER: US 08/286,889
10     / FILING DATE: 5-AUG-1994
11     / FILING DATE: 5-AUG-1994
12     / ATTORNEY/AGENT INFORMATION:
13     / NAME: Williams Jr., Joseph A.
14     / REGISTRATION NUMBER: 38,659
15     / REFERENCE/DOCKET NUMBER: 2/866/32391
16     / TELECOMMUNICATION INFORMATION:
17     / TELEPHONE: 312-474-6300
18     / TELEFAX: 312-474-0448
19     /
20     / TELEX: 25-1856
21     / INFORMATION FOR SEQ ID NO: 54:
22     / SEQUENCE CHARACTERISTICS:
23     / LENGTH: 3597 base pairs
24     / TYPE: nucleic acid
25     / STRANDEDNESS: single
26     / TOPOLOGY: linear
27     / MOLECULE TYPE: cDNA
28     / FEATURES:
29     /
30     / NAME/KEY: CDS
31     / LOCATION: 40..3525
32     /
33     / US-08-362-652-54

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Alignment scores:	
Pred. No.:	1,16e-07
Score:	138.50
Percent Similarity:	47.83%
Best Local Similarity:	28.26%
Query Match:	15.41%
Length:	3597
Matches:	52
Conservative:	36
Mismatches:	71
Indels:	25

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US-09-970-076-2_COPY_44_216 (1-173) x US-08-362-652-54 (1-3597)
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QY 20 TyrTyRpheValGluInLeuAlaH18LyseRpheileseRProGInLeuArgMetSerPhe 39
DB 553 AAGGACTTGTTCAAAGCTTTGATGGAGAGTTTGGACACACAGCACTGTCTCCCTG 612
QY 40 I1eValPheSerThrArgGlyThrThrLeuMetLyseLeuThrGlu----- 54
DB 613 ATGCAATACTGAACTGAACTGAACTTTTAACTTCACTGAATTCAAGAACATCCTG 672
QY 55 AsparGluGlnIleArgGlnGlyLeuGluGluLeuGlnLyseValLeuProGlyGlyAsp 74
DB 673 GACCTCGAGACCTGGTGATCCCATTTCTCCAGCTGCA-----GGCCTG 717
QY 75 ThrTyRmetH18GluGlyPheGluArgAlaSerGluGlnIleTyRtyRgluAsnArgGln 94
DB 718 ACCATACACAGCCACAGCATCGGACAGTATGGAGAGCTATTTCATAGCAAGATGG 777
QY 95 GlyTyRArgThrAla---SerValIleIleAlaLeuThrAspGlyGluLeuH18GluAsp 113
DB 778 TCCGTAAGAAGTCCCAAGAGATCTCTCTGTATCACAGATGGCAGAAATACAGAGAC 837
QY 114 LeuPhePheTyRserGlu-----ArgGluAlaAsnArgSerArgAspLeuGlyAlaIle 131
DB 838 CCCCTGAGTATGATGATCATTCGCCCGAGACAAAGCT-----GGCATCATTT 888
QY 132 ValTyRCysValGlyValIlyAsp---PheAsnGlu---ThrGlnLeuAlaArgIle--- 148
DB 889 CGTTATGCTATGGGGTGGAGATGCTTCCAGAGCCCACTGCCCTGAAGAGCTGAAC 948
QY 149 -----AlaAspSerLyseAspH18ValPheProValAsnAspGlyPheGlnAla 164
DB 949 ACCATTGGCTCAGCTCCGCCACAGAGCACCGTTCAAGTATGGCAAC---TTTGCAGCA 1005
QY 165 leuGlnGlyIle 168
DB 1006 CTTCGACAGCATC 1017

Search completed: December 18, 2005, 07:34:43
Job time : 133.458 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:01:37 ; Search time 127.075 Seconds
(without alignments)
2531.884 Million cell updates/sec

Title: US-09-970-076-2_COPY_42_222
Perfect score: 943
Sequence: 1 GFDLYFLIDKSGSVLHWNH.....DGFALQGIHSLKSCIE 181

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA -QFMT=fastcp -SUFFIX=rm -MINMATCH=0.1 -LOOFC=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO MMAP -LARGESUBERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database : Issued Patents NA:*

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3: /cgn2_6/ptodata/1/ina/6A/COMB.seq:*
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7: /cgn2_6/ptodata/1/ina/PP/COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE/COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfile01.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	943	100.0	1609	3	US-09-620-312D-8
2	542	57.5	2234	3	US-10-104-047-669
3	478	50.7	1492	3	US-09-774-528-297
4	478	50.7	1492	3	US-10-120-988-297
5	158	16.8	3981	3	US-09-799-451-250
6	141.5	15.0	3528	2	US-08-286-889-36
7	141.5	15.0	3528	2	US-08-485-618-54
8	141.5	15.0	3528	2	US-08-362-652-36
9	141.5	15.0	3528	2	US-08-605-672-36



10	141.5	15.0	3528	2	US-08-482-293A-36	Sequence 36, Appl
11	141.5	15.0	3528	2	US-08-943-363-36	Sequence 36, Appl
12	141.5	15.0	3528	3	US-09-193-043-36	Sequence 36, Appl
13	141.5	15.0	3528	3	US-09-688-307A-36	Sequence 36, Appl
14	141.5	15.0	3528	2	US-09-350-259-36	Sequence 36, Appl
15	141.5	15.0	3597	2	US-08-485-618-54	Sequence 54, Appl
16	141.5	15.0	3597	2	US-08-362-652-54	Sequence 54, Appl
17	141.5	15.0	3597	2	US-08-605-672-54	Sequence 54, Appl
18	141.5	15.0	3597	2	US-08-482-293A-54	Sequence 54, Appl
19	141.5	15.0	3597	2	US-08-943-363-54	Sequence 54, Appl
20	141.5	15.0	3597	3	US-09-193-043-54	Sequence 54, Appl
21	141.5	15.0	3597	3	US-09-688-307A-54	Sequence 54, Appl
22	141.5	15.0	3597	3	US-09-350-259-54	Sequence 54, Appl
23	138.5	14.7	3519	2	US-08-286-889-45	Sequence 45, Appl
24	138.5	14.7	3519	2	US-08-485-618-45	Sequence 45, Appl
25	138.5	14.7	3519	2	US-08-362-652-45	Sequence 45, Appl
26	138.5	14.7	3519	2	US-08-605-672-45	Sequence 45, Appl
27	138.5	14.7	3519	2	US-08-482-293A-45	Sequence 45, Appl
28	138.5	14.7	3519	2	US-08-943-363-45	Sequence 45, Appl
29	138.5	14.7	3519	3	US-09-193-043-45	Sequence 45, Appl
30	138.5	14.7	3519	3	US-09-688-307A-45	Sequence 45, Appl
31	138.5	14.7	3519	3	US-09-350-259-45	Sequence 45, Appl
32	138.5	14.7	3803	2	US-08-485-618-52	Sequence 52, Appl
33	138.5	14.7	3803	2	US-08-362-652-52	Sequence 52, Appl
34	138.5	14.7	3803	2	US-08-605-672-52	Sequence 52, Appl
35	138.5	14.7	3803	2	US-08-482-293A-52	Sequence 52, Appl
36	138.5	14.7	3803	2	US-08-943-363-52	Sequence 52, Appl
37	138.5	14.7	3803	3	US-09-193-043-52	Sequence 52, Appl
38	138.5	14.7	3803	3	US-09-688-307A-52	Sequence 52, Appl
39	138.5	14.7	3803	3	US-09-350-259-52	Sequence 52, Appl
40	132.5	14.1	3533	2	US-08-476-062A-40	Sequence 40, Appl
41	132.5	14.1	3533	6	PCT-US96-01314-40	Sequence 40, Appl
42	132.5	14.1	3533	9	PCT-US96-01314-40	Sequence 40, Appl
43	132.5	14.1	3533	3	US-09-023-655-1147	Sequence 37, Appl
44	132.5	14.1	4045	3	US-09-809-517A-37	Sequence 37, Appl
45	132.5	14.1	4124	3	US-09-023-655-1178	Sequence 1178, Ap

ALIGNMENTS

RESULT 1
US-09-620-312D-8
Sequence 8, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Dian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Dimaec, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_Fl_genes Version 1.0

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/ SEQ ID NO 8
/ LENGTH: 1609
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (309)..(1202)
US-09-620-312D-8

Alignment Scores:
Pred. No.: 3 05e-113 Length: 1609
Score: 943.00 Matches: 161
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-09-620-312D-8 (1-1609)

QY 1 G1YPheApleuTYrPhe1leuApleuSerg1yServal1euh1sh1strPaanglu 20
DB 432 GGAATTGACCTGACTTCTTGGACAAATCAGAAAGTGTGTCAGCCAGCTGAATGAA 491
QY 21 11eTYrTYrPheValGluGluLeuA1ah1elyPhe11eSergProGluLeuA1gmetSer 40
DB 492 ACTATTAATCTTGAGAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATGTC 551
QY 41 Phe11eValPheSergTharG1yThrThrLeuMetLysLeuThrGluAparGluGlu 60
DB 552 TTTATGTTTCTCCACCCAGAAACAACTTAAATGAACTGACAGAGACAGAAACAA 611
QY 61 11eArgGluGlyLeuGluGluLeuGluGlyValLeuProGlyGlyAparThyTyrMetHis 80
DB 612 ATCCGTCAGAGGCTAGAGAAATCCAGAAAGTTCTGCGAGAGAGACATTAATGAT 671
QY 81 GluGlyPheGluA1serGluGluGlyValLeuProGlyGlyAparThyTyrArgThr 100
DB 672 GAAGGATTTGAAAGGGCGAGTGAAGCAATTTATTAAGAAACAGACAGAGGTCAGACA 731
QY 101 AlaSerVal11e1leuA1euh1rAparGlyGluLeu1e1e1eVal1yTyrCyVal1yVal1y 120
DB 732 GCCAGGCTATCTTCTGCTGATGAGAACTCCATGAATCTCTTTTCTATTC 791
QY 121 GluArgGluA1aSerA1serA1serA1e1eVal1yTyrCyVal1yVal1y 140
DB 792 GAAGGAGGCTAATAGTCTCCAGATCTTGTCATCTTTAATCTGTTGTCGAGAA 851
QY 141 AapPheA1euh1rGluLeuA1ah1e1eA1aSerLysAparHisValPheProVal 160
DB 852 GATTCATAGACACAGCTGGCCCGGATTCGCGACGTAAAGATCTGTTGTTCCCGTG 911
QY 161 AapAapGlyPheGluA1euh1e1e1e1e1e1e1e1e1e1e1e1e1e1e1e1e1e1e 180
DB 912 AATGACGGCTTTCAGGCTCTGCAAGCATCATCACTCAATTTTGAAGAAAGTCTGATC 971
QY 181 Glu 181
DB 972 GAA 974

RESULT 2
US-10-104-047-669
/ Sequence 669, Application US/10104047
/ Patent No. 6943241
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: No. 6943241e1 full length cDNA
/ FILE REFERENCE: H1-A0105
/ CURRENT APPLICATION NUMBER: US/10/104, 047
/ PRIOR FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER:
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: PatentIn Ver. 2.1
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/ SEQ ID NO 669
/ LENGTH: 2234
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-104-047-669

Alignment Scores:
Pred. No.: 1 34e-60 Length: 2234
Score: 542.00 Matches: 107
Percent Similarity: 78.89% Conservative: 35
Best Local Similarity: 59.44% Mismatches: 36
Query Match: 57.48% Indels: 2
Gaps: 1

US-09-970-076-2_COPY_42_222 (1-181) x US-10-104-047-669 (1-2234)

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DB 655 TTTGATCTCTAATCTTGCTGCAAGTGTGAGAGTGTGCAAAATTAATGATGAAAT 714
QY 22 TYrTYrPheValGluGluLeuA1ah1elyPhe11eSergProGluLeuA1gmetSerPhe 41
DB 715 TATTAATTCGTACAGCACTTCGAGAGATTTGTGAGCCCTGAATGAGATTAATCTTTC 774
QY 42 11eValPheSergTharG1yThrThrLeuMetLysLeuThrGluAparGluGlu 61
DB 775 ATTGTTTCTTCTCAAGCACTTATTTTCCCTTAATCTGAGACAGAGCAAAATC 834
QY 62 ArgGluGlyLeuGluGluGluGlyValLeuProGlyGlyAparThyTyrArgThrA1a 81
DB 835 AATAAAGGCTGAGAGATTAATAAGCTGTAGTCCAGTGAAGACATATATCCATGAA 894
QY 82 GlyPheGluA1serGluGluGlyValLeuProGlyGlyAparThyTyrArgThrA1a 101
DB 895 GGACTAAAGCTGAGATTAATAAGCTGTAGTCCAGTGAAGACATATATCCATGAA 948
QY 102 SerVal11e1e1eA1euh1rAparGlyGluLeuH1e1eA1aSerLysAparPhePheTyrSerglu 121
DB 949 AGTATCATTAATGCTCTGCAAGTGTGAGAACTCCATGAATCTCTTTTCTATTC 1008
QY 122 ArgGluA1aSerA1serA1serA1e1eVal1yTyrCyVal1yVal1y 141
DB 1009 AAAGGCAAGATATCCAGTCACTTGAGGCTAAGTATTTGTTGTCCTTGAT 1068
QY 142 PheA1euh1rGluLeuA1ah1e1eA1aSerLysAparHisValPheProValA1a 161
DB 1069 TTTGAACAAGCACAGCTTAAAGATTTGATTCAGAGAGCAAGTTTCCCTGCAAA 1128
QY 162 AapGlyPheGluA1euh1e1e1e1e1e1e1e1e1e1e1e1e1e1e1e1e1e1e 181
DB 1129 GGTGATTCAGGCTCTTAAAGATTAATTTATTAATCTAATCTGATGATGATGAA 1188

RESULT 3
US-09-774-528-297
/ Sequence 297, Application US/09774528
/ Patent No. 6743619
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Zhou, Ping
/ APPLICANT: Goodrich, Ryle
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Xu, Aiding
/ APPLICANT: Ren, Feiyun
/ APPLICANT: Zhang, Jie
/ APPLICANT: Yang, Yonghong
/ APPLICANT: Wang, Jiao-Rui
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Wang, Jiao-Rui
/ APPLICANT: Dmanac, Radofe T.
/ TITLE OF INVENTION: No. 6743619e1 Nucleic Acids and
/ TITLE OF INVENTION: Polypeptides
```



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FILE REFERENCE: 802
CURRENT APPLICATION NUMBER: US/09/774.528
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: PL_FL_genes Version 2.0
SEQ ID NO 297
LENGTH: 1492
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (79)..(1434)
US-09-774-528-297

Alignment Scores:
Pred. No.: 1,75e-52 Length: 1492
Score: 478.00 Matches: 95
Percent Similarity: 77.71% Conservative: 34
Best Local Similarity: 57.23% Mismatches: 35
Query Match: 50.69% Indels: 2
Gaps: 1

US-09-970-076-2_COPY_42_222 (1-181) x US-09-774-528-297 (1-1492)

QY 16 HIEHSTRPANGIUIETRYTYRPhEVALGluGluLeuA1AH1bLYSPheH1ESerPro 35
Db 16 AATAACTGATGTAATTAATTATTCGTACAGCAACTTCGAGAGATTGTGAGCCCT 75
QY 36 GlnLeuArgMetSerPheH1EVALPheSerThrArgGlyThrThrLeuMetLYLeuThr 55
Db 76 GAATGAGATTATCTTCATGATGTTCTTCCTCAAGCAACTATTATTATTCCTCACTTA 135
QY 56 GlnAspArgGluGlnIleArgGlnGlyLeuGluGluLeuGlnLYsVALLeuProGlyGly 75
Db 136 GAGACAGAGGCAAAATCAAGAAAGCTTGAGAGATTAAACGTGTAGTCCAGTGA 195
QY 76 AspThrTYrMetH1EGLUGlyPheGluArgAlaSerGluGlnIleTYrTYrGluAsnArg 95
Db 196 GAGACATATATCCATGAAAGCACTAAGCTAGCAATGACAAATTT-----CAGAAAGCA 249
QY 96 GlnGlyTYrArgThrAlaSerVAL1Ile1AlaLeuThrAspGlyGluLeuH1EGLuAsp 115
Db 250 GAGAGCTTGAAACCTCCAGTATCATATATGCTTGACAGTGGCAAGTTGGACGCTGTG 309
QY 116 LeuPhePheTYrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAla1IleVALTYr 135
Db 310 GTGCCATCATATGCAAGAAAGAGGCAAGATATCCAGTCACTTGGGGCTAGCTTTAT 369
QY 136 CyEVALGlyVALyAspPheAsnGluThrGlnLeuAlaArg1Ile1AspSerLYsAsp 155
Db 370 TGTGTTGGGCTCTTGATTTTGAACAAGCAGCTTGAAAGATTTGCTGATTTCAAGAG 429
QY 156 H1EVALPheProVALAsnAspGlyPheGlnAlaLeuGlnGly1Ile1Eh1Ser1Ileu 175
Db 430 CAAGTTTCCCTGTCAAAGGTGATTTCAAGCTCTTAAGGAATTAATTATTTCTATCTA 489
QY 176 LyELySerCYs1IleGlu 181
Db 490 GCTCAGTCATGTACTGA 507

RESULT 4
US-10-120-988-297
Sequence 297, Application US/10120988
Patent No. 6919193
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Ren, Feiyun
APPLICANT: Wang, Dumin
APPLICANT: Demanc, Radoje T.
TITLE OF INVENTION: No. 6919193el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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FILE REFERENCE: 802CON
CURRENT APPLICATION NUMBER: US/10/120.988
CURRENT FILING DATE: 2002-04-11
PRIORITY APPLICATION NUMBER: 09/774,528
PRIORITY FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: PL_FL_genes Version 2.0
SEQ ID NO 297
LENGTH: 1492
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (79)..(1434)
US-10-120-988-297

Alignment Scores:
Pred. No.: 1,75e-52 Length: 1492
Score: 478.00 Matches: 95
Percent Similarity: 77.71% Conservative: 34
Best Local Similarity: 57.23% Mismatches: 35
Query Match: 50.69% Indels: 2
Gaps: 1

US-09-970-076-2_COPY_42_222 (1-181) x US-10-120-988-297 (1-1492)

QY 16 HIEHSTRPANGIUIETRYTYRPhEVALGluGluLeuA1AH1bLYSPheH1ESerPro 35
Db 16 AATAACTGATGTAATTAATTATTCGTACAGCAACTTCGAGAGATTGTGAGCCCT 75
QY 36 GlnLeuArgMetSerPheH1EVALPheSerThrArgGlyThrThrLeuMetLYLeuThr 55
Db 76 GAATGAGATTATCTTCATGATGTTCTTCCTCAAGCAACTATTATTATTCCTCACTTA 135
QY 56 GlnAspArgGluGlnIleArgGlnGlyLeuGluGluLeuGlnLYsVALLeuProGlyGly 75
Db 136 GAGACAGAGGCAAAATCAAGAAAGCTTGAGAGATTAAACGTGTAGTCCAGTGA 195
QY 76 AspThrTYrMetH1EGLUGlyPheGluArgAlaSerGluGlnIleTYrTYrGluAsnArg 95
Db 196 GAGACATATATCCATGAAAGCACTAAGCTAGCAATGACAAATTT-----CAGAAAGCA 249
QY 96 GlnGlyTYrArgThrAlaSerVAL1Ile1AlaLeuThrAspGlyGluLeuH1EGLuAsp 115
Db 250 GAGAGCTTGAAACCTCCAGTATCATATATGCTTGACAGTGGCAAGTTGGACGCTGTG 309
QY 116 LeuPhePheTYrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAla1IleVALTYr 135
Db 310 GTGCCATCATATGCAAGAAAGAGGCAAGATATCCAGTCACTTGGGGCTAGCTTTAT 369
QY 136 CyEVALGlyVALyAspPheAsnGluThrGlnLeuAlaArg1Ile1AspSerLYsAsp 155
Db 370 TGTGTTGGGCTCTTGATTTTGAACAAGCAGCTTGAAAGATTTGCTGATTTCAAGAG 429
QY 156 H1EVALPheProVALAsnAspGlyPheGlnAlaLeuGlnGly1Ile1Eh1Ser1Ileu 175
Db 430 CAAGTTTCCCTGTCAAAGGTGATTTCAAGCTCTTAAGGAATTAATTATTTCTATCTA 489
QY 176 LyELySerCYs1IleGlu 181
Db 490 GCTCAGTCATGTACTGA 507

RESULT 5
US-09-799-451-250
Sequence 250, Application US/09799451
Patent No. 6783969
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Aundt, Vinod
APPLICANT: Ren, Feiyun
APPLICANT: Zhang, Jie
```


Sequence 36, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3456
US-08-485-618-36
Alignment Scores:
Pred. No.: 6.12e-08 Length: 3528
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 15.01% Indels: 25
DB: 2 Gaps: 10
US-09-970-076-2_COPY_42_222 (1-181) x US-08-485-618-36 (1-3528)
Qy 3 AspleuYrPheileLeuApLySeRgLySeRvAl--LeuHlSHlStrPAsnglUle 21
Db 424 GACATTCGTTCCGATGATGCTTCGACGACATTAACCAAGGACTTGGCCCAATG 483
Qy 22 TyTrYrPheValGlugInLeuAlaHleYrPheileSeRProGInLeuAlYgMeSeRphe 41
Db 484 AAGGACTTTCGCAAGCTTTCGAGAGAGTTTCGAGACACACACCTTGTCTCCCTG 543
Qy 42 IlleValPheSeRThrArYgGlyThrThreUmeCtySeRThrgU-----56
Db 544 ATGCATTACTCGAATCTCTGAGACCCATTTACTCTTCACTGAATTCAAGACATCTCTG 603

Qy 57 AsPArgGlUGInIleArGInGlyLeuGlUGluLeuGInLySValLeuProGlyGlyAsP 76
Db 604 GACCTTCAGAGCCGTCGTCGATCCCATTCCTCCAGCTGCNA-----GGCCTG 648
Qy 77 ThrYrMetHlAsGInGlyPheGluArGAlSeRGlUGInIleYrYrGluAlaArGIn 96
Db 649 ACCTACACAGCCACAGCATCCGACAGTGAAGAGCTATTTCATACAGAGATGG 708
Qy 97 GLyYrArThrAla---SeRValIleleAlaLeuThrArPArGlyGluLeuHlSGluAsP 115
Db 709 TCCGTTAAAGTCGCAAGAGATCTCTCTGTACACAGATGGCAGAAATACAGAAC 768
Qy 116 LeuPhePheYrSeRglu-----ArgGluAlaArGSeRArGArPLeuGlyAlaIle 133
Db 769 CCCCTGAGATATAGATGATTCATTCGCGCAGACAAAGCT-----GGCATCAT 819
Qy 134 ValYrCySValGlyValYrAsP---PheAsnglu---ThrgInLeuAlArGile--- 150
Db 820 CGTATGCTATGTGGGGTGGAGATGCTTCAGAGGCCACTGCCGTGAAGAGCTGAAC 879
Qy 151 -----AlaAsPSeRlyAsPHeISeRlyAlPheProValaAsPglyPheGlnAla 166
Db 880 ACATTCGCTCAGCTCCGCCACAGACACAGTGTTCAGGTAGGCAC---TTTGACACA 936
Qy 167 LeuGInGlyIleIleHlSeRleLeuLyS 177
Db 937 CTTCGACATCCAGAGCAACTTCAGAGAA 969
RESULT 8
US-08-362-652-36
Sequence 36, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

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/ TOPOLOGY: linear
/ MOLECULE TYPE: CDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..3456
US-08-362-652-36

Alignment Scores:
Pred. No.: 6,12e-08 Length: 3528
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 15.01% Indels: 25
DB: Gaps: 10

US-09-970-076-2_COPY_42_222 (1-181) x US-08-362-652-36 (1-3528)
QY 3 AarLeuTyrrPheIleuAarLySerGlySerVal---LeuNHistTrpAengluile 21
DB 424 GACATTGCTTCTCTGATGATGCTTGGCAGCATTAACCAAGGACCTTGGCCCGAGATG 483
QY 22 TyrrTyrrPheValGluInleuAanIshLySerPheIleSerProGluInleuAargMetSerPhe 41
DB 484 AAGGACTTTGTCAAGCTTTGATGGAGAGTTTGGCAGACCAAGCAACCTTTGTTCTCCCTG 543
QY 42 ILeuAlpheSerThrArgGlyThrThyLeuMetLyLeuThrglu----- 56
DB 544 ATGCAATATCTCAACATCTCTGAAGACCTTTTAACTTCACTGAAATTAAGAAATCTCTG 603
QY 57 AarAargGluGlnIleAargGlnIleuGluGluLeuGlnValLeuProGluGlyAar 76
DB 604 GACCTTCAGAGCTGTGGATCCCATTTGCCATTTGCCAGCTGCA-----GGCCTG 648
QY 77 ThrTyrrMetIshGluGlyPheGluAargAlaSerGluGlnIleTyrrTyrrGluAenAargGln 96
DB 649 ACCTACACAGCCACAGGACCTCCGAGACGATGAAAGATATTGATATGCAAGAAATGGG 708
QY 97 GlyTyrrArgThrAla---SerValIleIleAlaLeuThrAarGlyGluInleuNHistGluAar 115
DB 709 TCCCGTAAAGTCCCAAGAAATCTCTGTCATCAAGATGGGCAAAATACAGAGAC 768
QY 116 LeuPhePheTyrrSerGlu-----AargGluAlaAarAargSerAargAarGluAlaIle 133
DB 769 CCGCTGAGATATGATGATGATCTCCCGCGCAGACAAAGCT-----GGCATCATT 819
QY 134 ValTyrrCysValGlyValLyAar---PheAenglu---ThrnIleuAlaAargIle--- 150
DB 820 CGTTATGCTATTTGGGTGGAGATGCTTCCAGAGACCCCACTGCTTGAAGAGCTGAAC 879
QY 151 -----AlaAarSerLyAarPheIshValPheProValAanAarGlyPheGlnAla 166
DB 880 ACCATTGGCTCAAGTCCCCCAAGACGACGATGTTCAAGGTATGAGCAAC---TTTGCAGCA 936
QY 167 LeuGlnGlyIleIleIshSerIleLeuLyAar 177
DB 937 CTTGCGAGATCCAGAGCAATTCAGAGAAA 969

RESULT 9
US-08-605-672-36
/ Sequence 36, Application US/08605672
/ Patent No. 5817515
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vlieten, Monica
/ TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerslein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402

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/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/605,672
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 36:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3528 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..3456
US-08-605-672-36

Alignment Scores:
Pred. No.: 6,12e-08 Length: 3528
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 15.01% Indels: 25
DB: Gaps: 10

US-09-970-076-2_COPY_42_222 (1-181) x US-08-605-672-36 (1-3528)
QY 3 AarLeuTyrrPheIleuAarLySerGlySerVal---LeuNHistTrpAengluile 21
DB 424 GACATTGCTTCTCTGATGATGCTTGGCAGCATTAACCAAGGACCTTGGCCCGAGATG 483
QY 22 TyrrTyrrPheValGluInleuAanIshLySerPheIleSerProGluInleuAargMetSerPhe 41
DB 484 AAGGACTTTGTCAAGCTTTGATGGAGAGTTTGGCAGACCAAGCAACCTTTGTTCTCCCTG 543
QY 42 ILeuAlpheSerThrArgGlyThrThyLeuMetLyLeuThrglu----- 56
DB 544 ATGCAATATCTCAACATCTCTGAAGACCTTTTAACTTCACTGAAATTAAGAAATCTCTG 603
QY 57 AarAargGluGlnIleAargGlnIleuGluGluLeuGlnValLeuProGluGlyAar 76
DB 604 GACCTTCAGAGCTGTGGATCCCATTTGCCATTTGCCAGCTGCA-----GGCCTG 648
QY 77 ThrTyrrMetIshGluGlyPheGluAargAlaSerGluGlnIleTyrrTyrrGluAenAargGln 96
DB 649 ACCTACACAGCCACAGGACCTCCGAGACGATGAAAGATATTGATATGCAAGAAATGGG 708
QY 97 GlyTyrrArgThrAla---SerValIleIleAlaLeuThrAarGlyGluInleuNHistGluAar 115
DB 709 TCCCGTAAAGTCCCAAGAAATCTCTGTCATCAAGATGGGCAAAATACAGAGAC 768
QY 116 LeuPhePheTyrrSerGlu-----AargGluAlaAarAargSerAargAarGluAlaIle 133

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DB 769 CCCCTGGAGTATAGTATGTCATTCCTCCCGCCGACGACAAAGCT-----GGCATTCATT 819
QY 134 ValTYrCyValGlyValIyAsp---Pheanglu---ThrgInLeuAlaArgIle--- 150
DB 820 CGTATGCTATTGGGTGGGAGATGCTTCCAGAGCCACCTGCTGAAGAGCTGAAC 879
QY 151 -----AlaAspSerIyAspHisValPheProValAsnAspGlyPheGlnAla 166
DB 880 ACCATTGGCTGAGCTCCCGCCACAGACACCGTGTCAAGTGAACAAC---TTTCAGACA 936
QY 167 LeuGlnGlyIleIleHisSerIleLeuIyAsp 177
DB 937 CTTCGACAGATCCAGAGCACTTCAGAGAGAA 969
RESULT 10
US-08-482-293A-36
Sequence 36, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDBESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3456
US-08-482-293A-36
Alignment Scores:
Pred. No.: 6,12e-08 Length: 3528
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38

Best Local Similarity: 27.75% Mismatch: 75
Query Match: 15.01% Indels: 25
DB: 2 Gaps: 10
US-09-970-076-2_copy_42_222 (1-181) x US-08-482-293A-36 (1-3528)
QY 3 AspleuTYrPheIleLeuAspIySergIySerVal---LeuHisIeTrpAsnGluIle 21
DB 424 GACATGGCTTTCCTGATGATGATGTTCTGGGACATTAACCAAGGACCTTGGCCAGATG 483
QY 22 TyrTYrPheValGlnIleuAlaHisIeAspPheIleSergProGlnLeuAspSerPhe 41
DB 484 AAGACCTTGTCAAGACCTTATGAGAGAGTTGGACACAGACCTTGTCTTCCTGG 543
QY 42 IleValPheSerThrArgIyThrTYrLeuSerIyLeuThrGlu----- 56
DB 544 ATGCAATACCTGAACATCTCGAAGCCCATTTACCTTCATGATTCAGAACATCTCG 603
QY 57 AspArgGlnIleArgIyLeuGlnIleuGlnIyValLeuProGlyGlyAsp 76
DB 604 GACCTTCAGAGCCTGGTGATCCATTGTCCAGCTGCAA-----GGCCTG 648
QY 77 ThrTYrMetHisGlnIyPheGluArgAlaSerGlnIleTYrTYrGluAsnArgGln 96
DB 649 ACCTACAGCCACAGGATCCGACAGTGAAGAGCTATTTCATAGCAAGATGG 708
QY 97 GlyTYrArgThrAla---SerValIleIleAlaLeuThrAspGlyGlnIleuHisGluAsp 115
DB 709 TCCGTAAGATGCGAAGAGATCTCTGTCATCACAGATGGCAGAAATACAGAC 768
QY 116 LeuPhePheTYrSergIu---ArgGluAlaAsnArgSerArgAspLeuGlyAlaIle 133
DB 769 CCCCTGGAGTATAGTATGTCATTCCTCCCGCCGACGACAAAGCT-----GGCATTCATT 819
QY 134 ValTYrCyValGlyValIyAsp---Pheanglu---ThrgInLeuAlaArgIle--- 150
DB 820 CGTATGCTATTGGGTGGGAGATGCTTCCAGAGCCACCTGCTGAAGAGCTGAAC 879
QY 151 -----AlaAspSerIyAspHisValPheProValAsnAspGlyPheGlnAla 166
DB 880 ACCATTGGCTGAGCTCCCGCCACAGACACCGTGTTCAGAGTGAACAAC---TTTCAGACA 936
QY 167 LeuGlnGlyIleIleHisSerIleLeuIyAsp 177
DB 937 CTTCGACAGATCCAGAGCACTTCAGAGAGAA 969
RESULT 11
US-08-943-363-36
Sequence 36, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497

[illegible]

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US-09-970-076-2_COPY_42_222 (1-181) x US-09-668-307A-36 (1-3528)
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Db 424 GACATGGCTTTCCTCATATGATGGTTCTGGCACACATTAACCAAGGACCTTGGCCAGAT 483
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QY 22 TYTYrPheValGIuGlnIleuA1h1slyvPheIISeSPrGlnIleuTYrMetSerPhe 41
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Db 484 AAGGACTTTGTCAAAAGCTTTGATGGAGAGTTTGGACGACCAAGCACCTTTGTTCTCCCTG 543
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QY 42 I1eValPheSerThrArgGIyThrThrIleuMetLyLeuThrGIu----- 56
    :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 544 ATGCAAATACTGCAGACATCTCGAAGACCCATTTTAACTCTCACTGAATTCAAAGACATCTCTG 603
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QY 57 AsPArGdGIuGlnI1eArGIuGlnIyLeuGIuGlnIyLeuGlnIyValLeuProGIyGIyAsP 76
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Db 604 GACCTCTCAGAGCTGTGGATCCCATCTGTCCAGCTGCAC-----GGCCTG 648
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QY 77 ThTYrMetH1eGIuGIyPheGIuArGIaSeSrgIuGlnI1eTYrTYrGIuAenArGIu 96
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QY 97 GIuTYrArGIhAla---SeValI1eIeAlaLeuThrAsPGIyGIuIleuH1eGIuAsP 115
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Db 709 TCCCGTAAAGTCCAGAGAAATCTCTCTTCATCAACAGATGGGAGAAATGCAGAGAC 768
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QY 116 LeuPhePheTYrSerGIu-----ArgGIuIaAenArGISeArGIaSerGIyAlaI1e 133
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 769 CCCCTGAGTATAGTATGATGTATCTCCCGCCGACAAAGCT-----GGCATCATT 819
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 134 ValTYrCyvValGIyValIyAsP---PheAenGIu---ThrGIuIleuA1ArGI1e--- 150
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Db 820 CGTATAGCTATTTGGGTGGAGATCCCTTCCAGAGCCCACTGCCCTGAAGAGCTGAAC 879
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 151 -----AlaAsPSeTyAsPArh1eValPheProValAsnAsPGIyPheGIuAla 166
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Db 880 ACCATGGCTCAGGCTCCCGCCACAGGACCAACGCTGTCAAGTATGAGCAAC---TTTGACAGCA 936
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 167 LeuGlnGIyI1eI1eH1eSerI1eIleuLyIyS 177
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Db 937 CTTCGACGATCCAGAGCAACTTCAGAGAA 969
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RESULT 14
US-09-350-259-36
? Sequence 36, Application US/09350259
? Patient No. 6620915
? GENERAL INFORMATION:
? APPLICANT: Gallatin, Michael W.
? APPLICANT: Van der Vlieten, Monica
? TITLE OF INVENTION: No. 6620915el Human 2
? FILE REFERENCE: 27866/35004
? CURRENT APPLICATION NUMBER: US/09/350,259
? EARLIER FILING DATE: 1999-07-08
? EARLIER APPLICATION NUMBER: 09/193,043
? EARLIER FILING DATE: 1998-11-16
? EARLIER APPLICATION NUMBER: 08/173,497
? EARLIER FILING DATE: 1993-12-23
? EARLIER APPLICATION NUMBER: 08/286,889
? EARLIER FILING DATE: 1994-08-05
? EARLIER APPLICATION NUMBER: 08/162,652
? EARLIER FILING DATE: 1994-12-21
? EARLIER APPLICATION NUMBER: 08/743,363
? EARLIER FILING DATE: 1997-10-03
? NUMBER OF SEQ ID NOS: 114
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 36
? LENGTH: 3528
? TYPE: DNA
? ORGANISM: Rattus rattus
? FEATURES:
? NAME/KEY: CDS
? LOCATION: (1)..(3453)

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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-350-259-36

Alignment Scores:
Pred. No.: 6.12e-08 Length: 3528
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 15.01% Indels: 25
Gaps: 10

US-09-970-076-2_COPY_42_222 (1-181) x US-09-350-259-36 (1-3528)

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QY 3 AepLeuTYrPheHleLeuAryLysSerGlySerVal---LeuNHleTTPaengluile 21
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Db 424 GACATTCCTTCTGATTCATGATGATTCCTGACAGCATTAACCAAGGACTTTCCTCCAGATG 483
QY 22 TYrTYrPheValGluGlnLeuAlaNHlyuPheHleSerProGlnLeuAryMetSerPhe 41
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 484 AAGGACTTTCCTCAAGCTTGTGAGAGAGTTGGAGACACAGACACCTGTTCTCCCTG 543
QY 42 lIeValPheSerThraArgLyThrThreuMetLyLeuThrglu----- 56
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 544 ATGCAATACCTGACATCCTGAAGACCCATTTCACCTTCATGAAATTCAGAACATCCTG 603
QY 57 AepAryGluGlnlIeAryGlnlYleuGlnlYleuGlnlYleuValLeuProGlyLysA 76
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 604 GACCTCGAGAGCTGTGATGATCCCATGCTGACAGTGCAGTGCAG-----GACCTG 648
QY 77 ThTYrMetNHleGluGlyPheGluAryGalaSerGluGlnlIeTYrTYrGluAryA 96
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 649 ACCTACACAGCCACAGGACCTCGGACAGATGAGAGAGCTATTCAGAACAGATGG 708
QY 97 GlyTYrAryThraA---SerValIleleAlaLeuThraArgGlyGluLeuNHleGluA 115
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 709 TCCCGTAAAGTCCAGAGAGATGCTCTGTCATCAGATGAGGAGAAATACAGAGAC 768
QY 116 LeuPhePheTYrSerGlu-----ArgGluAlaAryArySerAryAryLeuGlyAlaIle 133
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 769 CCCCTGAGATATGATGATCATTCCTCCCGCCGACAGAAAGCT-----GACATCAT 819
QY 134 ValTYrCyValGlyValLysAryPheAenglu---ThrglnLeuAlaAryGle--- 150
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 820 CCTATGCTATGCGGTGGAGATGCTTCACAGAGCCACAGCTGTAAGAGAGCTGAC 879
QY 151 -----AlaArySerLysAryAryNHlePheProValAryAryGlyPheGlnAla 166
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 880 ACCATTGCTCAGCTCCCGCCACAGACACGCTGTCAGAGTAGGACAACT---TTTGCAGCA 936
QY 167 LeuGlnGlylIleleHleSerlIeLeuLys 177
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 937 CTTCGAGCATCCAGAGCAATTCAGAGAGAAA 969
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RESULT 15
US-08-485-618-54
Sequence 54, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vliet, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Bear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 3597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 40..3525
US-08-485-618-54

Alignment Scores:
Pred. No.: 6.29e-08 Length: 3597
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 15.01% Indels: 25
Gaps: 10

US-09-970-076-2_COPY_42_222 (1-181) x US-08-485-618-54 (1-3597)

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QY 3 AepLeuTYrPheHleLeuAryLysSerGlySerVal---LeuNHleTTPaengluile 21
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Db 493 GACATTCCTTCTGATTCATGATGATTCCTGACAGCATTAACCAAGGACTTTCCTCCAGATG 552
QY 22 TYrTYrPheValGluGlnLeuAlaNHlyuPheHleSerProGlnLeuAryMetSerPhe 41
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 553 AAGGACTTTCCTCAAGCTTGTGAGAGAGTTGGAGACACAGACACCTGTTCTCCCTG 612
QY 42 lIeValPheSerThraArgLyThrThreuMetLyLeuThrglu----- 56
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 613 ATGCAATACCTGACATCCTGAAGACCCATTTCACCTTCATGAAATTCAGAACATCCTG 672
QY 57 AepAryGluGlnlIeAryGlnlYleuGlnlYleuGlnlYleuValLeuProGlyLysA 76
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 673 GACCTCGAGAGCTGTGATGATCCCATGCTGACAGTGCAGTGCAG-----GACCTG 717
QY 77 ThTYrMetNHleGluGlyPheGluAryGalaSerGluGlnlIeTYrTYrGluAryA 96
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 718 ACCTACACAGCCACAGGACCTCGGACAGATGAGAGAGCTATTCATGAGAACATGG 777
QY 97 GlyTYrAryThraA---SerValIleleAlaLeuThraArgGlyGluLeuNHleGluA 115
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 778 TCCCGTAAAGTCCAGAGAGATGCTCTGTCATCAGATGAGGAGAAATACAGAGAC 837
QY 116 LeuPhePheTYrSerGlu-----ArgGluAlaAryArySerAryAryLeuGlyAlaIle 133
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 838 CCCCTGAGATATGATGATCATTCCTCCCGCCGACAGAAAGCT-----GACATCAT 888
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QY 134 ValTyrGlyValIleAsp---Pheanglu---ThrGlnLeuAlaArgIle--- 150
Db CGTTATGCTATTGGGAGATGCTTTCCAGAGGCCACTGCGCTTGAAGAGCTGAAC 948
QY 151 -----AlaAspSerIleAspHisValPheProValAsnAspGlyPheGlnAla 166
Db ACCATTGGCTAGCTCCCCACAGGACCAACGGTTCACAGTAGGCAAC--TTTGCAACA 1005
QY 167 LeuGlnGlyIleIleHisSerIleLeuValys 177
Db CTTCCAGCATTCAGAGGCAACTTGAAGAGAAA 1038

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Search completed: December 18, 2005, 07:34:55
Job time : 139.075 sec

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:01:37 ; Search time 131.287 Seconds
(without alignments)
2531.884 Million cell updates/sec

Title: US-09-970-076-2_COPY_41_227

Perfect score: 970
Sequence: 1 GGFDFLYFLDKSGSVLHMN.....LOGIHSILKSCIEFLAAE 187

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_NA -QPM=fastap -SUFFIX=nni -WINMATCH=0.1 -LOOFL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09970076 @CGN 1.1 535 @runat 14122005 11850 20999 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEOUTERY -NEG_SCORE=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*

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- 2: /cg2_6/prodata/1/ina/5.COMB.seq:*
- 3: /cg2_6/prodata/1/ina/6.COMB.seq:*
- 4: /cg2_6/prodata/1/ina/6.COMB.seq:*
- 5: /cg2_6/prodata/1/ina/6.COMB.seq:*
- 6: /cg2_6/prodata/1/ina/6.COMB.seq:*
- 7: /cg2_6/prodata/1/ina/6.COMB.seq:*
- 8: /cg2_6/prodata/1/ina/6.COMB.seq:*
- 9: /cg2_6/prodata/1/ina/6.COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	970	100.0	3	US-09-620-312D-8 Sequence 8, Appl
2	550	56.7	2234	US-10-104-047-669 Sequence 699, App
3	486	50.1	1492	US-09-774-528-297 Sequence 297, App
4	486	50.1	1492	US-10-120-988-297 Sequence 297, App
5	179	18.5	3981	US-09-799-451-250 Sequence 250, App
6	141.5	14.6	3528	US-08-286-889-36 Sequence 36, Appl
7	141.5	14.6	3528	US-08-485-618-36 Sequence 36, Appl
8	141.5	14.6	3528	US-08-362-652-36 Sequence 36, Appl
9	141.5	14.6	3528	US-08-605-672-36 Sequence 36, Appl

10	141.5	14.6	3528	US-08-482-293A-36 Sequence 36, Appl
11	141.5	14.6	3528	US-08-943-363-36 Sequence 36, Appl
12	141.5	14.6	3528	US-09-193-043-36 Sequence 36, Appl
13	141.5	14.6	3528	US-09-688-307A-36 Sequence 36, Appl
14	141.5	14.6	3528	US-09-350-259-36 Sequence 36, Appl
15	141.5	14.6	3528	US-08-485-618-54 Sequence 54, Appl
16	141.5	14.6	3528	US-08-362-652-54 Sequence 54, Appl
17	141.5	14.6	3528	US-08-605-672-54 Sequence 54, Appl
18	141.5	14.6	3528	US-08-482-293A-54 Sequence 54, Appl
19	141.5	14.6	3528	US-08-943-363-54 Sequence 54, Appl
20	141.5	14.6	3528	US-09-193-043-54 Sequence 54, Appl
21	141.5	14.6	3528	US-09-688-307A-54 Sequence 54, Appl
22	141.5	14.6	3528	US-09-350-259-54 Sequence 54, Appl
23	138.5	14.3	3519	US-08-286-889-45 Sequence 45, Appl
24	138.5	14.3	3519	US-08-485-618-45 Sequence 45, Appl
25	138.5	14.3	3519	US-08-362-652-45 Sequence 45, Appl
26	138.5	14.3	3519	US-08-605-672-45 Sequence 45, Appl
27	138.5	14.3	3519	US-08-482-293A-45 Sequence 45, Appl
28	138.5	14.3	3519	US-08-943-363-45 Sequence 45, Appl
29	138.5	14.3	3519	US-09-193-043-45 Sequence 45, Appl
30	138.5	14.3	3519	US-09-688-307A-45 Sequence 45, Appl
31	138.5	14.3	3519	US-09-350-259-45 Sequence 45, Appl
32	138.5	14.3	3803	US-08-485-618-52 Sequence 52, Appl
33	138.5	14.3	3803	US-08-362-652-52 Sequence 52, Appl
34	138.5	14.3	3803	US-08-605-672-52 Sequence 52, Appl
35	138.5	14.3	3803	US-08-482-293A-52 Sequence 52, Appl
36	138.5	14.3	3803	US-08-943-363-52 Sequence 52, Appl
37	138.5	14.3	3803	US-09-193-043-52 Sequence 52, Appl
38	138.5	14.3	3803	US-09-688-307A-52 Sequence 52, Appl
39	138.5	14.3	3803	US-09-350-259-52 Sequence 52, Appl
40	132.5	13.7	3533	US-08-476-062A-40 Sequence 40, Appl
41	132.5	13.7	3533	PCT-US96-01314-40 Sequence 40, Appl
42	132.5	13.7	3533	Patent No. 5424399-1 Sequence 40, Appl
43	132.5	13.7	3595	US-09-023-655-1147 Sequence 1147, Ap
44	132.5	13.7	4045	US-09-809-517A-37 Sequence 37, Appl
45	132.5	13.7	4124	US-09-023-655-1178 Sequence 1178, Ap

ALIGNMENTS

RESULT 1
US-09-620-312D-8
Sequence 8, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyun
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Tonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_fl_genes Version 1.0

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/ SEQ ID NO 8
/ LENGTH: 1609
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (309)..(1202)
US-09-620-312D-8

Alignment Scores:
Pred. No.: 6,46e-116 Length: 1609
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-2_COPY_41_227 (1-187) x US-09-620-312D-8 (1-1609)

QY 1 G1YGIYpheaapleuTYrPheileuaplysSerGlySerValleuHishITrpaSn 20
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DB 429 GGGGATTGACCTGTACTTCTTGGACAAATCAGGAAGTGTGTCACACTGGAAT 488
QY 21 GluIleTYrTYrPheValGluGlnLeuAlahIshYpHeileSerProGlnLeuXMet 40
   |||||
DB 489 GAATCTAATTAATTGTGGAACTGTGCTCAAAATTCATCAGCCCACTGAAGATG 548
QY 41 SerPheileValPheSerThraGlyThrThreMetLysLeuThrGluAAspArgGlu 60
   |||||
DB 549 TCCATTATTTGTTTCTCCACCCGAGAACAACTTATGAACTGACAGAAAGACAGAA 608
QY 61 GlnIleArgGlnGlyLeuGlnLeuGlnLysValleuProGlyGlyAspThrTYrMet 80
   |||||
DB 609 CAATTCGTCAGGCGCTGAGAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 668
QY 81 HisGluGlyPheGluArgAlaSerGlnIleTYrTYrGluAAspArgGlnGlyTYrArg 100
   |||||
DB 669 CATAGAGATTGTGAAGGCGCAGAGAGCAAGATTATTTGAAACAGACAGGGTACAGG 728
QY 101 ThrIleSerValIleIleAlaLeuThraSpGlyLeuHishGluAAspLeuPhePheTYr 120
   |||||
DB 729 ACACGACGCTCATCATTTGCTTGACTATGAGAACTCCATGAAGATCTCTTTTTCAT 788
QY 121 SerGluArgGluAlaAspArgSerArgAspLeuGlyAlaIleValTYrCysValGlyVal 140
   |||||
DB 789 TCAGAGAGGAGGCTAATAGGTCTCGAGATCTTGTCATTTAATGTTTGTGTGTG 848
QY 141 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
   |||||
DB 849 AAAGATTTCATGAGACACAGCTGCGCGAATGCGGACAGTAAAGATCATGTGTTCC 908
QY 161 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 180
   |||||
DB 909 GTGAATGACGGCTTTCAGGCTCTGAAAGCATCACTCAATTTTAAAGAGTCTGTC 968
QY 181 IleguileuAlaIleGlu 187
   |||||
DB 969 ATCGAAATTCAGAGCTGAA 989

RESULT 2
US-10-104-047-669
; Sequence 669, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. 6943241el Full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
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/ SEQ ID NO 669
/ LENGTH: 2234
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-104-047-669

Alignment Scores:
Pred. No.: 3,64e-61 Length: 2234
Score: 550.00 Matches: 109
Percent Similarity: 79.12% Conservative: 35
Best Local Similarity: 59.89% Mismatches: 36
Query Match: 56.70% Indels: 2
DB: 3 Gaps: 1

US-09-970-076-2_COPY_41_227 (1-187) x US-10-104-047-669 (1-2234)

QY 3 PheaapleuTYrPheileuaplysSerGlySerValleuHishITrpaSnGluIle 22
   |||||
DB 655 TTGGATCTACTTCCTGCTGACCAAGTCTGGAGTGTGGCAATTAATCTGATTGAAT 714
QY 23 TYrTYrPheValGluGlnLeuAlahIshYpHeileSerProGlnLeuXMetSerPhe 42
   |||||
DB 715 TATTAATTCGTAACCACTTGGAGAGATTGTGAGCCCTGAAGTGAATTAATCTTTC 774
QY 43 IleValPheSerThraGlyThrThreMetLysLeuThrGluAAspArgGluGlnIle 62
   |||||
DB 775 ATGTGTTTCTTCTCAAGCACTTATTTTGCATTAATCTGAGACAGAGCAAAATC 834
QY 63 ArgGlnGlyLeuGlnGlnLeuGlnLysValleuProGlyGlyAspThrTYrMetHisGlu 82
   |||||
DB 835 AGTAAGGCTTGGAGGATTTAAACGTGTAGTCCAGTAAAGAGACATATATCCATGAA 894
QY 83 GlyPheGluArgAlaSerGlnIleTYrTYrGluAAspArgGlnGlyTYrArgThraIle 102
   |||||
DB 895 GAACTAAAGCTAGGAATGAACAAATTC-----CAGAAAGAGAGAGCTTAAACCTCC 948
QY 103 SerValIleIleAlaLeuThraSpGlyLeuHishGluAAspLeuPhePheTYrSerGlu 122
   |||||
DB 949 AGTATCAATTAATGCTTCAAGATGCAAGTGTGAACGCTCTGTGCTCATATGCAAG 1008
QY 123 ArgGluAlaAspArgSerArgAspLeuGlyAlaIleValTYrCysValGlyValAsp 142
   |||||
DB 1009 AAAGAGCAAAAGATCAAGCTCACTTGGGCTAGTGTATTTGTTGTTGTTGCTTGTAT 1068
QY 143 PheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPheProValAsn 162
   |||||
DB 1069 TTTGAACAGCACAGCTTGAAGAAATGCTGATTCAGAGGACAAAGTTTCCCTGTCAA 1128
QY 163 AspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCysIlegu 182
   |||||
DB 1129 GGTGAATTTTCAGGCTTTAAGAAATTAATTAATTAATTAATTAATTAATTAATTA 1188
QY 183 IleLeu 184
   |||||
DB 1189 ATCTTA 1194

RESULT 3
US-09-774-528-297
; Sequence 297, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Peiyuan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehtman, Tom
; APPLICANT: Wang, Jian-Rui
```

```
/ APPLICANT: Wang, Dunrui
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: No. 6743619e1 Nucleic Acids and
/ TITLE OF INVENTION: Polypeptides
/ FILE REFERENCE: 802
/ CURRENT APPLICATION NUMBER: US/09/774,528
/ CURRENT FILING DATE: 2001-01-30
/ NUMBER OF SEQ ID NOS: 441
/ SOFTWARE: pc_fl_genes Version 2.0
/ SEQ ID NO 297
/ LENGTH: 1492
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (79) .. (1434)
US-09-774-528-297

Alignment Scores:
Pred. No.: 4,16e-53 Length: 1492
Score: 486.00 Matches: 97
Percent Similarity: 77.98% Conservative: 34
Best Local Similarity: 57.74% Mismatches: 35
Query Match: 50.10% Indels: 2
DB: 3 Gaps: 1

US-09-970-076-2_copy_41_227 (1-187) x US-09-774-528-297 (1-1492)

QY 17 HishstTPaengluileTyTyrrPheValGluGlnLeuAlaHslyPheHleSerPro 36
D 16 AATAACGATGATGAATTAATTATTAATTCGTACAGCAACTGGGAGAGATTGTGTAGCCCT 75
QY 37 GlnleuArmetSerPheHleValPheSerThrArgGlyThrThLeuMetLeuLeuThr 56
D 76 GAATGAGATTAATCTTCAATGTGTCTCTCAAGCACTATTAATTTGGCATTACT 135
QY 57 GluAPArGluGlnIleArgGlnIleuGlnIleuGlnIleuValLeuProGly 76
D 136 GAGACAGAGCCAAATCAGTAAGGCTTGAGATTAAACGTGTAGTCCAGTAGA 195
QY 77 AspThrTyrrMetHsleGlnIlePheGlnArgAlaSerGlnIleTyTyrrGluAsnArg 96
D 196 GAGCATATATCCATGAAGGACTAAAGCTAGCAATGAACAAATT-----CAGAAAGCA 249
QY 97 GlnGlyTyrrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHsleGluAsp 116
D 250 GGAAGCTTGAAACCTCCAGATATCAATATGCTGTGACAGATGCGAAGTTGACGCTG 309
QY 117 LeuPhePheTyrrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrr 136
D 310 GTGCCATCATATGACGAGAAAGGCAAAAGATATCCAGTCACTGGGGCTAGTGTAT 369
QY 137 CysValGlyValIleAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerIleAsp 156
D 370 TGTGTGGGGCTCTGATTTGAAACACACAGCTTGAAGAATGTGATTCCAAGAG 429
QY 157 HisValPheProValaAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHsSerIleLeu 176
D 430 CAAATTTTCCCTGCAAAAGGTGATTTTCAAGCTCTTAAAGAAATTAATTTCTATCTA 489
QY 177 LysLeuSerCysIleGlnIleLeu 184
D 490 GCTCAGTCATGACTGAATCTTA 513

RESULT 4
US-10-120-988-297
/ Sequence 297, Application US/10120988
/ Patent No. 6919193
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Goodrich, Ryle
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Ren, Feiyan
```

```
/ APPLICANT: Wang, Dunrui
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: No. 6919193e1 Nucleic Acids and
/ TITLE OF INVENTION: Polypeptides
/ FILE REFERENCE: 802CON
/ CURRENT APPLICATION NUMBER: US/10/120,988
/ CURRENT FILING DATE: 2002-04-11
/ PRIOR APPLICATION NUMBER: 09/774,528
/ PRIOR FILING DATE: 2001-01-30
/ NUMBER OF SEQ ID NOS: 441
/ SOFTWARE: pc_fl_genes Version 2.0
/ SEQ ID NO 297
/ LENGTH: 1492
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (79) .. (1434)
US-10-120-988-297

Alignment Scores:
Pred. No.: 4,16e-53 Length: 1492
Score: 486.00 Matches: 97
Percent Similarity: 77.98% Conservative: 34
Best Local Similarity: 57.74% Mismatches: 35
Query Match: 50.10% Indels: 2
DB: 3 Gaps: 1

US-09-970-076-2_copy_41_227 (1-187) x US-10-120-988-297 (1-1492)

QY 17 HishstTPaengluileTyTyrrPheValGluGlnLeuAlaHslyPheHleSerPro 36
D 16 AATAACGATGATGAATTAATTATTAATTCGTACAGCAACTGGGAGAGATTGTGTAGCCCT 75
QY 37 GlnleuArmetSerPheHleValPheSerThrArgGlyThrThLeuMetLeuLeuThr 56
D 76 GAATGAGATTAATCTTCAATGTGTCTCTCAAGCACTATTAATTTGGCATTACT 135
QY 57 GluAPArGluGlnIleArgGlnIleuGlnIleuGlnIleuValLeuProGly 76
D 136 GAGACAGAGCCAAATCAGTAAGGCTTGAGATTAAACGTGTAGTCCAGTAGA 195
QY 77 AspThrTyrrMetHsleGlnIlePheGlnArgAlaSerGlnIleTyTyrrGluAsnArg 96
D 196 GAGCATATATCCATGAAGGACTAAAGCTAGCAATGAACAAATT-----CAGAAAGCA 249
QY 97 GlnGlyTyrrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHsleGluAsp 116
D 250 GGAAGCTTGAAACCTCCAGATATCAATATGCTGTGACAGATGCGAAGTTGACGCTG 309
QY 117 LeuPhePheTyrrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrr 136
D 310 GTGCCATCATATGACGAGAAAGGCAAAAGATATCCAGTCACTGGGGCTAGTGTAT 369
QY 137 CysValGlyValIleAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerIleAsp 156
D 370 TGTGTGGGGCTCTGATTTGAAACACACAGCTTGAAGAATGTGATTCCAAGAG 429
QY 157 HisValPheProValaAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHsSerIleLeu 176
D 430 CAAATTTTCCCTGCAAAAGGTGATTTTCAAGCTCTTAAAGAAATTAATTTCTATCTA 489
QY 177 LysLeuSerCysIleGlnIleLeu 184
D 490 GCTCAGTCATGACTGAATCTTA 513

RESULT 5
US-09-799-451-250
/ Sequence 250, Application US/09799451
/ Patent No. 6783969
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Zhou, Ping
```


Db 937 CTTGCGAGCATCCAGAGGCACTTCAGAGAAA 969

RESULT 7

US-08-485-618-36

Sequence 36 Application US/08485618

Patient No. 5728533

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Van der Vieren, Monica

TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum

STREET: 233 South Wacker Drive, 6300 Sear Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,618

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/32797

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 3528 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..3456

US-08-485-618-36

Alignment Scores:

Pred. No.:	7.93e-08	Length:	3528
Score:	141.50	Matches:	53
Percent Similarity:	47.64%	Conservative:	38
Best Local Similarity:	27.75%	Mismatches:	75
Query Match:	14.59%	Indels:	25
DB:	2	Gaps:	10

US-09-970-076-2_COPY_41_227 (1-187) x US-08-485-618-36 (1-3528)

Qy 4 AspleuTyRheleuaplysergylserVal--LeuHieHieTtpaenglulie 22

Db 424 GACATTGCTTCTGATGATGCTTGCAGACATTAACCAAGGACTTGCACAGATG 483

Qy 23 TyTyTyRheValGluGluLeuAlaHblyRhelelesterProGluLeuAlaRgmetserPhe 42

Db 484 AAGACATTGTCAAGCTTGTATGGAGATTGGCGAGACACAGACCTGTGTCTCCCTG 543

Qy 43 IleValPheSerThrArgGlyThrThreuletylsleuThrglu----- 57

Db 544 ATGCATATCTGCAGATCATCTGTAAGACCCATTTCCTTACCTGATTCAGAAATCTCTG 603

Qy 58 AsparGluGlnIleArgGlnGlyLeuGluGluGlnIleValLeuProGluGlyAsp 77

Db 604 GACCTTGAGAGCTGTGTGATCCATGTCTGACGCTGCA-----GCCCTG 648

Qy 78 ThrTyMetHieGluGlyPheGluArgAlaSerGluGlnIleTyTyRgluAsnArgGln 97

Db 649 ACCTACAGACGACGATCCGACAGATGAGAGGCTATTCATGACAAATGAG 708

Qy 98 GlyTyArgThrAla--SerValIleIleAlaLeuThrArgGlyGluLeuHieGluAsp 116

Db 709 TCCCGTAAAGTCCAGAGATCTCTTGTCTGACAGATGAGGAGGAGAAATACAGAGAC 768

Qy 117 LeuPhePheTyRserGlu-----ArgGluAlaAsnArgSerArgAspLeuGlyAlaIle 134

Db 769 CCCCTGAGATATGATGATCTATCCGCCGCGACAAAGCT-----GCCATCAT 819

Qy 135 ValTyCyValGlyValIleAsp--PheAsnGlu--ThrgluLeuAlaArgGlu 151

Db 820 CGTATGCTATGAGGTGGAGATGCTTCCAGAGGCCCACTGCCCTGAAAGAGCTGAAC 879

Qy 152 -----AlaAspSerIleAspHieValPheProValAsnAspGlyPheGluAla 167

Db 880 ACCATTGGCTGCTGCTCCCGACAGGACCGAGTTCAGATGAGCAAC---TTTCAGCA 936

Qy 168 LeuGlnGlyIleIleHieSerIleLeuAlaGly 178

Db 937 CTTGCGAGCATCCAGAGGCACTTCAGAGAAA 969

RESULT 8

US-08-362-652-36

Sequence 36 Application US/08362652

Patient No. 576850

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Van der Vieren, Monica

TITLE OF INVENTION: No. 576850el Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum

STREET: 233 South Wacker Drive, 6300 Sear Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/362,652

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/32391

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

INFORMATION FOR SEQ ID NO: 36:

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? SEQUENCE CHARACTERISTICS:
? LENGTH: 3528 base pair
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..3456
US-08-362-652-36

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h3:grimmencocccccc:	7.93e-08	Length:	3528
Pred. No.:		Matches:	53
Score:	11.150	Conservative:	38
Percent Similarity:	47.644	Mismatches:	75
Best Local Similarity:	27.754	Indels:	25
Query Match:	14.594	Gaps:	10
DB:	2		

US-09-970-076-2_COPY_41_227 (1-187) x US-08-362-652-36 (1-3528)

QY 4 LeuLeuLeuThrPheIleLeuLeuArgLysSerGlySerVal---LeuH1sh1eTrpAsnGluIle 22
 Db 424 GACATTTGCTTCTCTGATATGATAGTGTGTGGAGACATTAAACCAAGGACATTGGCCCAAGT 483
 QY 23 TyrTyrPheValGluGlnLeuAlaIsh1yLysPheIleSerProGlnLeuArgMetSerPhe 42
 Db 484 AAGACCTTTGTGCAGACCTTTGATGGGAGATTTGGACGACCCAGACACTGTGTTCTCCCTG 543
 QY 43 IleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGlu----- 57
 Db 544 ATGCATATCTCCAGACATCTCTGGAAGCCCAATTTTACCTTCATGAATTCAGAAACATCTTG 603
 QY 58 AspArgGlnGlnIleArgGlnGlyLeuGlnGlnLeuGlnLysValLeuProGlyGlyAsp 77
 Db 604 GACCTTCAGACGCTGTGGATGCCCATTTGCSACCTGCA-----GGCTCG 648
 QY 78 ThrTyrMetHisGluGlnIlyrPheGluArgAlaSerGluGlnIleTyrTyrGlnAsnArgGln 97
 Db 649 ACCTTACAGACGCCACAGACATCTCCGACACAGTATGAGAGACCTTATTCACCAAGAAATGGG 708
 QY 98 GlyTyrArgValThrAla---SerValIleIleAlaLeuThrAspGlyGluMetHisGluAsp 116
 Db 709 TCCCGTAAAGTGGCCCAAGAAATCTCTCTGTGCATCACAATGGGCGAATAATCAGAGAC 768
 QY 117 LeuPhePheThrSerGln-----ArgGluAlaAsnArgSerArgAspLeuGlyAlaIle 134
 Db 769 CCCCCTGGAGATATATGATATGATGATCTCCCGCCGCGACACAAACT-----GGCATATT 81.9
 QY 135 ValTyrCysValGlyValIlyAsp---PheAsnGlu--ThrGlnLeuAlaArgIle-- 151
 Db 820 CGTTATGCGATTTGGGTGGGAGATGCTCTTCAGAGAGCCCACTGCCCTGGAAGGAGCTGAC 87.7
 QY 152 -----AlaAspSerLysAspHisValPheProValAsnAspArgLyrPheGlnAla 167
 Db 880 ACCATTGGCTCAAGCTCCCCCAGACAGACACAGTGTTCAGAGTAGGCAAC---TTTGACAGA 936
 QY 168 LeuGlnGlyIleIleHisSerIleLeuLys 178
 Db 937 CTTTCGACGATCCAGAGGCACTTTCAGGAGAA 969

RESULT 9
US-08-605-672-36
Sequence 36, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESSES:
ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seat Tower

CITY:	Chicago		
STATE:	Illinois		
COUNTRY:	United States		
ZIP:	60606-6402		
COMPUTER READABLE FORM:			
MEDIUM TYPE:	Floppy disk		
COMPUTER:	IBM PC compatible		
OPERATING SYSTEM:	PC-DOS/MS-DOS		
SOFTWARE:	Patentin Release #1.0, Version #1.25		
CURRENT APPLICATION DATA:			
APPLICATION NUMBER:	US/08/605,672		
FILING DATE:			
CLASSIFICATION:	530		
PRIOR APPLICATION DATA:			
APPLICATION NUMBER:	US 08/173,497		
FILING DATE:	23-DEC-1993		
PRIOR APPLICATION DATA:			
APPLICATION NUMBER:	US 08/286,889		
FILING DATE:	5-AUG-1994		
PRIOR APPLICATION DATA:			
APPLICATION NUMBER:	US 08/362,652		
FILING DATE:	21-DEC-1994		
ATTORNEY/AGENT INFORMATION:			
NAME:	Williams Jr., Joseph A.		
REGISTRATION NUMBER:	38,659		
REFERENCE/DOCKET NUMBER:	27866/32684		
TELECOMMUNICATION INFORMATION:			
TELEPHONE:	312-474-6300		
TELEFAX:	312-474-0448		
TELEX:	25-3856		
INFORMATION FOR SEQ ID NO:	36:		
SEQUENCE CHARACTERISTICS:			
LENGTH:	3528 base pairs		
TYPE:	nucleic acid		
STRANDEDNESS:	single		
TOPOLOGY:	linear		
MOLECULE TYPE:	CDNA		
FEATURE:			
NAME/KEY:	CDS		
LOCATION:	1..3456		
US-08-605-672-36			
Alignment Scores:			
Pred. No.:	7,93e-08	Length:	3528
Score:	141.50	Matches:	53
Percent Similarity:	47.64%	Conservative:	38
Best Local Similarity:	27.75%	Mismatches:	75
Query Match:	14.59%	Indels:	25
DB:	2	Gaps:	10

US-09-970-076-2_COPY_41_227 (1-187) x US-08-605-672-36 (1-3528)

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QY      4 AaPLeuTYrPheIleuAaRbLYSeRGISeRvaL----LeuNhiNhiStrPaNgIuLe 22
DB      424 GACATTTGGTTTCTTCTATGATGGTTCTTGCGACACATTAAACCAAAAGGACTTTGCCCAAGTg 483
QY      23 TYrTYrPheValGluGlnLeuAlaNIhLYSPheIleSeRProGlnLeuAaRgMeSeRphe 42
DB      484 AAGGACCTTGTAAGACTTTGATGGAGAGAGTTTGCGAAGCAACAGACACTTTGTCTCCtG 543
QY      43 ILeValPheSeRThrArgGlyThrThrLeuMeCtLYSeuThrGlu-----57
DB      544 ATGCAATACTGCAACATCCGTAAGACCCATTTTACCTTCACCTGAATTCAAAGAACATCCtG 603
QY      58 AaPaRgGluGlnIleAaRgGlnLYLeuGluGluLeuGlnLYValLeuProGlyGlyAaR 77
DB      604 GACCCtCAAGCCGTGATGATCCCATTTGtCCAGtCCAA-----GGCCTG 648
QY      78 ThrTYrMeChISeGluGlyPheGluAaRgAlaSeRGIuGlnIleTYrTYrGluAaRgGln 97
DB      649 ACCtACACAGCCACAGGCAATCCGCAACAGTGAAGAAAGACATTATTCATGACCAAGAAATGGG 708
QY      98 GtLYrTAaRgThAla---SeRValIleIleAlaLeuThrAaRbLYGluMeNIhISeGluAaR 116

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Db	709	TCCTGGAAAAAGTGGCAAGAAAGATCTCTCTTGTATCATCAGATGGGGCAGAAATACAGAGAC	766
Qy	117	LeuPhePhyTysSerGlu-----ArgGluAlaAsnArgSerArgLeuGlyAlaIle	134
Db	769	CCCCCGAGATATAGTATGATGTCATTCCTCCCGCCGACAGACAAAGCT-----GGCATATTT	819
Qy	135	ValTyrCysValGlyValIlyAsp---PheAsnGlu---ThrgInLeuAlaArgIle--	151
Db	820	CGTATATGCTATTGGGGTGGAGAGTGGCTTCCAGAGAGCCCTCCCTCGAAGGAGAGCTGAC	879
Qy	152	-----AlaAspSerIlyAspPheIValPheProValAsnAspGlyPheGlnAla	167
Db	880	ACCATTGGCTCAGCTCCCCCACAAGACACAGTTCATCAAGTATAGCAAC---TTTGCAGCA	936
Qy	168	LeuGlnGlyIleIleHisSerIleLeuIlyAsp	178
Db	937	CTTCGACGATCCAGAGGCAACTTTCAGGACAA 969	

QY 117 Leuphetheryserglu-----Arglnu1aasnargserargleuGlyAla11e 134
 |||||
 DB 769 CCCCTGGAGTATGATGATTCATTCGCCGCCAGACAAAGCT-----GGCATCATTT 819
 QY 135 ValTyrcyValGlyValLysAsp---PheasnGlu---ThrglnLeuAlaArg11e--- 151
 |||||
 DB 820 CGTATGCTATGTTGGGGTGGAGATGCCCTTCAGAGCCCTGCTGAAAGAGCTGAAAC 879
 QY 152 -----AlaaspseryLysAspHisValPheProValaasnargGlyPheGlnAla 167
 |||||
 DB 880 ACCATTGGCTCAGCTCCGCCACAGACACCGATGTTCAAGTAGGCAAC---TTTGCAGCA 936
 QY 168 LeuGlnGly11e11eHisser11eLeuLys 178
 |||||
 DB 937 CTTCGACGATCCAGAGCACTTCAGAGAAA 969
 RESULT 13
 US-09-688-307A-36
 / Sequence 36, Application US/09688307A
 / Patent No. 6432404
 / GENERAL INFORMATION:
 / APPLICANT: Gallatin, Michael W.
 / APPLICANT: Van der Vlieten, Monica
 / TITLE OF INVENTION: No. 6432404e1 Human Beta-2
 / FILE REFERENCE: 27866/36646
 / CURRENT APPLICATION NUMBER: US/09/688,307A
 / PRIOR FILING DATE: 2000-10-13
 / PRIOR APPLICATION NUMBER: 09/193,043
 / PRIOR FILING DATE: 1998-11-16
 / PRIOR APPLICATION NUMBER: 08/605,672
 / PRIOR FILING DATE: 1996-02-22
 / PRIOR APPLICATION NUMBER: 08/173,497
 / PRIOR FILING DATE: 1993-12-23
 / PRIOR APPLICATION NUMBER: 08/286,889
 / PRIOR FILING DATE: 1994-08-05
 / PRIOR APPLICATION NUMBER: 08/362,652
 / PRIOR FILING DATE: 1994-12-21
 / PRIOR APPLICATION NUMBER: 08/943,363
 / PRIOR FILING DATE: 1997-10-03
 / NUMBER OF SEQ ID NOS: 114
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 36
 / LENGTH: 3528
 / TYPE: DNA
 / ORGANISM: Rattus rattus
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (1)..(3453)
 / OTHER INFORMATION: Description of Artificial Sequence: primer
 / NAME/KEY: misc_feature
 / LOCATION: 361
 / OTHER INFORMATION: Xaa = any or unknown amino acid
 / NAME/KEY: misc_feature
 / LOCATION: 464
 / OTHER INFORMATION: Xaa = any or unknown amino acid
 / NAME/KEY: misc_feature
 / LOCATION: 486
 / OTHER INFORMATION: Xaa = any or unknown amino acid
 / NAME/KEY: misc_feature
 / LOCATION: 506
 / OTHER INFORMATION: Xaa = any or unknown amino acid
 / NAME/KEY: misc_feature
 / LOCATION: 1117
 / OTHER INFORMATION: Xaa = any or unknown amino acid
 / NAME/KEY: misc_feature
 / LOCATION: 1118
 / OTHER INFORMATION: Xaa = any or unknown amino acid
 / OTHER INFORMATION: Xaa = any or unknown amino acid
 / US-09-688-307A-36
 Alignment Scores: 7.93e-08 Length: 3528
 Pred. No.: 141.50 Matches: 53
 Score:

Percent Similarity: 47.64% Conservative: 38%
 Best Local Similarity: 27.75% Mismatches: 75
 Query Match: 14.59% Indels: 25
 DB: 3 Gaps: 10
 US-09-970-076-2_COPY_41_227 (1-187) x US-09-688-307A-36 (1-3528)
 QY 4 AspleutyrrheileleuAspLysSerglyServal--LeuHisThrPasnGlu11e 22
 |||||
 DB 424 GACATTCCTTCCCTGATGATGTTCTGCGACAGCATTAACCAAGAGACTTTCGCCAGATG 483
 QY 23 TyrryrrheValGlnGlnLeuAlaHisLeuPheLeuSerrProGlnLeuAspMetSerphe 42
 |||||
 DB 484 AAGCACTTTCACAACTTTCAGTGGAGAGTTCGAGCAACCAACACCTTGTCTCCCTG 543
 QY 43 IlleValPheSerrThrArgGlyThrThrLeuMetLysLeuThrGlu----- 57
 |||||
 DB 544 ATGCAATACCTGAAACATCCCGAAGACCCCATTTTACCTTCACTGATTCAGAACATCCTG 603
 QY 58 AspArgGlnGlnleargGlnGlyLeuGlnGlyLeuGlnGlyValLeuProGlyLysAsp 77
 |||||
 DB 604 GACCTCAGAGCCTGGTGGATCCCATGTCACAGTGCAG-----GGCCTG 648
 QY 78 ThrTyrrmethisGlnGlyPheGluArgAlasergGlnGlnleTyrryrrGluAsnArgGln 97
 |||||
 DB 649 ACCATCACAGCCACAGGCAATCCGACAGTAGAAGCTATTTCATACGACAAATGGC 708
 QY 98 GlyTyrrargThrAla---Serval11e11eAlaLeuThrAspGlyGluLeuHisGluAsp 116
 |||||
 DB 709 TCCCGTAAAGTCCGAAGAAGATCCCTCTTGATCACAAGTGGCAGAAATACAGAGAC 768
 QY 117 Leuphetheryserglu-----Arglnu1aasnargserargleuGlyAla11e 134
 |||||
 DB 769 CCCCTGGAGTATGATGATTCATTCGCCGCCAGACAAAGCT-----GGCATCATTT 819
 QY 135 ValTyrcyValGlyValLysAsp---PheasnGlu---ThrglnLeuAlaArg11e--- 151
 |||||
 DB 820 CGTATGCTATGTTGGGGTGGAGATGCCCTTCAGAGCCCTGCTGAAAGAGCTGAAAC 879
 QY 152 -----AlaaspseryLysAspHisValPheProValaasnargGlyPheGlnAla 167
 |||||
 DB 880 ACCATTGGCTCAGCTCCGCCACAGACACCGATGTTCAAGTAGGCAAC---TTTGCAGCA 936
 QY 168 LeuGlnGly11e11eHisser11eLeuLys 178
 |||||
 DB 937 CTTCGACGATCCAGAGCACTTCAGAGAAA 969
 RESULT 14
 US-09-350-259-36
 / Sequence 36, Application US/09350259
 / Patent No. 6620915
 / GENERAL INFORMATION:
 / APPLICANT: Gallatin, Michael W.
 / APPLICANT: Van der Vlieten, Monica
 / TITLE OF INVENTION: No. 6620915e1 Human 2
 / FILE REFERENCE: 27866/35004
 / CURRENT APPLICATION NUMBER: US/09/350,259
 / PRIOR FILING DATE: 1999-07-08
 / PRIOR APPLICATION NUMBER: 09/193,043
 / PRIOR FILING DATE: 1998-11-16
 / PRIOR APPLICATION NUMBER: 08/173,497
 / PRIOR FILING DATE: 1993-12-23
 / PRIOR APPLICATION NUMBER: 08/286,889
 / PRIOR FILING DATE: 1994-08-05
 / PRIOR APPLICATION NUMBER: 08/362,652
 / PRIOR FILING DATE: 1994-12-21
 / PRIOR APPLICATION NUMBER: 08/943,363
 / PRIOR FILING DATE: 1997-10-03
 / NUMBER OF SEQ ID NOS: 114
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 36
 / LENGTH: 3528
 / TYPE: DNA

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ORGANISM: Rattus rattus
FEATURE:
NAME/KEY: CDS
LOCATION: (1) .. (3453)
FEATURE: (1) .. (3453)
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-350-259-36

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Alignment Scores:
Pred. No.: 7,93e-08 Length: 3528
Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
Best Local Similarity: 27.75% Mismatches: 75
Query Match: 14.59% Indels: 25
Gaps: 10

```

US-09-970-076-2_COPY_41_227 (1-187) x US-09-350-259-36 (1-3528)

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QY 4 AapLeuTyrrPheileLeuAapLySerGlySerVal---LeuHihIeTrpAenGluile 22
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 424 GACATGCTTCTTCATGATGATGTTCTGGACACATTAAACMAAGGACCTTGCCAGATG 483
QY 23 TyrrTyrrPheValGluGlnLeuAhiSyrrPheileSerProGlnLeuArygMetSerPhe 42
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 484 AAGGACTTGTCAAGCTTGTATGGAGAGTTGGAGAGCTTGGACAGACACCTTGTTCCTCG 543
QY 43 IleValPheSerThrArgGlyThrThrLeuMetLySerValLeuThrglu----- 57
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 544 ATGCAATCTCGAACAATCTCGAAGCCCTTTACCTTCATCGAATTCAGAAACATCTCG 603
QY 58 AapArgGluGlnIleArgGlnIleuGlnIleuGlnIleValLeuProGlyGlyAap 77
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 604 GACCTCAGAGCTGTGGATGCCATTTGCCAGCTGCAA-----GGCCTG 648
QY 78 ThrTyrrMetHieGluGlyPheGluArgAlaSerGluGlnIleTyrrTyrrGluAenArgGln 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 649 ACCTACAGACGACGAGCATCCGACAGTGAAGAGACATTCATACAGAAATGGG 708
QY 98 GlyTyrrArgThrAla---SerValIleIleAlaLeuThraArgGlyGluLeuHieGluAap 116
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 709 TCCCTTAAGAGGCCAAGAAAGATCTCTCTTCATCAGATGGGACAAATACAGAGAC 768
QY 117 LeuPhePheTyrrSerGlu---ArgGluAlaAenArySerArgAapLeuGlyAlaIle 134
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 769 CCCCTGAGATATGATGATCATCTCCCGCCGACAAAGCT-----GGCATCATT 819
QY 135 ValTyrrCyrrValGlyValLyAap---PheAenGlu---ThrglnLeuAlaArgIle--- 151
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 820 CGTTATGCTATGGGGGTGGAGATGCTTCACAGAGCCCACTGCTCGAAGAGCTGAAC 879
QY 152 -----AlaAapSerLyAapHieValPheProValAenAapGlyPheGlnAla 167
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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RESULT 15
US-08-485-618-54
Sequence 54, Application US/08485618
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GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Bear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States

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ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 3597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 40..3525
US-08-485-618-54
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Score: 141.50 Matches: 53
Percent Similarity: 47.64% Conservative: 38
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ACCESSION	AF421380			
VERSION	AF421380.1	GI:16566412		
KEYWORDS				
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hominoidea; Homo.
1 (bases) 1 to 1414

REFERENCE
 1. Moore, K.A., Collier, R.J., Mourer, M., and Young, J.A.
 Bradley, K.A., and Collier, R.J. (2001)
 TITLE Identification of the cellular receptor for anthrax toxin
 JOURNAL Nature 414 (6860), 225-229 (2001)
 PUBMED 11700562

REMARK	REFERENCE
2 (bases 1 to 1414)	http://www.nature.com
BRADLEY, K.A., MCGRIDGIE, J., MOURER, M., COLLIER, R.J. and YOUNG, J.A.T.	
TITLE	
Direct Submission	
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 LOCUS Sequence 176 from Patent WO0210217.
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 ACCESSION AX393246
 VERSION AX393246.1 GI:19701296
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Homnidae; Homo.
 REFERENCE
 1 St Croix, B., Kinzler, K.W. and Vogelstein, B.
 Endothelial cell expression patterns
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VERSION AX393301.1 GI:19701322
KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
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AUTHORS St Croix,B., Kinzler,K.W. and Vogelstein,B.
TITLE Endothelial cell expression patterns
JOURNAL Patent: WO 0210217-A 231 07-FEB-2002;
The Johns Hopkins University (US)
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Qy | 241 | CTTCAATTTTGAAGAAATGAGAAAGTGTGTGACCACTGGAATGAATTTATCTTGT | 300
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Qy | 421 | AGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATGATGAGAAATTTGAAG | 480
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Db | 521 | GGCCAGTGAAGATTATATGAAAAAGAGAGGGTCAAGAGACGCCAGCTCATCAT | 580
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Qy | 601 | TAGGTCTCGAGATCTTTGGTGAATGTTTACTGTGTGTGTGAAGATTTCATGAGAC | 660
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Db | 761 | GGCTCTGCAAGGACATCATCACTCAATTTTGAAGAGTCTGATGAGAAATTTCTAGAC | 820
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RESULT 5
AX458370 5540 bp DNA linear PAT 08-JUL-2002
LOCUS Definition Sequence 5 from Patent WO0246228.
ACCESSION AX458370 GI:21725040
VERSION AX458370.1 GI:21725040
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1
REFERENCE
AUTHORS Young, J.A., Bradley, K.A., Collier, R.J. and Mowbride, J.S.
TITLE Receptor for b. Anthracis toxin
JOURNAL Patent: WO 0246228-A 5 13 JUN-2002;
WISCONSIN ALUMNI RESEARCH FOUNDATION (US)
FEATURES
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ORIGIN
Query Match 84.4%; Score 1193.8; DB 6; Length 5540;
Best Local Similarity 99.8%; Pred. No. 1.7e-286;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 401 CACCCGAGGACACCTTATATGAATCTGACAGAGACAGAGAAACAAATCCGTCAGGCT 460
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RESULT 6
AF279145 5540 bp mRNA linear PRI 09-MAY-2001
LOCUS Homo sapiens tumor endothelial marker 8 precursor (TEM8) mRNA,
DEFINITION complete cds.
ACCESSION AF279145
VERSION AF279145.2 GI:14017380
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 5540)
AUTHORS St. Croix,B., Rago,C., Velculescu,V., Traverso,G., Romans,K.E.,
Montgomery,E., Lal,A., Riggin,G.J., Lengauer,C., Vogelstein,B. and
Kinzler,K.W.
Gene expressed in human tumor endothelium
JOURNAL Science 289 (5482), 1197-1202 (2000)
PUBMED 10947988
REFERENCE 2 (bases 1 to 5540)
AUTHORS St. Croix,B., Vogelstein,B. and Kinzler,K.W.
Direct Submission
JOURNAL Submitted (16-JUN-2000) Johns Hopkins Oncology Center, Johns
Hopkins University, 1650 Orleans Street, Baltimore, MD 21231, USA
3 (bases 1 to 5540)
AUTHORS St. Croix,B., Vogelstein,B. and Kinzler,K.W.
Direct Submission
JOURNAL Submitted (09-MAY-2001) Johns Hopkins Oncology Center, Johns
Hopkins University, 1650 Orleans Street, Baltimore, MD 21231, USA
Sequence update by submitter
REMARK On May 9, 2001 this sequence version replaced gi:9857405.
COMMENT
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ORIGIN
Query Match 84.4%; Score 1193.8; DB 8; Length 5540;
Best Local Similarity 99.8%; Pred. No. 1.7e-288;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 AGACCCGCGAGAAAGGCGCGGATGCGCGTCCCTGAGGCTGTGGCGAGTTCCGCG 60
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Db 41 AGACCCGCGAGAAAGGCGCGGATGCGCGTCCCTGAGGCTGTGGCGAGTTCCGCG 100
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RESULT 7
AY928975 1576 bp mRNA linear PRI 10-MAY-2005
LOCUS Homo sapiens anthrax toxin receptor/neuroblastoma fusion protein
DEFINITION transcript variant 2 (ANTXR1/NGG1 fusion) mRNA, complete cds.
ACCESSION AY928975
VERSION AY928975.1 GI:62870686
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1576)
Oberthuer, A., Kahlert, Y., Spitz, R., Skowron, M., Westermann, F.,
Mehler, K., Berthold, F. and Fischer, M.
SAGE-based discovery and characterization of a novel fusion gene in
the neuroblastoma cell lines IMR-5, IMR-5/75 and IMR-32
Unpublished
2 (bases 1 to 1576)
Oberthuer, A., Kahlert, Y., Spitz, R., Skowron, M., Westermann, F.,
Mehler, K., Berthold, F. and Fischer, M.
Direct Submission
Submitted (14-FEB-2005) Pediatric Oncology and Hematology, Cologne
Childrens Hospital, University of Cologne, Joseph-Steitzmann-Strasse
9, Cologne, NRW D-50924, Germany
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ORIGIN
Query Match 84.4%; Score 1193.4; DB 8; Length 1576;
Best Local Similarity 99.5%; Pred. No. 1,6e-288;
Matches 1197; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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RESULT 8
AY928977 1658 bp mRNA linear PRI 10-MAY-2005
LOCUS Homo sapiens anthrax toxin receptor/neuroblastoma fusion protein
DEFINITION transcript variant 4 (ANTXR1/NG1 fusion) mRNA, complete cds.
ACCESSION AY928977.1 GI:62870690
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 1658)
AUTHORS Oberthuer, A., Kahle, Y., Spitz, R., Skowron, M., Westermann, F.,
Mehler, K., Berthold, F. and Fischer, M.
TITLE SAGE-based discovery and characterization of a novel fusion gene in
the neuroblastoma cell lines IMR-5, IMR-5/75 and IMR-32
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1658)
AUTHORS Oberthuer, A., Kahle, Y., Spitz, R., Skowron, M., Westermann, F.,
Mehler, K., Berthold, F. and Fischer, M.
TITLE Direct Submission
JOURNAL Submitted (14-FEB-2005) Pediatric Oncology and Hematology, Cologne
Childrens Hospital, University of Cologne, Joseph-Stelzmann-Strasse
9, Cologne, NRW D-50924, Germany
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 VERSION AY928974.1 GI:62870684
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 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Oberthur, A., Kahler, Y., Spitz, R., Skowron, M., Westermann, F.,
 Mehler, K., Berthold, F. and Fischer, M.
 TITLE SAGE-based discovery and characterization of a novel fusion gene in
 the neuroblastoma cell lines IMR-5, IMR-5/75 and IMR-32
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1496)
 AUTHORS Oberthur, A., Kahler, Y., Spitz, R., Skowron, M., Westermann, F.,
 Mehler, K., Berthold, F. and Fischer, M.
 TITLE Direct Submission
 JOURNAL Submitted (14-FEB-2005) Pediatric Oncology and Hematology, Cologne
 Childrens Hospital, University of Cologne, Joseph-Stelzmann-Strasse
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transcript variant 3 (ANTXR1/NG1 fusion) mRNA, complete cds.
ACCESSION AY928976
VERSION AY928976.1 GI:62870688
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Homidae; Homo.
REFERENCE 1 (bases 1 to 1578)
Oberthuer, A., Kahler, Y., Spitz, R., Skowron, M., Westermann, F.,
Mehler, K., Berthold, F. and Fischer, M.
SAGE-based discovery and characterization of a novel fusion gene in
the neuroblastoma cell lines IMR-5, IMR-5/75 and IMR-32
Unpublished
2 (bases 1 to 1578)
Oberthuer, A., Kahler, Y., Spitz, R., Skowron, M., Westermann, F.,
Mehler, K., Berthold, F. and Fischer, M.
Direct Submision
Submitted (14-FEB-2005) Pediatric Oncology and Hematology, Cologne
Childrens Hospital, University of Cologne, Joseph-Stelzmann-Strasse
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 VERSION AX458372.1 GI:21725042
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 Homnidae; Homo.
 REFERENCE
 AUTHORS Young, J. A., Bradley, K. A., Collier, R. J. and Mogridge, J. S.
 TITLE Receptor for b. Anthracis toxin
 JOURNAL Patent: WO 0246228-A 7 13-JUN-2002;
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ACCESSION BC012074 GI:15082332
VERSION BC012074.1 GI:15082332
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
1 (bases 1 to 2112)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Scheener,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haleh,F.,
Datchenko,L., Marziani,K., Parker,A.A., Rubin,G.M., Hong,L.,
Sapichon,M., Soares,M.B., Bonaldo,M.F., Casavant,L.,
Schaefer,T.E., Brownstein,M.J., Uedin,T.B., Toshiyuki,S.,
Carinci,P., Prange,C., Raha,S.S., Loggellano,N.A., Peters,G.U.,
Abramson,R.D., Mulhaly,S.J., Bosak,S.A., McEwan,P.J.,
Mckernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.U., Lu,X., Gibbs,R.A.,
Fahney,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalek,U., Smalls,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2112)
Strausberg,R.
Direct Submission
Submitted (02-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Nasson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lissa Pribbu,
Parvaneh Saeedi, Jr Santos, Angeliue Schnerch, Ursula Skalek,
Diane Smalls, Jeff Stolt, Miranda Tsai, George Yang, Jacquiie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/ULNL at: <http://image.llnl.gov>
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This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 1693552.
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Best Local Similarity 99.9%; Pred. No. 4,7e-253; Indels 0; Gaps 0;
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 ACCESSION AK23273.1 GI:62898106
 VERSION FLI_CDNA; o11go capping.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Matuyama, K. and Sugano, S.
 TITLE Oligo-capping: a simple method to replace the cap structure of eukaryotic mRNAs with oligoribonucleotides
 JOURNAL Gene 138 (1-2), 171-174 (1994)
 PUBMED 8125298
 REFERENCE
 AUTHORS Suzuki, Y., Yoshitomo-Nakagawa, K., Matuyama, K., Suyama, A. and Sugano, S.
 TITLE Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library
 JOURNAL Gene 200 (1-2), 149-156 (1997)
 PUBMED 9373149
 REFERENCE
 AUTHORS Suzuki, Y., Sugano, S., Totoki, Y., Toyoda, A., Takeda, T., Sakaki, Y., Tanaka, A. and Yokoyama, S.
 TITLE Direct Submision
 JOURNAL Submitted (22-APR-2005) Akiko Tanaka, RIKEN Yokohama Institute, Protein Research Group, 1-7-22 Suehiro, Tsukumi, Yokohama, Kanagawa, 230-0045, Japan (E-mail: aketanaka@riken.jp, URL: http://protein.gsc.riken.jp/, Tel: 81-45-503-9452,

COMMENT
 Fax: 81-45-503-9450
 This work was supported in part by the National Project on Protein Structural and Functional Analysis, Ministry of Education, Culture, Sports, Science and Technology of Japan.
 Sumio Sugano, Yutaka Suzuki
 Laboratory of Functional Genomics Department of Medical Genome Sciences Graduate School of Frontier Sciences The University of Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639 Japan email: saugano@k.u-tokyo.ac.jp
 URL: http://www.k.u-tokyo.ac.jp/index.html.en.
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 Best Local Similarity 99.7%; Pred. No. 5.2e-253;
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DEFINITION Sequence 8 from patent US 6569662.
ACCESSION AR338517
VERSION AR338517.1 GI:33725374
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1609)
AUTHORS Tang, Y.T., Zhou, P. and Drmanac, R.T.
TITLE Nucleic acids and polypeptides
JOURNAL Patent: US 6569662-A 8 27-MAY-2003;
Hyeq, Inc.; Sunnyvale, CA
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Best Local Similarity 99.8%; Pred. No. 1.7e-216;
Matches 908; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1106 ACTCAATGAG 1115

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DEFINITION Sequence 30300 from Patent WO0160860.
ACCESSION CQ498433
VERSION CQ498433.1 GI:41464069
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: December 17, 2005, 13:37:50 ; Search time 941.731 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

SUMMARIES

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	6	1193.8	84.4	5540	10	ABV72003	Abv72003 DNA encod
	7	1193.8	84.4	5540	13	ADx48215	Adx48215 Human tum
	8	1193.8	84.4	5540	14	ADx70742	Adx70742 Tumor end
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29	950.8	67.2	1650	10	AD100541	Human	TAN
30	950.8	67.2	1650	11	AD100541	Human	TAN
31	914.4	64.7	1047	10	AD100553	Human	TAN
32	914.4	64.7	1047	11	AD100553	Human	TAN
33	906.8	64.1	1402	4	AA159918	Human	pol
34	906.8	64.1	1609	9	AA159918	Human	pol
35	906.8	64.1	1609	5	AD098338	DNA	encod
36	906.8	64.1	1609	9	AD098338	DNA	encod
37	906.2	64.0	1718	5	ABV30282	Human	pro
38	894.6	63.3	1608	10	AD100567	Human	TAN
39	890	62.9	1436	6	AAH14331	Human	cdn
40	890	62.9	1436	6	ABV73884	Human	ant
41	867.6	61.4	1623	10	AD100543	Human	TAN
42	867.6	61.4	1623	11	AD100543	Human	TAN
43	853.4	60.4	5220	6	AB192085	Mouse	Tum
44	853.4	60.4	5220	6	AB192085	Mouse	Tum
45	853.4	60.4	5220	10	ABX72010	DNA	encod

ALIGNMENTS

```

XX RESULT 1
XX ABV73881
ID ABV73881 standard; cDNA; 1414 BP.
XX
XX ABV73881;
XX
XX 08-JAN-2003 (first entry)
XX
XX Human anthrax toxin receptor cDNA.
XX
XX Anthrax; toxin; receptor; human; antibacterial; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 104..1210
XX FT /*tag= a
XX FT /*product= "anthrax toxin receptor"
XX FT sig_peptide 104..182
XX FT /*tag= b
XX FT mat_peptide 183..1207
XX FT /*tag= c
XX
XX WO200246228-A2.
XX
XX
XX 13-JUN-2002.
XX
XX 03-OCT-2001; 2001WO-US030941.
XX
XX 05-DEC-2000; 2000US-0251481P.
XX
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX Young JAT, Bradley KA, Collier RJ, Mogridge JS;
XX
XX WPI; 2002-713235/77.
XX
XX P-PSDB; ABP54903.
XX
XX Novel isolated polypeptide useful for identifying agent that prevents or
XX reduces effect of anthrax toxin on host cell, for treating human or non-
XX human animal suffering from anthrax.
XX

```

PS Claim 7; Page 27-29; 45bp; English.
 XX The present sequence is that of cDNA encoding a human surface-bound
 CC anthrax toxin receptor (ATR). The cDNA is a PCR amplification product
 CC from HeLa cells and human placenta cDNA libraries. Anthrax toxin
 CC protective antigen (PA) binds to the ATR at a von Willebrand factor A
 CC domain located in the extracellular domain of ATR. The invention provides
 CC ATR polypeptides and polynucleotides, vectors, host cells, and transgenic
 CC and knock-out animals. The invention also provides methods for
 CC identifying molecules that bind the ATR and which reduce the toxicity of
 CC anthrax toxin. A claimed method for treating anthrax in a human or animal
 CC involves administering an agent that inhibits binding between PA and ATR
 CC at a level effective to reduce the severity of anthrax. Suitable agents
 CC include ATR or a PA-binding fragment of ATR, a PA-binding polypeptide at
 CC least 80% identical to these, a fusion protein, a monoclonal or
 CC polyclonal antibody, a polysaccharide, a lipid or a nucleic acid. ATR
 CC polynucleotides can also be used in the recombinant production of ATR
 CC polypeptides, and as molecular probes
 XX
 SQ Sequence 1414 BP; 394 A; 344 C; 344 G; 332 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1414; DB 6; Length 1414;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGGACCCGCGAGGAGGCGCGGATGCGCGTCCCTGAGAGTCTGGAGGTTGCGCG 60
 DB 1 AGGACCCGCGAGGAGGCGCGGATGCGCGTCCCTGAGAGTCTGGAGGTTGCGCG 60
 QY 61 AGCGTGGAGAGAGAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGGCCACGGGGAGCG 120
 DB 61 AGCGTGGAGAGAGAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGGCCACGGGGAGCG 120
 QY 121 GAGAGCCCTGGGCACTCGGCTTCCAGTGGCTCTCTTTGGGCACTGGGTCATCTGCGC 180
 DB 121 GAGAGCCCTGGGCACTCGGCTTCCAGTGGCTCTCTTTGGGCACTGGGTCATCTGCGC 180
 QY 121 GAGAGCCCTGGGCACTCGGCTTCCAGTGGCTCTCTTTGGGCACTGGGTCATCTGCGC 180
 DB 121 GAGAGCCCTGGGCACTCGGCTTCCAGTGGCTCTCTTTGGGCACTGGGTCATCTGCGC 180
 QY 181 CGGGCAAGGGGGAGCGAGGAGATGGGGGTCCAGCTGCTACGCGGATTTGACTGTA 240
 DB 181 CGGGCAAGGGGGAGCGAGGAGATGGGGGTCCAGCTGCTACGCGGATTTGACTGTA 240
 QY 181 CGGGCAAGGGGGAGCGAGGAGATGGGGGTCCAGCTGCTACGCGGATTTGACTGTA 240
 DB 181 CGGGCAAGGGGGAGCGAGGAGATGGGGGTCCAGCTGCTACGCGGATTTGACTGTA 240
 QY 241 CTTTCATTTTGGACAAATCAGGAATGTGCTGCACCTGGAATGGAATCTTATCTTGT 300
 DB 241 CTTTCATTTTGGACAAATCAGGAATGTGCTGCACCTGGAATGGAATCTTATCTTGT 300
 QY 241 CTTTCATTTTGGACAAATCAGGAATGTGCTGCACCTGGAATGGAATCTTATCTTGT 300
 DB 241 CTTTCATTTTGGACAAATCAGGAATGTGCTGCACCTGGAATGGAATCTTATCTTGT 300
 QY 301 GGAACAGTTGGCTCACAATTCATCAGCCACAGTTGGAATGTCCTTATTTGTTTCTC 360
 DB 301 GGAACAGTTGGCTCACAATTCATCAGCCACAGTTGGAATGTCCTTATTTGTTTCTC 360
 QY 361 CACCGAGGAGCAACCTTATGAACTGACAGAAAGACAGAGAACAAATCCGTCAAGGCT 420
 DB 361 CACCGAGGAGCAACCTTATGAACTGACAGAAAGACAGAGAACAAATCCGTCAAGGCT 420
 QY 421 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGATGAAGATTGAAAG 480
 DB 421 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGATGAAGATTGAAAG 480
 QY 481 GGCACAGAGAGAGATTTATTAAGAAACAGACAGGGGTACAGACAGCAGTCATCAT 540
 DB 481 GGCACAGAGAGAGATTTATTAAGAAACAGACAGGGGTACAGACAGCAGTCATCAT 540
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 DB 601 TAGGTCTCGAGATCTTGGTGAATTTGTTTACTGTGTGGTGAAGATTTCATGAGAC 660
 QY 661 ACAGCTGGCCCGGATTTGGGACAGTAAGATCATGTGTTCCCGTGAATGAGCGGCTTCA 720
 DB 661 ACAGCTGGCCCGGATTTGGGACAGTAAGATCATGTGTTCCCGTGAATGAGCGGCTTCA 720

QY 721 GGCTTCGCAAGGATCATCTCAATTTTGAAGAGTCTCGCATGGAATTTCTAGACG 780
 DB 721 GGCTTCGCAAGGATCATCTCAATTTTGAAGAGTCTCGCATGGAATTTCTAGACG 780
 QY 781 TGAACCATCCACATATGTCAGAGAGATCTTCAAGTTGTCGTGAGAGAAACGGCTT 840
 DB 781 TGAACCATCCACATATGTCAGAGAGATCTTCAAGTTGTCGTGAGAGAAACGGCTT 840
 QY 841 CGGACATGCCCGGACGTCGACAGGCTCTCTGACGTTCAAGATCAATGACTGGTAC 900
 DB 841 CGGACATGCCCGGACGTCGACAGGCTCTCTGACGTTCAAGATCAATGACTGGTAC 900
 QY 901 ACTCAATGAGAACCCCTTTTCTGGAAGACACTTATTTCTGTGTCAGGCGCTATCTT 960
 DB 901 ACTCAATGAGAACCCCTTTTCTGGAAGACACTTATTTCTGTGTCAGGCGCTATCTT 960
 QY 961 AAAAGAAAGTGGATGAGAAAGCTGACCTGACAGTCAAGATGAAGAGGCTCTTTTAT 1020
 DB 961 AAAAGAAAGTGGATGAGAAAGCTGACCTGACAGTCAAGATGAAGAGGCTCTTTTAT 1020
 QY 1021 CTCGAGTTCTGTATCATCAACACACACACTGTTCTGACGTTCAATCTGCGCATGCG 1080
 DB 1021 CTCGAGTTCTGTATCATCAACACACACACTGTTCTGACGTTCAATCTGCGCATGCG 1080
 QY 1081 CTTGCTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 DB 1081 CTTGCTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 QY 1141 CTCGACTGTGATTTATCAAGAGGTCCTCCACCCCTGCGAGAGAGTGAAGAAATTA 1200
 DB 1141 CTCGACTGTGATTTATCAAGAGGTCCTCCACCCCTGCGAGAGAGTGAAGAAATTA 1200
 QY 1201 AATTAATAAACAAG 1260
 DB 1201 AATTAATAAACAAG 1260
 QY 1261 CCGTGCAAGCTATTTTATTAAGTCTGTAAGTCAATGCTCAATCTAGACAGTCTTT 1320
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 QY 1381 CAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1440
 DB 1381 CAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1440
 RESULT 2
 ABL92078 standard; cDNA; 5540 BP.
 XX ABL92078;
 AC ABL92078;
 XX
 DT 30-MAY-2002 (first entry)
 XX
 DE Human Tumour Endothelial Marker polynucleotide SEQ ID NO 176.
 XX Human; mouse; rat; TBM; tumour endothelial marker; immunosuppressant;
 KW normal endothelial marker; pan-endothelial marker; immunosuppressant;
 KW antiangiogenic; tumour; neovascularisation; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200210217-A2.
 XX
 XX 07-FEB-2002.
 XX
 XX PD
 XX 01-AUG-2001; 2001MO-US024031.
 XX
 XX

PR 02-AUG-2000; 2000US-0222599P.
PR 11-AUG-2000; 2000US-0224360P.
PR 11-APR-2001; 2001US-0282850P.
XX
XX
XX (UYJO) UNIV JOHNS HOPKINS.
PI St Croix B, Kinzler KM, Vogelstein B;
DR WPI; 2002-291856/33.
XX
XX An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
marker (TEM) protein, useful for inhibiting tumor growth.
XX
XX Disclosure; Page 121-123; 331pp; English.
XX
XX The invention relates to an isolated molecule comprising an antibody
CC variable region which specifically binds to an extracellular domain of a
CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects
CC bearing a vascularised tumour, polycystic kidney disease, diabetic
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
CC are disclosed, as are marker oligonucleotide sequences: tumour
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191, normal
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
CC (PEM) ABL91903-ABL91995
XX
SQ Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
Query Match 84.4%; Score 1193.8; DB 6; Length 5540;
Best Local Similarity 99.8%; Pred. No. 2.4e-285;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGAAGCCGCGAGAGAGGCGCGGATGGCGGCTCCGAGAGGCGGAGTTCGCGG 60
DB 41 AGAAGCCGCGAGAGAGGCGCGGATGGCGGCTCCGAGAGGCGGAGTTCGCGG 100
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DB 101 AGCGTGGAGAGAGAGAGGCGGAGTTCGCGGCTCCGAGAGGCGGAGTTCGCGG 160
QY 121 GAGAGCCCTCGGATCGGCTTCAGTGGCTCTCTTGGCCATCTGTGCTCATCTGCGC 180
DB 161 GAGAGCCCTCGGATCGGCTTCAGTGGCTCTCTTGGCCATCTGTGCTCATCTGCGC 220
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QY 241 CTTGATTTTGGACAATCAGAGAGTGTGCTGACCACTGGAATGAAATCTTACTTGT 300
DB 281 CTTGATTTTGGACAATCAGAGAGTGTGCTGACCACTGGAATGAAATCTTACTTGT 340
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DB 341 GGAACAGTGGCTCACAATTCATCAGCCACAGTTGGAATGTCTTATTTGTTTCTC 400
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QY 421 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGACCTTACATGCTAGTAAGATTGAAAG 480
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QY 481 GGCCAGTGGAGATTTATTTATGAAACAGACAAAGGATACAGACAGCCAGCTCATCAT 540
DB 521 GGCCAGTGGAGATTTATTTATGAAACAGACAAAGGATACAGACAGCCAGCTCATCAT 580
QY 541 TGCTTTGACTGATGAGAACTCCATGAAGATCTTTTCTATTCAGAGAGGAGCTAA 600

DB 581 TGCTTTGACTGATGAGAACTCCATGAAGATCTTTTCTATTCAGAGAGGAGCTAA 640
QY 601 TAGGCTCGAGATCTTGGTGCAATTTGTTTACTGTGTGGTGGAAGATTCAATAGAC 660
DB 641 TAGGCTCGAGATCTTGGTGCAATTTGTTTACTGTGTGGTGGAAGATTCAATAGAC 700
QY 661 ACAGCTGGCCCGGATGGCGGACAGTAAAGATCATGTGTTTCCCGTAATGACGGCTTCA 720
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DB 761 GGCTTCGAGAGGATCATCATCTCAATTTTGAAGAGTCTGATCGAAATTTAGACG 820
QY 781 TGAACCATCCACATATTTGTCAGAGAGATCTTCAAGTTGTGTGAGAGAAACGGCTT 840
DB 821 TGAACCATCCACATATTTGTCAGAGAGATCTTCAAGTTGTGTGAGAGAAACGGCTT 880
QY 841 CGGACATGCGCCGAGAGGAGGAGGAGGCTCTGAGCTTCAAGATCAATGACTCGGTAC 900
DB 881 CGGACATGCGCCGAGAGGAGGAGGAGGCTCTGAGCTTCAAGATCAATGACTCGGTAC 940
QY 901 ACTCAATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
DB 941 ACTCAATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1000
QY 961 AAAAGAAAGTTGGATGAGAAAGTCACTCCAGGTCAGATGAGAGAGGAGGAGGAGGAG 1020
DB 1001 AAAAGAAAGTTGGATGAGAAAGTCACTCCAGGTCAGATGAGAGAGGAGGAGGAGGAG 1060
QY 1021 CTCAGATCTGTGATATATCAACACACACACACACACACACACACACACACACACACAC 1080
DB 1061 CTCAGATCTGTGATATATCAACACACACACACACACACACACACACACACACACACAC 1120
QY 1081 CTTGCTGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
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QY 1141 CTGCACTGTGATATATCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1197
DB 1181 CTGCACTGTGATATATCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1237
RESULT 3
ABL92104
ID ABL92104 standard; cDNA; 5540 BP.
XX
XX ABL92104;
AC
XX 30-MAY-2002 (first entry)
DT
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XX Human Tumour Endothelial Marker polynucleotide SEQ ID NO 231.
DE
XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200210217-A2.
FN
XX
XX 07-FEB-2002.
PD
XX
XX 01-AUG-2001; 2001WO-US024031.
PE
XX
XX 02-AUG-2000; 2000US-0222599P.
PR 11-AUG-2000; 2000US-0224360P.
PR 11-APR-2001; 2001US-0282850P.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
PA

XX St Croix B, Kinzler KM, Vogelstein B;
 XX MPI: 2002-291856/33.
 DR P-PSDB; ABB90750.
 XX
 XX An isolated molecule comprising an antibody variable region which
 PT specifically binds to an extracellular domain of a tumor endothelial
 PT marker (TEM) protein, useful for inhibiting tumor growth.
 XX
 PS Claim 30; Page 207-209; 33pp; English.
 XX
 CC The invention relates to an isolated molecule comprising an antibody
 CC variable region which specifically binds to an extracellular domain of a
 CC tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
 CC They are useful for inhibiting tumor growth, neoangiogenesis in subjects
 CC bearing a vascularised tumour, polycystic kidney disease, diabetic
 CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
 CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
 CC are disclosed, as are marker oligonucleotide sequences; tumour
 CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
 CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
 CC (PEM) ABL91903-ABL91995
 XX
 SQ Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
 Query Match 84.4%; Score 1193.8; DB 6; Length 5540;
 Best Local Similarity 99.8%; Pred. No. 2.4e-285;
 Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 641 TAGGTCGAGATCTTGGGCAATGTTTACGTGTGTGTGGAAGATTTCAATGAGAC 700
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 DB 701 AAGCTGGCCGGATTTGGGACAGTAAAGATCATGTGTTCCCGAATAGACGGCTTTCA 760
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 DB 761 GGCTGTGACAGGATCATCTCAATTTTGAAGAAGTCTTCATCGAATTTCTAGCAGC 820
 QY 781 TGAACATTCACCATATGTGACAGAGAGTCAATTTCAAGTTGTCGTAAGAGAAACGGCTT 840
 DB 821 TGAACATTCACCATATGTGACAGAGAGTCAATTTCAAGTTGTCGTAAGAGAAACGGCTT 880
 QY 841 CCGACATGCCGCAACGTGGAAGAGGATCTCTGACGCTTCAAGATCAATGATCGGTAC 900
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 DB 1061 CTCGAGTTCTGATCATCATACACACACAGTGTGACGGTTCATCTGGCCATCGC 1120
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 DB 1121 CCTGTGATCTCTGTTCTCTGCTCTAGCCCTGCTCTCTGTGTGTTCTGAGCCCTCTG 1180
 QY 1141 CTGCACTGTGATTTATCAAGAGGTCCTTCACCCCTGCGAGAGAGTGAAGAAA 1197
 DB 1181 CTGCACTGTGATTTATCAAGAGGTCCTTCACCCCTGCGAGAGAGTGAAGAAA 1237

RESULT 4
 ABV73882
 ID ABV73882 standard; cDNA; 5540 BP.
 XX
 AC ABV73882;
 XX
 DT 08-JAN-2003 (first entry)
 XX
 DE Human anthrax toxin receptor cDNA.
 XX
 KM Anthrax; toxin; receptor; human; TEM8; antibacterial; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 144..1838
 FT FT /*tag= a
 FT sig_peptide 144..224
 FT mat_peptide 225..1838
 FT FT /*tag= b
 FT FT /*tag= c
 PN MO200246228-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 03-OCT-2001; 2001WO-US030941.
 XX
 PR 05-DEC-2000; 2000US-0251481P.
 XX
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX

PI Young JAT, Bradley KA, Collier RJ, Mogridge US;
XX MPI, 2002-713235/77.
DR P-PSDB; ABP54904.
XX Novel isolated polypeptide useful for identifying agent that prevents or
PT reduces effect of anthrax toxin on host cell, for treating human or non-
human animal suffering from anthrax.
XX disclosure; Page 32-37; 45pp; English.
XX
XX The present sequence is that of cDNA encoding a human anthrax toxin
CC receptor (ATR). The cDNA, previously designated TEM8, was originally
CC isolated by PCR from HeLa cell and human placenta cDNA libraries. It was
CC identified in a database screening using a newly isolated human cDNA (see
CC ABV7881) which encodes an ATR (see ABP54903) that is identical to the
CC TEM8 polypeptide except in the cytoplasmic tail, suggesting differential
CC splicing of a primary mRNA transcript. TEM8 was not previously identified
CC as an ATR. The invention provides ATR polypeptides and polynucleotides,
CC host cells, vectors, and transgenic and knock-out animals. It also
CC provides methods for identifying molecules that bind the ATR and which
CC reduce the toxicity of anthrax toxin. A claimed method for treating
CC anthrax in a human or animal involves administering an agent that
CC inhibits binding between anthrax toxin protective antigen (PA) and ATR at
CC a level effective to reduce the severity of anthrax. Suitable agents
CC include the TEM8 polypeptide or a PA-binding fragment of it, a PA-binding
CC polypeptide at least 80% identical to these, a fusion protein, a
CC monoclonal or polyclonal antibody, a polysaccharide, a lipid or a nucleic
CC acid. ATR polynucleotides can also be used in the recombinant production
CC of ATR polypeptides, and as molecular probes
XX
SQ Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other:
Query Match 84.4%; Score 1193.8; DB 6; Length 5540;
Best Local Similarity 99.8%; Pred. No. 2.4e-285;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGAAGCCGCGAGAGAGGCGCCGCGATGGCGGCTCTCTGAGGAGTCTGGGAGTTCCGG 60
DB 41 AGAAGCCGCGAGAGAGGCGCCGCGATGGCGGCTCTCTGAGGAGTCTGGGAGTTCCGG 100
QY 61 AGGCTGGGAGAGAGCGGAGCCCTGCTCCCGGGCTGCGGGCCATGGCCAGCGGAGCG 120
DB 101 AGGCTGGGAGAGAGCGGAGCCCTGCTCCCGGGCTGCGGGCCATGGCCAGCGGAGCG 160
QY 121 GAGAGCCCTCGGATCGGCTTCCAGTGGCTCTCTTTGGCCATCTGTGCTCATCTGCGC 180
DB 161 GAGAGCCCTCGGATCGGCTTCCAGTGGCTCTCTTTGGCCATCTGTGCTCATCTGCGC 220
QY 181 CGGCGAAGGGGAGCGAGGAGATGGGGGCTCCAGCTGCTACCGGCGGATTTGACCTGTA 240
DB 221 CGGCGAAGGGGAGCGAGGAGATGGGGGCTCCAGCTGCTACCGGCGGATTTGACCTGTA 280
QY 241 CTTCAATTTTGGACAAATCAGGAAGTGTGCTGACCACTGGAAATGAATCTATTCTTGT 300
DB 281 CTTCAATTTTGGACAAATCAGGAAGTGTGCTGACCACTGGAAATGAATCTATTCTTGT 340
QY 301 GGAACAGTGTGCTCAAAATTCATCAGCCCAAGTTGAGATGTCTTTATTTGTTTCTC 360
DB 341 GGAACAGTGTGCTCAAAATTCATCAGCCCAAGTTGAGATGTCTTTATTTGTTTCTC 400
QY 361 CACCCGAGGAACAACCTTAATGAATGACAGAAACAGAGACAAATCCGTCAGGCT 420
DB 401 CACCCGAGGAACAACCTTAATGAATGACAGAAACAGAGACAAATCCGTCAGGCT 460
QY 421 AGAAGACTCCAGAAATTCGCAAGAGAGAGACTTAACATGATGAAGATTGAAG 480
DB 461 AGAAGACTCCAGAAATTCGCAAGAGAGAGACTTAACATGATGAAGATTGAAG 520
QY 481 GGCCAGTGAAGATTTATTAAGAAAAGAGAGAGGATACAGAGACAGCGTCATCAT 540
DB 521 GGCCAGTGAAGATTTATTAAGAAAAGAGAGAGGATACAGAGACAGCGTCATCAT 580

QY 541 TGCTTGAATGATGAGAACTCCATGAAGATCTCTTTTCTATTCAGAGAGAGCTTAA 600
DB 581 TGCTTGAATGATGAGAACTCCATGAAGATCTCTTTTCTATTCAGAGAGAGCTTAA 640
QY 601 TAGGTCTGAGATCTTGTGCAATTTTACTGTGTGTGTGAAGAAATTTCAATGAGAC 660
DB 641 TAGGTCTGAGATCTTGTGCAATTTTACTGTGTGTGTGAAGAAATTTCAATGAGAC 700
QY 661 ACAGCTGGCCCGGATTCGGGACAGTAAAGATCATGTGTTCCCGTAAATGACGGCTTCA 720
DB 701 ACAGCTGGCCCGGATTCGGGACAGTAAAGATCATGTGTTCCCGTAAATGACGGCTTCA 760
QY 721 GGCTCTGAAGGATCATCATCAATTTTGAAGAGTCTGTGATGGAATTTAGCAGC 780
DB 761 GGCTCTGAAGGATCATCATCAATTTTGAAGAGTCTGTGATGGAATTTAGCAGC 820
QY 781 TGAACATCCACCATATGTGACAGAGAGTCAATTTCAAGTTGTGTGAGAGAAAAGGCTT 840
DB 821 TGAACATCCACCATATGTGACAGAGAGTCAATTTCAAGTTGTGTGAGAGAAAAGGCTT 880
QY 841 CCGACATGCCCGGACAGTGAAGAGGCTCTGTGACGTTCAAGATCAATGACTCGGTAC 900
DB 881 CCGACATGCCCGGACAGTGAAGAGGCTCTGTGACGTTCAAGATCAATGACTCGGTAC 940
QY 901 ACTCAATGAGAGCCCTTTCTGTGAGAGACCTTAATTTACTGTGTCCAGCGCTATCTT 960
DB 941 ACTCAATGAGAGCCCTTTCTGTGAGAGACCTTAATTTACTGTGTCCAGCGCTATCTT 1000
QY 961 AAAAGAGTTGGATGAGAAAGCTGCACTCCAGGTCAAGATGAAGATGCGCTCTTTTAT 1020
DB 1001 AAAAGAGTTGGATGAGAAAGCTGCACTCCAGGTCAAGATGAAGATGCGCTCTTTTAT 1060
QY 1021 CTCGAGTTCTGTATCATATCAACACACACACTGTGTTGAGAGGTTCCATCTGTGCGCATCCG 1080
DB 1061 CTCGAGTTCTGTATCATATCAACACACACTGTGTTGAGAGGTTCCATCTGTGCGCATCCG 1120
QY 1081 CTTGCTGATCTGTCTTCCTGCTCCAGGCTGTGCTCTCTGTGGGTTCTGGCCCTCTG 1140
DB 1121 CTTGCTGATCTGTCTTCCTGCTCCAGGCTGTGCTCTCTGTGGGTTCTGGCCCTCTG 1180
QY 1141 CTCGACTGTGATTAATCAAGAGAGTCCCTCCAGCCCTGCGAGAGAGTGAAGAAA 1197
DB 1181 CTCGACTGTGATTAATCAAGAGAGTCCCTCCAGCCCTGCGAGAGAGTGAAGAAA 1237
RESULT 5
ABX72029
ID ABX72029 standard; DNA; 5540 BP.
XX
AC ABX72029;
XX
DT 12-MAR-2003 (first entry)
XX
DE DNA encoding human tumour endothelial marker TEM 19.
XX
KW Human; endothelial cell; BC; tumour endothelial cell; TEM; NEM;
KW tumour endothelial marker; normal endothelial marker; PEM;
KW pan-endothelial marker; polycystic kidney disease; psoriasis;
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
KW neovascularization; immune response; cytotoxic; antidiabetic; gene;
KW ophthalmological; antineumatic; antirheumatic; antipsoriatic; ds.
XX
OS Homo sapiens.
XX
PN WO200283874-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US008253.
XX
PR 11-APR-2001; 2001US-0282850P.
XX
PR 06-FEB-2002; 2002US-0354262P.
XX

PA (UYJO) UNIV JOHNS HOPKINS.
 XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
 XX WPI; 2003-093016/08.
 DR P-PSDB; AB054457.
 XX
 XX New purified human transmembrane protein, designated as tumor endothelial
 PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
 PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
 PT psoriasis.
 XX
 XX Disclosure; Page 223-225; 374pp; English.
 XX
 XX The present invention relates to a novel method for the isolation of
 CC endothelial cells (ECs), and the identification of genes expressed in
 CC normal and tumor ECs. Tumour endothelial marker (TEM), normal
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
 CC identified in human ECs. The human EC marker proteins and the
 CC polynucleotide sequences encoding them are useful for detecting,
 CC diagnosing or treating tumours as well as polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
 CC useful for inhibiting neovascularization or tumour angiogenesis, for
 CC inducing an immune response to tumour endothelial cells in a patient, or
 CC for identifying candidate drugs for treating tumours. The present
 CC sequence represents a human TEM or NEM gene of the invention
 XX
 SQ Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
 Query Match 84.4%; Score 1193.8; DB 10; Length 5540;
 Best Local Similarity 99.8%; Pred. No. 2.4e-285;
 Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AGGACCCCGGAGAAAGGCGCCCGATGCGCGTCCCTGAGGTGCTGCGAGTTGCGCG 60
 DB 41 AGGACCCCGGAGAAAGGCGCCCGATGCGCGTCCCTGAGGTGCTGCGAGTTGCGCG 100
 QY 61 AGCGTGGAGAGAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGGCCAGCGGAGCG 120
 DB 101 AGCGTGGAGAGAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGGCCAGCGGAGCG 160
 QY 121 GAGAGCCCTCGGCATCGGCTTCAGTGCTCTTTGGCCACTCTGGTCTCATCTGCGC 180
 DB 161 GAGAGCCCTCGGCATCGGCTTCAGTGCTCTTTGGCCACTCTGGTCTCATCTGCGC 220
 QY 181 CGGGCAAGGGGAGCGAGGAGAGATGGGGTCCAGCTGCTCGGGAGTTGAGCCTGTA 240
 DB 221 CGGGCAAGGGGAGCGAGGAGAGATGGGGTCCAGCTGCTCGGGAGTTGAGCCTGTA 280
 QY 241 CTTCAATTTTGGACAAATCAGAAAGTGTGCTGACCACTGGAATGAATCTAATCTTGT 300
 DB 281 CTTCAATTTTGGACAAATCAGAAAGTGTGCTGACCACTGGAATGAATCTAATCTTGT 340
 QY 301 GGAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGATGCTTTATTTGTTCTC 360
 DB 341 GGAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGATGCTTTATTTGTTCTC 400
 QY 361 CACCCGAGGAACAACCTTATGAAACTGACAGAGACAGAGAACTCCGTCAAGGCTT 420
 DB 401 CACCCGAGGAACAACCTTATGAAACTGACAGAGACAGAGAACTCCGTCAAGGCTT 460
 QY 421 AGAAGAACTCCAGAAAGTCTGCGAGAGAGACACTTACATGATGAAGATTTGAAG 480
 DB 461 AGAAGAACTCCAGAAAGTCTGCGAGAGAGACACTTACATGATGAAGATTTGAAG 520
 QY 481 GGCCAGTAGAGAGATTTATGAAAAACAGACAAAGGTAACAGACAGCCGCTCATCAT 540
 DB 521 GGCCAGTAGAGAGATTTATGAAAAACAGACAAAGGTAACAGACAGCCGCTCATCAT 580
 QY 541 TGGTTGACTGATGAGAACTCATGAATCTCTTTTCTATTCAGAGAGGAGCTTAA 600
 DB 581 TGGTTGACTGATGAGAACTCATGAATCTCTTTTCTATTCAGAGAGGAGCTTAA 640

QY 601 TAGCTCGAGATCTTGGTGCATATGTTACTGTGTGTGTGAAGATTTCAATGAGAC 660
 DB 641 TAGCTCGAGATCTTGGTGCATATGTTACTGTGTGTGTGAAGATTTCAATGAGAC 700
 QY 661 ACAGCTGGCCCGGATTTGGGAGACAGTAAGATCATGTGTTCCCGTGAATGAGCGCTTCA 720
 DB 701 ACAGCTGGCCCGGATTTGGGAGACAGTAAGATCATGTGTTCCCGTGAATGAGCGCTTCA 760
 QY 721 GGCCTGCAAGGACATCATCACTCAATTTTGAAGAAAGTCTGCATGCAATTTCTAGCAGC 780
 DB 761 GGCCTGCAAGGACATCATCACTCAATTTTGAAGAAAGTCTGCATGCAATTTCTAGCAGC 820
 QY 781 TGAACCATTCACCATATGTGACAGAGAGTCAATTTCAAGTTGTGTGAGAGAAAACGGCTT 840
 DB 821 TGAACCATTCACCATATGTGACAGAGAGTCAATTTCAAGTTGTGTGAGAGAAAACGGCTT 880
 QY 841 CCGAATGCCCCCAACGTGAGACAGAGGTCTCTGCAAGCTTCAAGTCAATGACTCGGCTAC 900
 DB 881 CCGAATGCCCCCAACGTGAGACAGAGGTCTCTGCAAGCTTCAAGTCAATGACTCGGCTAC 940
 QY 901 ACTCAATGAGAGCCCTTTTGTGTGAAAGACACTTATTTACTGTGTCCAGCGCTATCTT 960
 DB 941 ACTCAATGAGAGCCCTTTTGTGTGAAAGACACTTATTTACTGTGTCCAGCGCTATCTT 1000
 QY 961 AAAAGAAATTGGCATGAAGAGCTGCACTCCAGGTCAAGATGAAGATGCGCTCTTTTAT 1020
 DB 1001 AAAAGAAATTGGCATGAAGAGCTGCACTCCAGGTCAAGATGAAGATGCGCTCTTTTAT 1060
 QY 1021 CTCGATTTGTGCATCATCATACCAACACACAGTTCTGACGGTTCCATCTGCGCATTCG 1080
 DB 1061 CTCGATTTGTGCATCATCATACCAACACACAGTTCTGACGGTTCCATCTGCGCATTCG 1120
 QY 1081 CCGTGTGATCTGTTCTCTGCTCTCTAGCCCTGAGCTCTCTCTGATGTTCTGCGCCCTCTG 1140
 DB 1121 CCGTGTGATCTGTTCTCTGCTCTCTAGCCCTGAGCTCTCTCTGATGTTCTGCGCCCTCTG 1180
 QY 1141 CTGCACTGTGATTCAGAGAGGTCCTTCACCCCTCTGCGAGAGATGAGAGAAA 1197
 DB 1181 CTGCACTGTGATTCAGAGAGGTCCTTCACCCCTCTGCGAGAGATGAGAGAAA 1237
 RESULT 6
 ABX72003
 ID ABX72003 standard; DNA; 5540 BP.
 XX
 AC ABX72003;
 XX
 DT 12-MAR-2003 (first entry)
 XX
 DE DNA encoding human tumour endothelial marker TEM 8.
 XX
 KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
 KW Tumour endothelial marker; normal endothelial marker; PEM;
 KW pan-endothelial marker; polycystic kidney disease; psoriasis;
 KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
 KW neovascularization; immune response; cytotoxic; antidiabetic; gene;
 KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic; de.
 XX
 OS Homo sapiens.
 XX
 PN WO200283874-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US008253.
 XX
 XX 11-APR-2001; 2001US-0282850P.
 PR 06-FEB-2002; 2002US-0354262P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
 PI

DR WPI: 2003-093016/08.
 DR P-PSDB; ABUS4430.
 XX
 PT New purified human transmembrane protein, designated as tumor endothelial
 PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
 PT polyarthritis kidney disease, diabetic retinopathy, rheumatoid arthritis or
 PT psoriasis.
 XX
 PS Disclosure; Page 117-120; 374pp; English.
 XX
 CC The present invention relates to a novel method for the isolation of
 CC endothelial cells (ECs), and the identification of genes expressed in
 CC normal and tumor ECs. Tumor endothelial marker (TEM), normal
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
 CC identified in human ECs. The human EC marker proteins and the
 CC polynucleotide sequences encoding them are useful for detecting,
 CC diagnosing or treating tumors as well as polyarthritis kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
 CC useful for inhibiting neovascularization or tumor angiogenesis, for
 CC inducing an immune response to tumor endothelial cells in a patient, or
 CC for identifying candidate drugs for treating tumors. The present
 CC sequence represents a human TEM or NEM gene of the invention.
 CC
 SO Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
 Query Match 84.4%; Score 1193.8; DB 10; Length 5540;
 Best Local Similarity 99.8%; Pred. No. 2,46-285;
 Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACCCGCGAGGAGGCGCGGAGTGGCGGCTCCCTGAGGAGGCTGGGAGTTCCGCG 60
 DB 41 AGGACCCGCGAGGAGGCGCGGAGTGGCGGCTCCCTGAGGAGGCTGGGAGTTCCGCG 100
 QY 61 AGCGTGGAGAGAGCGGAGCCTGCTCTCCCGGCGCTCGGCGCAAGCGGAGCG 120
 DB 101 AGCGTGGAGAGAGCGGAGCCTGCTCTCCCGGCGCTCGGCGCAAGCGGAGCG 160
 QY 121 GAGAGCCCTGGGCGCTCGGCTCTCCCTGAGGAGGCTGGGAGTTCCGCG 180
 DB 161 GAGAGCCCTGGGCGCTCGGCTCTCCCTGAGGAGGCTGGGAGTTCCGCG 220
 QY 181 CGGCGAAGGGGAGGAGGAGGAGTGGGCGCTCGGCGCAAGCGGAGTTCCGCG 240
 DB 221 CGGCGAAGGGGAGGAGGAGGAGTGGGCGCTCGGCGCAAGCGGAGTTCCGCG 280
 QY 241 CTTGATTTGGACAATTCAGGAGTGTCTGACCACTGAGTAATCTATTACTTTGT 300
 DB 281 CTTGATTTGGACAATTCAGGAGTGTCTGACCACTGAGTAATCTATTACTTTGT 340
 QY 301 GGAACAGTTGGCTCACAATTCATCAGCCACAGTTGAGAAATGTCCTTATTTGTTCTC 360
 DB 341 GGAACAGTTGGCTCACAATTCATCAGCCACAGTTGAGAAATGTCCTTATTTGTTCTC 400
 QY 361 CACCGGAGGAGCACTTAATGAACTGACAGAGAGAGAAATCCGTCAGAGGCT 420
 DB 401 CACCGGAGGAGCACTTAATGAACTGACAGAGAGAGAAATCCGTCAGAGGCT 460
 QY 421 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACATTAATCATGATGAGATTGAAAG 480
 DB 461 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACATTAATCATGATGAGATTGAAAG 520
 QY 481 GGGCAGTAGAGATTTATTAATGAAACAGACAGAGGATCAGAGACGCGTCATCAT 540
 DB 521 GGGCAGTAGAGATTTATTAATGAAACAGACAGAGGATCAGAGACGCGTCATCAT 580
 QY 541 TGCTTTGATGATGAGAACTCAATGAGATCTGTTTTTCAATTCAGAGAGGAGCTAA 600
 DB 581 TGCTTTGATGATGAGAACTCAATGAGATCTGTTTTTCAATTCAGAGAGGAGCTAA 640
 QY 601 TAGGCTTCGAGATCTTGGTGCATTTGTTTACATGTTGGTGTGAAGAATTTCAATGAGAC 660
 DB 641 TAGGCTTCGAGATCTTGGTGCATTTGTTTACATGTTGGTGTGAAGAATTTCAATGAGAC 700

QY 661 ACAGCTGGCCCGGATTCGCGACAGTAAGATCATGTGTTCCCGTAATGACGCGCTTCA 720
 DB 701 ACAGCTGGCCCGGATTCGCGACAGTAAGATCATGTGTTCCCGTAATGACGCGCTTCA 760
 QY 721 GGGCTTCGAGAGGATCATTCACATTTTGAAGAAATCTGATGAAATTTAGCAGC 780
 DB 761 GGGCTTCGAGAGGATCATTCACATTTTGAAGAAATCTGATGAAATTTAGCAGC 820
 QY 781 TGAACCATCCACATATGTGACAGAGATGATTTCAAGTTGTGTGAGAGAAACGGCTT 840
 DB 821 TGAACCATCCACATATGTGACAGAGATGATTTCAAGTTGTGTGAGAGAAACGGCTT 880
 QY 841 CCGACATGCCCGGACAGTGAAGAGGCTCTGACGCTTCAATCAATCAATCAATCAATCA 900
 DB 881 CCGACATGCCCGGACAGTGAAGAGGCTCTGACGCTTCAATCAATCAATCAATCAATCA 940
 QY 901 ACTCAATGAGAAAGCCCTTTTCTGTGAAAGACATTTATTAAGTGTGACGCGCTATCTT 960
 DB 941 ACTCAATGAGAAAGCCCTTTTCTGTGAAAGATCTTATTTATGTTGTCAGCGCTATCTT 1000
 QY 961 AAAAGAAAGTTGGATGAAAGCTGCACTCCAGGTCAGAGTAAGATGAGGCGCTTTAT 1020
 DB 1001 AAAAGAAAGTTGGATGAAAGCTGCACTCCAGGTCAGAGTAAGATGAGGCGCTTTAT 1060
 QY 1021 CTCAGTTCTGTATCATCAACACACACACTGTTCTGAGGTTCCATCCTGGCCATCGC 1080
 DB 1061 CTCAGTTCTGTATCATCAACACACACTGTTCTGAGGTTCCATCCTGGCCATCGC 1120
 QY 1081 CTTGCTGATCTGTCTGCTGCTGAGCCCTGAGCTTCTCTGTGAGTTGAGCCCTCTG 1140
 DB 1121 CTTGCTGATCTGTCTGCTGCTGAGCCCTGAGCTTCTCTGTGAGTTGAGCCCTCTG 1180
 QY 1141 CTGCACTGTGATTTATCAAGAGGTCCTCCACCCCTCCGAGAGAGTGAAGAAA 1197
 DB 1181 CTGCACTGTGATTTATCAAGAGGTCCTCCACCCCTCCGAGAGAGTGAAGAAA 1237

RESULT 7
 ADR48215
 ID ADR48215 standard; cDNA; 5540 BP.
 XX
 AC ADR48215;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human tumour endothelial marker 8 precursor encoding cDNA SEQ.3.
 XX
 KW pancreatic cancer-associated transcript; pancreatic cancer; human;
 KW cytosolic; gene therapy; protein therapy;
 KW tumour endothelial marker 8 precursor; TEM8; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 144..1838
 FT /tag= a
 FT /product= "tumour endothelial marker 8 precursor (TEM8)"
 PN W02004074510-A1.
 PD 02-SEP-2004.
 XX
 XX 18-FEB-2004; 2004MO-AU000194.
 XX
 XX 18-FEB-2003; 2003AU-00900747.
 XX
 XX (GARV-) GARVAN INST MEDICAL RES.
 XX
 XX Blankin A, Segara D, Henshall S, Sutherland R;
 DR WPI: 2004-635591/61.
 DR P-PSDB; ADR48216.
 XX

PT Detecting pancreatic cancer-associated transcript in a biological sample,
PT useful for diagnosing or treating the disease, comprises contacting the
PT sample with a polynucleotide that selectively hybridizes to a specific
PT sequence.

PS Claim 70; SEQ ID NO 3; 263bp; English.

XX The present invention describes a method for detecting a pancreatic
XX cancer-associated transcript in a biological sample. The method comprises
XX contacting the biological sample with a polynucleotide that selectively
XX hybridizes to a sequence at least 80% identical to a sequence as shown in
XX any one of Tables 3 to 25 in the specification or having the Genbank
XX Accession Number AF279145. Also described: (1) diagnosing pancreatic
XX cancer in a human or animal subject being tested, determining the
XX likelihood that a subject having a pancreatic cancer will survive, or
XX determining the suitability of a subject having a pancreatic cancer for
XX surgical resection therapy; (2) detecting a pancreatic cancer-associated
XX polypeptide in a biological sample; (3) determining the likelihood that a
XX subject having a pancreatic cancer will survive; and (4) monitoring the
XX efficacy of a therapeutic treatment of pancreatic cancer. A pancreatic
XX cancer-associated transcript has cytosolic activity, and can be used in
XX gene and protein therapy. A pancreatic cancer-associated transcript
XX polynucleotide, a vector comprising the polynucleotide, an isolated
XX polypeptide or an antibody that binds to the isolated polypeptide can be
XX used for diagnosing or prognosing pancreatic cancer or for preparing a
XX medicament for the treatment of pancreatic cancer. The prognostic or
XX diagnostic methods are useful for the early detection of pancreatic
XX cancer or its metastases, and for monitoring the progress of disease such
XX as during remission or following surgery or chemotherapy. The present
XX sequence encodes human tumour endothelial marker 8 precursor (Tem8),
XX which is used in the exemplification of the present invention.

SQ Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;

Query Match 84.4%; Score 1193.8; DB 13; Length 5540;

Best Local Similarity 99.8%; Pred. No. 2.4e-285;

Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACCCGCGAGGAGGCGCGGATGCGGCTCCCTGAGGGTCGTGCGAAGTTGGCGG 60
DB 41 AGGACCCGCGAGGAGGCGCGGATGCGGCTCCCTGAGGGTCGTGCGAAGTTGGCGG 100
QY 61 AGCGTGGAGAGAGCGGACCTCTCTCCCGGGCTGCGGGCCATGSCCAACGCGGAGCG 120
DB 101 AGCGTGGAGAGAGCGGACCTCTCTCCCGGGCTGCGGGCCATGSCCAACGCGGAGCG 160
QY 121 GAGAGCCCTCGGATGCGCTTCCAGTGGCTCTTTGGCCACTCTGTCTATCTGCGC 180
DB 161 GAGAGCCCTCGGATGCGCTTCCAGTGGCTCTTTGGCCACTCTGTCTATCTGCGC 220
QY 181 CGGGCAAGGGGAGCGAGGAGATGGGGGTCAGGCTGTAAGGCGAATTTGACCTGTA 240
DB 221 CGGGCAAGGGGAGCGAGGAGATGGGGGTCAGGCTGTAAGGCGAATTTGACCTGTA 280
QY 241 CTTTCATTTTGAACAAATCAAGAAAGTGTCTGCAACACTGGAATGAATCTATTACTTTGT 300
DB 281 CTTTCATTTTGAACAAATCAAGAAAGTGTCTGCAACACTGGAATGAATCTATTACTTTGT 340
QY 301 GGAACAGTTGGCTCAACAAATTCATCAGCCCAAGTTGAAGTCTCTTATTGTTTTTC 360
DB 341 GGAACAGTTGGCTCAACAAATTCATCAGCCCAAGTTGAAGTCTCTTATTGTTTTTC 400
QY 361 CACCGAGGAAACCTTAATGAACCTGACAGAAAGACAGAAACAAATCCGTAAGGCTT 420
DB 401 CACCGAGGAAACCTTAATGAACCTGACAGAAAGACAGAAACAAATCCGTAAGGCTT 460
QY 421 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATGATGAAGATTTGAAAG 480
DB 461 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATGATGAAGATTTGAAAG 520
QY 481 GGCAGTGAAGCATTTTATTAAGAAACAGACAGAGGTACAGACAGCCAGGCTCATCAT 540
DB 521 GGCAGTGAAGCATTTTATTAAGAAACAGACAGAGGTACAGACAGCCAGGCTCATCAT 580

QY 541 TGCCTTGAAGTGAAGAACTCCATGAAGATCTTTTCTATTTCAGAGGAGGCTTA 600
DB 581 TGCCTTGAAGTGAAGAACTCCATGAAGATCTTTTCTATTTCAGAGGAGGCTTA 640
QY 601 TGGCTTCGAGATCTTTGGTGAATTTGTACTGTGTGTGTGAAAGATTTCAATAGAC 660
DB 641 TGGCTTCGAGATCTTTGGTGAATTTGTACTGTGTGTGAAAGATTTCAATAGAC 700
QY 661 ACAGCTGGCCGGATTTGGGAGAGTAAAGATCATGTTTCCCGTAATGACGGCTTTCA 720
DB 701 ACAGCTGGCCGGATTTGGGAGAGTAAAGATCATGTTTCCCGTAATGACGGCTTTCA 760
QY 721 GGCCTGCAAGGATCATCTCAATTTTGAAGAAGTCTCGATGAATTTCTAGCAG 780
DB 761 GGCCTGCAAGGATCATCTCAATTTTGAAGAAGTCTCGATGAATTTCTAGCAG 820
QY 781 TGAACCATCCATCATTTGTGCAAGAGATCATTTTCAAGTTGTCTGAGAGAAACGGCTT 840
DB 821 TGAACCATCCATCATTTGTGCAAGAGATCATTTTCAAGTTGTCTGAGAGAAACGGCTT 880
QY 841 CCGACATGCCCGCAAGTGAAGAGGAGTCTGACAGCTTCAAGATCAATGACTCGCTCAC 900
DB 881 CCGACATGCCCGCAAGTGAAGAGGAGTCTGACAGCTTCAAGATCAATGACTCGCTCAC 940
QY 901 ACTCAATGAAGACCTTTTCTGTGAGAGACATTAATTTACTGTGTCCAGCGCTTATTT 960
DB 941 ACTCAATGAAGACCTTTTCTGTGAGAGATTAATTTACTGTGTCCAGCGCTTATTT 1000
QY 961 AAAAGAGTTGGCATGAAGAAGTGCACATCCAGGTCAAGATGAAGAGTGGCTCTTTTAT 1020
DB 1001 AAAAGAGTTGGCATGAAGAAGTGCACATCCAGGTCAAGATGAAGAGTGGCTCTTTTAT 1060
QY 1021 CTCGAGTTCTGATCATCATCACCACACACACACTGTTTGAAGGTTCCATCTGGCCATGCG 1080
DB 1061 CTCGAGTTCTGATCATCATCACCACACACACTGTTTGAAGGTTCCATCTGGCCATGCG 1120
QY 1081 CCTGTGATCTGTTCTCTGCTCTTACCCCTGAGCTCTCTGTGGTGTCTGGCCCTCTG 1140
DB 1121 CCGTGTGATCTGTTCTCTGCTCTTACCCCTGAGCTCTCTGTGGTGTCTGGCCCTCTG 1180
QY 1141 CTGCACTGTGATTTCAAGAGAGTCCCTCACACCCCTGCGAGAGAGTGAAGAA 1197
DB 1181 CTGCACTGTGATTTCAAGAGAGTCCCTCACACCCCTGCGAGAGAGTGAAGAA 1237

RESULT 8
AD270742
ID AD270742 standard; cDNA; 5540 BP.
AC AD270742;
XX
DT 14-JUL-2005 (first entry)
XX
DE Tumor endothelial marker 8 precursor (Tem8) cDNA.
XX
KW osteopathic; antiarthritic; gene expression; differentiation;
XX transcription; bone disease; osteoarthritis; antiarthritic; osteopathic;
XX musculoskeletal disease; tumor endothelial marker 8 precursor; Tem8; gene;
XX 8.
XX
XX Homo sapiens.
XX OS
XX PN MO2005038022-A1.
XX
XX 28-APR-2005.
XX
XX 20-OCT-2004; 2004MO-JP015879.
XX PF
XX 20-OCT-2003; 2003JP-00359172.
XX PR
XX (TEIJ-) TEIJIN PHARMA LTD.
XX PA (KOMORI) KOMORI T.
PA

XX Komori T, Kanatani N, Yoshida CA, Zama A, Kobayashi S, Yamana K,
 PI MPI; 2005-322866/33.
 DR P-PSDB; AD270743.
 XX
 PT Acquiring chondrogenic differentiation control related gene Runx2/Cbfa1,
 PT by forcibly expressing transcriptional factor related to pathological
 PT condition in cell strain lacking transcriptional factor and screening for
 PT gene.
 XX
 PS Claim 15; SEQ ID NO 27; 357bp; Japanese.
 XX
 CC The invention describes acquiring (M1) a pathological condition related
 CC gene, preferably chondrogenic differentiation control related gene
 CC Runx2/Cbfa1, comprising forcibly expressing a transcriptional factor
 CC related to pathological condition, preferably Runx2/Cbfa1 in a cell
 CC strain or a primary culture cell lacking the transcriptional factor, and
 CC screening for the gene whose expression is induced or suppressed. (M1) is
 CC useful for acquiring a pathological condition related gene, preferably
 CC chondrogenic differentiation control related gene Runx2/Cbfa1.
 CC Polynucleotides detailed in the invention are useful for screening a
 CC preventive and/or therapeutic agent of bone and/or articular disease such
 CC as osteoarthritis. This sequence encodes tumor endothelial marker 8
 CC precursor (Temb) associated with isolation of a pathological condition
 CC related gene.
 CC
 XX Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
 SQ
 Query Match 84.4%; Score 1193.8; DB 14; Length 5540;
 Best Local Similarity 99.8%; Pred. No. 2.4e-285;
 Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACCCGCGAGAGAGGCGCGGATGGCGCTCCCTGAGAGGCTGAGGCGAGTTCCGG 60
 DB 41 AGGACCCGCGAGAGAGGCGCGGATGGCGCTCCCTGAGAGGCTGAGGCGAGTTCCGG 100
 QY 61 AGCGTGGAGAGAGAGCGGACCTCTCTCCCGGCGCTCGGCGCATGGCGAGCGGAGCG 120
 DB 101 AGCGTGGAGAGAGAGCGGACCTCTCTCCCGGCGCTCGGCGCATGGCGAGCGGAGCG 160
 QY 121 GAGAGCCCTCGGCGATCGGCTTCCAGTGGCTCTCTTTGGCCACTGTGGTGCATCTCGC 180
 DB 161 GAGAGCCCTCGGCGATCGGCTTCCAGTGGCTCTCTTTGGCCACTGTGGTGCATCTCGC 220
 QY 181 CGGCGAAGGGGAGCGAGGAGATGGGGTCCAGCCTGCTACGCGCGATTGACTGTA 240
 DB 221 CGGCGAAGGGGAGCGAGGAGATGGGGTCCAGCCTGCTACGCGCGATTGACTGTA 280
 QY 241 CTTCAATTTTGGACAATTCAGAGAGTGTGCTGCACCACTGGAATTAATCTTATCTTTGT 300
 DB 281 CTTCAATTTTGGACAATTCAGAGAGTGTGCTGCACCACTGGAATTAATCTTATCTTTGT 340
 QY 301 GGAACAGTTGGCTCAAAATTCATCAGCCCAAGTGGAGATGCTCTTATTTGTTTCTC 360
 DB 341 GGAACAGTTGGCTCAAAATTCATCAGCCCAAGTGGAGATGCTCTTATTTGTTTCTC 400
 QY 361 CACCCGAGAACCACTTAAATGAATGACAGAGAACAGAACAAATCCGCTCAAGCCT 420
 DB 401 CACCCGAGAACCACTTAAATGAATGACAGAGAACAGAACAAATCCGCTCAAGCCT 460
 QY 421 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATGATGAAGATTGAAAG 480
 DB 461 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATGATGAAGATTGAAAG 520
 QY 481 GGCAGTGAAGAGATTTATTATGAAGAACAGACAGGGTACAGAGCAGCGCTCATCAT 540
 DB 521 GGCAGTGAAGAGATTTATTATGAAGAACAGACAGGGTACAGAGCAGCGCTCATCAT 580
 QY 541 TGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTCTATTCAAGAGAGAGGCTAA 600
 DB 581 TGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTCTATTCAAGAGAGAGGCTAA 640

QY 601 TAGGTCTCGAGATCTTGTCGCAATGTTTACTGTGTGTGTGAAGATTCAATGAGAC 660
 DB 641 TAGGTCTCGAGATCTTGTCGCAATGTTTACTGTGTGTGTGAAGATTCAATGAGAC 700
 QY 661 ACAAGTGGCCCGGATTCGGAGACAGTAAGATCATGTGTTTCCGTCGATGACGGCTTTCA 720
 DB 701 ACAAGTGGCCCGGATTCGGAGACAGTAAGATCATGTGTTTCCGTCGATGACGGCTTTCA 760
 QY 721 GGCTTCGACAGGATCATTCATCAATTTTGAAGAGTCTGATGATGAATTTCTAGAGC 780
 DB 761 GGCTTCGACAGGATCATTCATCAATTTTGAAGAGTCTGATGATGAATTTCTAGAGC 820
 QY 781 TGAACCATCCACCATATGTGTCAGAGAGATGATTTCAAGTTGTGTGAGAGAAACGGCTT 840
 DB 821 TGAACCATCCACCATATGTGTCAGAGAGATGATTTCAAGTTGTGTGAGAGAAACGGCTT 880
 QY 841 CCGACATGCCCGGACGTCGACAGGGTCTCTGCACTTCAAGATCAATGATCTCGGTAC 900
 DB 881 CCGACATGCCCGGACGTCGACAGGGTCTCTGCACTTCAAGATCAATGATCTCGGTAC 940
 QY 901 ACTCAATGAGAGCCCTTTTCTGTGAGAGACATTTATCTGTGTCAGCGCTATCTT 960
 DB 941 ACTCAATGAGAGCCCTTTTCTGTGAGAGATTAATTTATCTGTGTCAGCGCTATCTT 1000
 QY 961 AAAAGAAAGTGGGATGAAAGCTGCACTCCAGTCCAGTCAAGATGAGATGAGCTCTTTAT 1020
 DB 1001 AAAAGAAAGTGGGATGAAAGCTGCACTCCAGTCCAGTCAAGATGAGATGAGCTCTTTAT 1060
 QY 1021 CTCGAGTTCTGTATCATCAACACACACACACTGTTTCAAGGTTCCATCTGCGCATCGC 1080
 DB 1061 CTCGAGTTCTGTATCATCAACACACACACTGTTTCAAGGTTCCATCTGCGCATCGC 1120
 QY 1081 CTGCTCATATCTGTTCTGCTCTCTGAGGCTGCTCTCTCTGAGTTCGAGCCCTCTG 1140
 DB 1121 CTGCTCATATCTGTTCTGCTCTCTGAGGCTGCTCTCTGAGTTCGAGCCCTCTG 1180
 QY 1141 CTGCACTGTATTAATCAAGAGGTCCTCCACCCCTGCGAGAGAGATGAGAGAA 1197
 DB 1181 CTGCACTGTATTAATCAAGAGGTCCTCCACCCCTGCGAGAGAGATGAGAGAA 1237

RESULT 9
 AEA29804
 ID AEA29804 standard; DNA; 5540 BP.
 XX
 AC AEA29804;
 XX
 DT 11-AUG-2005 (first entry)
 XX
 DB DNA encoding a human tumor endothelial marker 8 protein.
 XX
 KW synergistic induction; tumor-associated antigen; vaccine;
 KW tumor endothelial marker 8; immune stimulation; cytostatic; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 144..1838
 FT /*tag= a
 FT /product= "Human tumor endothelial marker 8 protein"
 XX
 PN W02005048943-A2.
 XX
 PD 02-JUN-2005.
 XX
 PP 15-NOV-2004; 2004WO-US038022.
 XX
 PR 13-NOV-2003; 2003US-051948P.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX
 PI Gregor P, Houghton A, Concelti A, Venzani FM;
 XX

XX 17-MAY-2001.
PD 01-NOV-2000; 2000MO-US030045.
PF 05-NOV-1999; 99US-0163581P.
PR 30-JUN-2000; 2000US-0215133P.
XX (HUMA-) HUMAN GENOME SCI INC.
PI Ruben SM, Komatsoulis GA, Moore PA, Birse CE, Ni J;
XX WPI: 2001-308778/32.
DR P-PSDB; AAE01439.
PT New nucleic acid molecules encoding 28 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
PS Claim 1; Page 425-426; 562pp; English.
XX AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted
XX protein genes, and AAE01436-AAE01513 represent the proteins they encode.
CC AAE01514-AAE01544 represent human secreted protein fragments or variants.
CC The genes and their secreted proteins are useful for preventing, treating
CC or ameliorating medical conditions, e.g., by protein or gene therapy.
CC Pathological conditions can be diagnosed by determining the amount of the
CC new protein in a sample or by determining the presence of mutations in
CC the new genes. Specific uses are described for each of the 28 genes,
CC based on the tissues in which they are most highly expressed, and include
CC developing products for the diagnosis or treatment of proliferative
CC disorders, cancer, tumors, foetal and developmental abnormalities,
CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
CC pregnancy-related disorders, endocrine disorders, and infections. The
CC proteins can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues, to identify their cognate ligands or binding
CC partners, and in chemotaxis, and can be used as a food additive or
CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
CC cDNA sequence represents a human secreted protein-encoding cDNA of the
CC invention
XX
SQ Sequence 2447 BP; 673 A; 562 C; 587 G; 625 T; 0 U; 0 Other;
Query Match 84.4%; Score 1193.6; DB 4; Length 2447;
Best Local Similarity 99.7%; Pred. No. 1.9e-285;
Matches 1196; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 AGGACCCCGAGAGAGGCGCCGCGATGCGCGTCCCTGAGAGGCTGATGGAGTTCCGG 60
DB 37 AGGACCCCGAGAGAGGCGCCGCGATGCGCGTCCCTGAGAGGCTGATGGAGTTCCGG 96
QY 61 AGCGTGGAG 120
DB 97 AGCGTGGAG 156
QY 121 GAGAGCCCTGGGATCGGCTTCCAGTGGCTCTCTTTGGGCACTGTGAGTCACTCTGCGC 180
DB 157 GAGAGCCCTGGGATCGGCTTCCAGTGGCTCTCTTTGGGCACTGTGAGTCACTCTGCGC 216
QY 181 CGGCGAAGGGGAG 240
DB 217 CGGCGAAGGGGAG 276

QY 241 CTTCAATTTTGGACAAATCAGAGAGAGTGTCTGACCACTGGAATGAATCTATCTTGT 300
DB 277 CTTCAATTTTGGACAAATCAGAGAGAGTGTCTGACCACTGGAATGAATCTATCTTGT 336
QY 301 GGAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGAAATGCTTTATGTTTTC 360
DB 337 GGAACAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGAAATGCTTTATGTTTTC 396
QY 361 CACCCGAGAGAACAACTTAATGAATCTGACAGAGAGACAGAGAACAAATCCGCAAGCCT 420
DB 397 CACCCGAGAGAACAACTTAATGAATCTGACAGAGAGACAGAGAACAAATCCGCAAGCCT 456
QY 421 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGACCTTACATGATGAAGATTGAAAG 480
DB 457 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGACCTTACATGATGAAGATTGAAAG 516
QY 481 GGCAGTAGAGAGATTTATTTATGAAGACAGACAGAGGTACAGAGACGCCAGCTCAT 540
DB 517 GGCAGTAGAGAGATTTATTTATGAAGACAGACAGAGGTACAGAGACGCCAGCTCAT 576
QY 541 TGCTTTGACGTGATGAGAACTCCATGAGATCTTTCTATTCAGAGAGGAGCTTA 600
DB 577 TGCTTTGACGTGATGAGAACTCCATGAGATCTTTCTATTCAGAGAGGAGCTTA 636
QY 601 TAGGTCGAGATCTTGTGTGCAATGTTTACTGTGTGTGTGAAAGATTTCATGAGAC 660
DB 637 TAGGTCGAGATCTTGTGTGCAATGTTTACTGTGTGTGTGAAAGATTTCATGAGAC 696
QY 661 ACAGCTGGCCCGGATGCGGACAGTAAAGATCATGTTTCCCGTAAATGACGCTTTCA 720
DB 697 ACAGCTGGCCCGGATGCGGACAGTAAAGATCATGTTTCCCGTAAATGACGCTTTCA 756
QY 721 GGTCTGCAAGGATATCATCTCAATTTTGAAGAGCTCTGATGGAATCTATACAC 780
DB 757 GGTCTGCAAGGATATCATCTCAATTTTGAAGAGCTCTGATGGAATCTATACAC 816
QY 781 TGAACCATCAACCATATGTGACAGAGAGTCAATTTCAAGTTGTGTGAGAGAAACGCTT 840
DB 817 TGAACCATCAACCATATGTGACAGAGAGTCAATTTCAAGTTGTGTGAGAGAAACGCTT 876
QY 841 CGGACATGCCCGGACAGTGAAGAGGTCCTCTGACGCTTCAAGATCAATGATCTGGTCA 900
DB 877 CGGACATGCCCGGACAGTGAAGAGGTCCTCTGACGCTTCAAGATCAATGATCTGGTCA 936
QY 901 ACTCAATGAGAAACCTTTTCTGTGAAGACATTTATTAATCTGTCCAGCGCTATCTT 960
DB 937 ACTCAATGAGAAACCTTTTCTGTGAAGATCTTTATTAATCTGTCCAGCGCTATCTT 996
QY 961 AAAAGAAGTTGGATGAAGAGCTGCACTCCAGATCAGCATGAAGATGAGCTCTCTTTAT 1020
DB 997 AAAAGAAGTTGGATGAAGAGCTGCACTCCAGATCAGCATGAAGATGAGCTCTCTTTAT 1056
QY 1021 CTCAGTCTGTGATGATCAACACACACTGTTTGAAGGTTCCATCTCTGCAATCGC 1080
DB 1057 CTCAGTCTGTGATGATCAACACACACTGTTTGAAGGTTCCATCTCTGCAATCGC 1116
QY 1081 CTTGCTGATCTCTGTTCTGCTCTTCAAGCCCTGCTCTCTTGTGATCTTGGCCCTCTG 1140
DB 1117 CTTGCTGATCTCTGTTCTGCTCTTCAAGCCCTGCTCTCTTGTGATCTTGGCCCTCTG 1176
QY 1141 CTGCACTGATATATCAAGAGAGTCCCTCCACCCCTGCGAGAGAGATGAGAGAAATAA 1200
DB 1177 CTGCACTGATATATCAAGAGAGTCCCTCCACCCCTGCGAGAGAGATGAGAGTAAGTGA 1236
RESULT 11
AAD05334
ID AAD05334 standard; cDNA; 2086 BP.
XX AAD05334;
XX AC
XX DT 17-JUL-2001 (first entry)
XX

DE	Human secreted protein-encoding gene 4 CDNA clone HMLFR02, SEQ ID NO:45.
XX	
KW	Human; secreted protein; proliferative disorder; cancer; tumour;
KM	focal abnormality; developmental abnormality; haematopoietic disorder;
KV	immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW	inflammation; allergy; neurological disorder; Alzheimer's disease;
KM	Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KV	skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW	cardiovascular disorder; angiotensin receptor; kidney disorder;
KM	gastrointestinal disorder; pregnancy-related disorder;
KV	endocrine disorder; infection; wound healing; vulnerability; cell culture;
KW	chemotaxis; food additive; gene therapy; binding partner identification;
KM	chromosome 19; SE.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	location/Qualifiers
FT	CDS
FT	166..1377
FT	/tag= a
FT	/product= "Human secreted protein"
FT	/transl_except= (pos:688..690, aa:Xaa)
FT	/transl_except= (pos:1123..1125, aa:Xaa)
FT	/transl_except= (pos:1156..1158, aa:Xaa)
FT	/transl_except= (pos:1267..1269, aa:Xaa)
FT	/note= "Xaa equals any of the twenty naturally occurring L
FT	-amino acids"
FT	166..246
FT	/tag= b
FT	247..1374
FT	/tag= c
FT	/product= "Mature human secreted protein"
PN	WO200134626-A1.
XX	
PD	17-MAY-2001.
XX	
PF	01-NOV-2000; 2000MO-US030045.
XX	
PR	05-NOV-1999; 99US-0163581P.
PR	30-JUN-2000; 2000US-0215133P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Ruben SM, Komatsoulis GA, Moore PA, Blaise CE, Ni J;
DR	WPI; 2001-308778/32.
XX	
PT	New nucleic acid molecules encoding 28 human secreted proteins for
PT	diagnosing, preventing, treating or ameliorating medical conditions and
PT	used as food additives or preservatives.
XX	
PS	Claim 1; Page 449; 562pp; English.
XX	
CC	AAD05300-AA05379 represent cDNAs corresponding to 28 human secreted
CC	protein genes, and AAE01436-AAE01513 represent the proteins they encode.
CC	AAE01514-AAE01544 represent human secreted protein fragments or variants.
CC	The genes and their secreted proteins are useful for preventing, treating
CC	or ameliorating medical conditions, e.g., by protein or gene therapy.
CC	Pathological conditions can be diagnosed by determining the amount of the
CC	new protein in a sample or by determining the presence of mutations in
CC	the new genes. Specific uses are described for each of the 28 genes,
CC	based on the tissues in which they are most highly expressed, and include
CC	developing products for the diagnosis or treatment of proliferative
CC	disorders, cancer, tumours, foetal and developmental abnormalities,
CC	haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC	diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC	neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC	cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC	psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC	angiogenic disorders, kidney disorders, gastrointestinal disorders,
CC	pregnancy-related disorders, endocrine disorders, and infections. The
CC	proteins can also be used to aid wound healing and epithelial cell

CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues, to identify their cognate ligands or binding
CC partners, and in chemotaxis, and can be used as a food additive or
CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
CC present sequence represents a human secreted protein-encoding cDNA of the
CC invention
XX
XX
SQ Sequence 2086 BP; 544 A; 491 C; 538 G; 501 T; 0 U; 12 Other;

Query Match: 84.3%; Score 1192.4; DB: 4; Length 2086;
Best Local Similarity 99.4%; Pred. NO. 3.5e-285;
Matches 1193; Conservative 3; Mismatches 4; Indels 0; Gaps 0

Query Match	84.3%	Score 1192.4	DB 4	Length 2086	
Best Local Similarity	99.4%	Pred. No. 3.5e-285			
Matches 1193	Conservative 3	Mismatches 4	Indels 0	Gaps 0	
QY	1	AGGACCCCGCAGAGAAAGGCGCCGCGATGAGCGGTCCCTTGAGGGTGTGGCGAGTTCCGCG	60		
DB	63	AGGACCCGCGAGAAAGGCGCCGCGATGCGCGTCCCTGAGGGTGTGGCGAGTTCCGCG	122		
QY	61	AGCGTGGGAAAGAGCGGACCTGCTCTCTCCCGGGCTGCGGGCATGCGACGCGGAGG	120		
DB	123	AGCGTGGGAAAGAGCGGACCTGCTCTCTCCCGGGCTGCGGGCGAATGCGCGAGG	182		
QY	121	GAGAGCCCTGGGCTTCGAGCTTCGAGTGGCTCTCTTTGGCCACTCTGATGCTCATCTGCGC	180		
DB	183	GAGAGCCCTGGGCTTCGAGCTTCGAGTGGCTCTCTTTGGCCACTCTGATGCTCATCTGCGC	242		
QY	181	CGGGCAAGGGGAGCGCAGGAGAGATGGGGGTCCAGCTTGCTAGCGCGATTGACTGTGA	240		
DB	243	CGGGCAAGGGGAGCGCAGGAGAGATGGGGGTCCAGCTTGCTAGCGCGATTGACTGTGA	302		
QY	241	CTTCAATTTTGGACAAATCAGGAAGTGTCTGCACACCTGGAATGAAATCTAATTAATCTGT	300		
DB	303	CTTCAATTTTGGACAAATCAGGAAGTGTCTGCACACCTGGAATGAAATCTAATTAATCTGT	362		
QY	301	GGAACAGTTGGCTCCAAATTCATCAGCCACAGTTGGAATGTCTTATTTGTTTCTC	360		
DB	363	GGAACAGTTGGCTCCAAATTCATCAGCCACAGTTGGAATGTCTTATTTGTTTCTC	422		
QY	361	CACCCGAGGAACAACCTTATATGAACTGCACAGAAACAGAGAAACAAATCCGTCAGGCTT	420		
DB	423	CACCCGAGGAACAACCTTATATGAACTGCACAGAAACAGAGAAACAAATCCGTCAGGCTT	482		
QY	421	AGAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGCATGAGAGATTGGAAG	480		
DB	483	AGAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGCATGAGAGATTGGAAG	542		
QY	481	GGCCAGTAGAGATTTATATGAAAACAGACAAAGGGTACAGGACAGCCAGCTCATCAT	540		
DB	543	GGCCAGTAGAGATTTATATGAAAACAGACAAAGGGTACAGGACAGCCAGCTCATCAT	602		
QY	541	TGCTTTGACATATGGAGAACTCCATGAAAGATCTCTTTTCTATTCAGAGAGGAGGCTAA	600		
DB	603	TGCTTTGACATATGGAGAACTCCATGAAAGATCTCTTTTCTATTCAGAGAGGAGGCTAA	662		
QY	601	TAGGCTTCGAGATCTTGGTGCAAATGTATTACTGTGTGGTGTGAAGAATTTCAATGAGAC	660		
DB	663	TAGGCTTCGAGATCTTGGTGCAAATGTATTACTGTGTGGTGTGAAGAATTTCAATGAGAC	722		
QY	661	ACAGCTGGCCCGGATTCGGACAGTAAAGATCATGTGTTCCCGTGAATGACGCGCTTTCA	720		
DB	723	ACAGCTGGCCCGGATTCGGACAGTAAAGATCATGTGTTCCCGTGAATGACGCGCTTTCA	782		
QY	721	GAGCTTCGAAAGCATCATCCCACTCAATTTTGAAGAAAGTCTGATCGAAATTCATGACAG	780		
DB	783	GAGCTTCGAAAGCATCATCCCACTCAATTTTGAAGAAAGTCTGATCGAAATTCATGACAG	842		
QY	781	TGAACCATCCACCAATATGTGCAGAGAGTCAATTTCAAGTTGTCTGTAGAGAAACGCGCTT	840		
DB	843	TGAACCATCCACCAATATGTGCAGAGAGTCAATTTCAAGTTGTCTGTAGAGAAACGCGCTT	902		

Oy		841	CCGACATCCCCCGCAACGTGGAGCAGGGTCTCTGCAGCTTCAAAGATCAAATGA CTGGTCCAC	900
Db		903	CCGACATCCCCCGCAACGTGGAGCAGGGTCTCTGCAGCTTCAAAGATCAAATGA CTGGTCCAC	962
Oy		901	ACTCAATGAGAAGGCCCTTTTCTGTGGAAGACACTTAATTACTGTGTCCAGGCCCTATCTT	960
Db		963	ACTCAATGAGAAGGCCCTTTTCTGTGGAAGATTAATTATTACTGTGTCCAGGCCCTATCTT	1022
Oy		961	AAAAGAACTTGAGCATGAAAGCTGCACCTCCAGGTCCAGTCAGATGAACGATGGCCTCTCTTTAT	1020
Db		1023	AAAAGAACTTGAGCATGAAAGCTGCACCTCCAGGTCCAGTCAGATGAACGATGGCCTCTCTTTAT	1082
Oy		1021	CTCCAGTTCTGTGCATCATCACACACACA CTTGTTCTTCAAGCTTCCAATCCGGGCATCCG	1080
Db		1083	CTCCAGTTCTGTGCATCATCACACACACA CTTGTTCTTCAAGCTTCCAATCCGGGCATCCG	1142
Oy		1081	CCTGCTGATCCGTGTTCTCTGCTCTCTTCAAGCTTCCAATCCGGGCATCCG	1140
Db		1143	CCTGCTGATCCGTGTTCTCTGCTCTCTTCAAGCTTCCAATCCGGGCATCCG	1202
Oy		1141	CTGCACCTGATTTATCAAGAGAGTCCCTCCACCCTCCGAGAGAGTAGAGAAAAATAA	1200
Db		1203	CTGCACCTGATTTATCAAGAGAGTCCCTCCACCCTCCGAGAGAGTAGAGATAAGTA	1262
RESULT 12				
ABV73883	ID	ABV73883	standard; cDNA; 2112 BP.	
XX				
AC		ABV73883;		
XX				
DT		08-JAN-2003	(first entry)	
XX				
DE		Human anthrax toxin receptor cDNA.		
XX				
KM		Anthrax; toxin; receptor; human; antibacterial; gene; ss.		
OS		Homo sapiens.		
XX				
FH		Key	Location/Qualifiers	
FT		CDS	113..1114	
FT			/+tag= a	
FT		s1g_peptide	/product= "anthrax toxin receptor"	
FT			113..193	
FT		mat_peptide	/+tag= b	
FT			194..1111	
FT			/+tag= c	
PN		WO200246228-A2.		
PD		13-JUN-2002.		
XX				
PP		03-OCT-2001; 2001MO-US030941.		
XX				
PR		05-DEC-2000; 2000US-0251481P.		
PA		(WISC) WISCONSIN ALUMNI RES FOUND.		
PI		Young JAT, Bradley KA, Collier RJ, Mogridge JS;		
DR		MPJ; 2002-713335/77.		
DR		P-PsDB; ABPS4905.		
PT		Noval isolated polypeptide useful for identifying agent that prevents or		
PT		reduces effect of anthrax toxin on host cell, for treating human or non-		
PS		human animal suffering from anthrax.		
XX				
XX		Disclosure; Page 39-41; 45pp; English.		
CC		The present sequence is that of cDNA encoding a human anthrax toxin		
CC		receptor (ATR). The cDNA, previously designated IMAGE CLONE 4563020,		
CC		encodes a polypeptide that is identical to amino acids 1-317 of a newly		
CC		identified ATR (see ABPS4904), differing thereafter at the C-terminus. No		

CC function was previously known for this polypeptide, nor was there any
CC prior indication that it is a complete or partial ATR. The invention
CC provides ATR polypeptides and polynucleotides, host cells, vectors, and
CC transgenic and knock-out animals. It also provides methods for
CC identifying molecules that bind the ATR and which reduce the toxicity of
CC anthrax toxin. A claimed method for creating anthrax in a human or animal
CC involves administering an agent that inhibits binding between anthrax
CC toxin protective antigen (PA) and ATR at a level effective to reduce the
CC severity of anthrax. Suitable agents include the 4563020 polypeptide or a
CC PA-binding fragment of it, a PA-binding polypeptide at least 80%
CC identical to these, a fusion protein, a monoclonal or polyclonal
CC antibody, a polysaccharide, a lipid or a nucleic acid. ATR
CC polynucleotides can also be used in the recombinant production of ATR
CC polypeptides, and as molecular probes

Query Match	74.4%	Score 1052.4	DB 6	Length 2112
Best Local Similarity	99.9%	Pred. No. 1.9e-250		
Matches 1053	0	Mismatches 1	Indels 0	Gaps 0

QY 1 AGGACCCGGGAGAGAGGCGCCGCGGATGGCGCGTCCCTGAGGGTCCGTGGCCAGTTCGCGG 60
Dbb 10 AGGACCCGGGAGAGAGGCGCCGCGGATGGCGCGTCCCTGAGGGTCCGTGGCCAGTTCGCGG 69

QY 61 AGCGTGGGAAAGAGAGCGGACCCCTGCTCTCCCGGGCGGCGGCATATGGCCACGGCGGACGC 120

Db 70 AGCGTGGGAAAGAGAGCGGACCCCTGCTCTCCCGGGCGGCGGCATATGGCCACGGCGGACGC 129

QY	122	GAGAGCCCTCGGCATCGGCTTCGATGGCTCTCTTTGGCCACTCTGGTGCATCTGGCG	180
Db	130	GAGAGCCCTCGGCATCGGCTTCGATGGCTCTCTTTGGCCACTCTGGTGCATCTGGCG	189

QY	181	CGGGCAAGGGGGGAGCGCAGGGAGGATGGGGGTCACGCTGTCTACACGGGATTTGACCTGTA	240
	190	CGGGCAAGGGGGGAGCGCAGGGAGGATGGGGGTCACGCTGTCTACACGGGCGATTTGACCTGTA	249
Dbb			

QY	241	CTTCAATTTGGACAACAAATCAGGAGGTGCTGCACCACTGGAGATGAAATCTATTACCTTGT	300
Db	250	CTTCAATTTGGACAACAAATCAGGAGGTGCTGCACCACTGGAGATGAAATCTATTACCTTGT	309

QY 301 GGACAGTGGGCTCAAAATTCATCAGCCACAGTTGAGATGTCCTTATGTGTTCTC 360
310 GGAACAGTGGCTCAAAATTCATCAGCCACAGTTGAGATGTCCTTATGTGTTCTC 369
Db

QY	361	CACCGAGGAAACCTTATGAACTGCAGAGCAGAGAAACAATCCGTCAAGGCT	420
Db	370	CACCGAGGAAACCTTATGAACTGCAGAGCAGAGAAACAATCCGTCAAGGCT	429

QY	422	AGAA	GA	ACTC	CGA	AG	TTCT	GC	CG	AG	AG	GA	CA	CTT	CA	TG	CA	GA	AG	ATT	G	AA	480
Db	430	AGAA	GA	ACTC	CGA	AG	TTCT	GC	CG	AG	AG	GA	CA	CTT	CA	TG	CA	GA	AG	ATT	G	AA	489

QY 481 GGCCAGTACAGATTATATGAACAACAGCAAGGTAACGACACAGCCAGCTCATCAT 540

Db 490 GGCCAGTACAGATTATATGAACAACAGCAAGGTAACGACACAGCCAGCTCATCAT 549

541 TGCCTTGACGATGAGAACTCCATGAGAGATCTCTTTTCTAATTCAGAGAGGGAGCCTAA 600
 550 TGCCTTGACGATGAGAACTCCATGAGAGATCTCTTTTCTAATTCAGAGAGGGAGCCTAA 609

QY TAGGCTCGAGATCTGGTGAATGTTTACGTGTGGTGAAGAATTTCATGAGAC 601
601 TAGGCTCGAGATCTGGTGAATGTTTACGTGTGGTGAAGAATTTCATGAGAC 660
Db 610 TAGGCTCGAGATCTGGTGAATGTTTACGTGTGGTGAAGAATTTCATGAGAC 669

Qy	661	720
ACAGCTGGCCCCGATTCGCGACAGTAAAGATCATGTGTTCCCGTAATGACGGCTTCA		
Db	670	729
ACAGCTGGCCCCGATTCGCGACAGTAAAGATCATGTGTTCCCGTAATGACGGCTTCA		

Qy	721	780
GGCTGCAAGGCATCATCCACTCAATTTTGAAGAGTCCGTCATGAAATTTCTAGCAGC		
Db	730	789
GGCTGCAAGGCATCATCCACTCAATTTTGAAGAGTCCGTCATGAAATTTCTAGCAGC		

QY 781 TGAACCATCCACCATATGTGACAGAGATCATTTCAAGTTGTCGTAGAGAAACGGCTT 840
DB 790 TGAACCATCCACCATATGTGACAGAGATCATTTCAAGTTGTCGTAGAGAAACGGCTT 849
QY 841 CCGACATGCCCCGACAGTGTGACAGAGTCTCTCTGACCTTCAAGATTAATGATCTGGTAC 900
DB 850 CCGACATGCCCCGACAGTGTGACAGAGTCTCTCTGACCTTCAAGATTAATGATCTGGTAC 909
QY 901 ACTCAATGAGAAAGCCCTTTTCTGTGAGAAACATTTATTTACTGTGTCCAGCCCTATCTT 960
DB 910 ACTCAATGAGAAAGCCCTTTTCTGTGAGAAATTAATTTATTTACTGTGTCCAGCCCTATCTT 969
QY 961 AAAAGAGTTGGATGAGAAAGCTGACCTCAAGTCAAGATGAACGATGSCCTCTTTTAT 1020
DB 970 AAAAGAGTTGGATGAGAAAGCTGACCTCAAGTCAAGATGAACGATGSCCTCTTTTAT 1029
QY 1021 CTCAGTTTGTTCATCATCATCACCAACACATCT 1054
DB 1030 CTCAGTTTGTTCATCATCATCACCAACACATCT 1063

RESULT 13
AAAA7455
ID AAAA7455 standard; cDNA, 2272 BP.
XX
XX AAAA7455;
AC
XX
DT 20-OCT-2000 (first entry)
DE Human TANGO 197 coding sequence.
XX
XX TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma;
KM graft versus-host disease; rheumatoid arthritis; psoriasis;
KM inflammatory bowel disease; septic shock; ulcerative colitis;
KM Crohn's disease; chronic myelogenous leukemia; cancer; liver disease;
KM Hodgkin's disease; osteoarthritis; Lyme's disease; cachexia;
KM autoimmune disease; myasthenia gravis; autoimmune diabetes;
KM systemic lupus erythematosus; transgenic animal; diagnosis; prognosis;
KM prophylactic; therapeutic; human; ds.
XX
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH 213. 1214
FT /*tag= a
FT /product= "TANGO 197"
XX
XX
XX WO200039284-A1.
XX
XX
XX PD 06-JUL-2000.
XX
XX PF 23-DEC-1999; 99WO-US031025.
XX
XX PR 30-DEC-1998; 98US-00223546.
XX
XX PA (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Holzman DA;
XX
XX DR WPI; 2000-465743/40.
XX
XX P-PSDB; AAB01422.
PT Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224
PT and 239 polypeptides useful for the treatment of asthma, rheumatoid
PT arthritis, psoriasis and autoimmune diseases.
XX
XX
XX Claim 1; Fig 4; 209pp; English.
XX
XX
XX Nucleic acids encoding TANGO polypeptides are useful as modulating agents
XX for regulating cellular processes like asthma, graft versus-host
XX diseases, rheumatoid arthritis, psoriasis, inflammatory bowel disease,
XX septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous
XX leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis,

CC Lyme's disease, cachexia and autoimmune diseases e.g. myasthenia gravis,
CC autoimmune diabetes and systemic lupus erythematosus. The nucleic acids
CC are also useful for producing transgenic animals and the TANGO
CC polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239
CC sequences are useful in forensic biology, for diagnostic assays.
CC prognostic assays, pharmacogenomics and for monitoring clinical trials.
CC TANGO polypeptides are suitable for both prophylactic and therapeutic
CC methods for treating a subject at risk of a disorder or having a disorder
CC associated with aberrant TANGO expression. A wide range of cellular
CC disorders can be treated
XX
SQ Sequence 2272 BP; 638 A; 554 C; 558 G; 522 T; 0 U; 0 Other;

Query Match 74.4%; Score 1052.4; DB 3; Length 2272;
Best Local Similarity 99.9%; Pred. No. 2e-250;
Matches 1053; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 350 CTTCAATTTTGGCAATCAGAAAGTGTGTGACACACATGGAATTAATTAATCTTGT 409
QY 301 GGAAAGTTGGCTCAAAATTCATCAGCCACAGTTGGAATGTCCTTATTTGTTTCTC 360
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QY 421 AGAAGAACCTCCAGAAAGTTCTGCGAGAGAGACCTTAACATGAGATTTGAAG 480
DB 530 AGAAGAACCTCCAGAAAGTTCTGCGAGAGAGACCTTAACATGAGATTTGAAG 589
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DB 590 GGCCAGTGAAGCATTTTATGAAAGAGCAAGAGGTACAGAGACAGCCAGGTCATAT 649
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DB 710 TAGATCTGAGATCTTGTGCAATGTTTACTGTGTGTGGAAGATTTCAATGAGAC 769
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QY 781 TGAACCATCCACCATATGTGACAGAGATCATTTCAAGTTGTCGTAGAGAAACGGCTT 840
DB 890 TGAACCATCCACCATATGTGACAGAGATCATTTCAAGTTGTCGTAGAGAAACGGCTT 949

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RESULT 14
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XX
DT 22-APR-2004 (first entry)
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KM fusion; von Willebrand factor A-like domain; vWF; antibacterial;
XX cutaneous; inhalation anthrax; human; TANGO 197; ss; gene.
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OS Homo sapiens.
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PN US2003144193-A1.
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PD 31-JUL-2003.
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PF 24-JUL-2002; 2002US-00201292.
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PR 20-DEC-2001; 2001US-00038307.
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PA (OKEE/) O'KEEFE T L.
PA (OZKA/) OZKAYNAK E.
PA (HEAL/) HEALEY J J.
XX
PI Rottman JB, O'Keefe TL, Ozkaynak E, Healey JJ;
XX WPI; 2003-720708/68.
XX DR P-PSDB; AD100534.
XX
XX New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or
XX ameliorating symptoms of anthrax comprises a von Willebrand factor A-like
XX domain (vWF) amino acid sequence and an amino acid sequence heterologous
XX to the vWF.
XX
XX Example; SEQ ID NO 1; 86bp; English.
XX
CC The invention relates to a novel fusion polypeptide comprising a von
CC Willebrand factor A-like domain (vWF) amino acid sequence and an amino
CC acid sequence heterologous to the vWF. The polypeptide of the invention
CC demonstrates antibacterial activities whilst the composition and method
CC may be useful in preventing or ameliorating the symptoms of cutaneous
CC and/or inhalation anthrax. The current sequence is that of the human
CC TANGO 197 cDNA of the invention.
XX
SQ Sequence 2272 BP; 638 A; 554 C; 558 G; 522 T; 0 U; 0 Other;
Query Match 74.4%; Score 1052.4; DB 10; Length 2272;
Best Local Similarity 99.9%; Pred. NO. 2e-250;
Matches 1053; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 410 GGAACAGTTGGCTCACAATAATTCATCAGCCACAGTTGAGAAATGCTTTATTGTTTCTC 469
QY 361 CACCCGAGGAAACAACCTTAATGAACTGACAGAGACAGAGAACAAATCCGTCAAGCCT 420
DB 470 CACCCGAGGAAACAACCTTAATGAACTGACAGAGACAGAGAACAAATCCGTCAAGCCT 529
QY 421 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGAACACTTTCATGCAATGAGATTTGAAG 480
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DB 650 TGCTTTGACTGATGAGAACTCCATGAGATCTTTTCTTATTCAGAGAGGAGCTTA 709
QY 601 TAGGTCTGAGATCTTGTGCAATTTGTTTACTGTGTGTGAGAAAGATTCAATGAGC 660
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QY 721 GGCTTCGAAAGGATCATCTCAATTTTGAAGAAATCTGTGATGAAATTTAGAGC 780
DB 830 GGCTTCGAAAGGATCATCTCAATTTTGAAGAAATCTGTGATGAAATTTAGAGC 889
QY 781 TGAACCATCCACATATATGTCAGAGAGATCAATTTCAAGTTGTGTGAGAGAAACGGCTT 840
DB 890 TGAACCATCCACATATATGTCAGAGAGATCAATTTCAAGTTGTGTGAGAGAAACGGCTT 949
QY 841 CCGACATGCCCCGCAAGCTGGACAGGGCTCTCTGACGTTCAAGTCAATGACTCGGTAC 900
DB 950 CCGACATGCCCCGCAAGCTGGACAGGGCTCTCTGACGTTCAAGTCAATGACTCGGTAC 1009
QY 901 ACTCAATGAGAGAGCCCTTTTCTGTGAGAGACACTTATTATCTGTTCAGCGGCTATCTT 960
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DB 1070 AAAAGAAAGTTGGCATGAAAGCTGCACTCCAGGTTCAGATGACATGAGGCTCTCTTTAT 1129
QY 1021 CTCGAGTTCTGTCTATCATCACACACACTGT 1054
DB 1130 CTCGAGTTCTGTCTATCATCACACACACTGT 1163

RESULT 15
ADMG4567
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ID ADM64567 standard; cDNA; 2272 BP.
 XX
 AC ADM64567;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human von Willebrand factor A-like domain protein TANGO197 cDNA.
 XX
 KW antibacterial; gene therapy;
 KM von Willebrand factor A-like domain amino acid sequence;
 KM vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
 KM inhalation anthrax; human; TANGO197; gene; ss.
 OS Homo sapiens.
 XX
 PN US2003134786-A1.
 XX
 PD 17-JUL-2003.
 XX
 PF 20-DEC-2001; 2001US-00038307.
 XX
 PR 20-DEC-2001; 2001US-00038307.
 XX
 PA (ROTT/) ROTTMAN J B.
 PA (OKEE/) O'KEEFE T L.
 PA (OZKA/) OZKAYNAK E.
 PA (HEAL/) HEALEY J J.
 XX
 PI Rotman JB, O'keefe TL, Ozkaynak E, Healey JJ;
 XX
 DR WPI; 2003-829643/77.
 DR P-PSDB; ADM64568.
 XX
 PT New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or
 PT ameliorating symptoms of anthrax comprises a von Willebrand factor A-like
 PT domain (vWF) amino acid sequence and an amino acid sequence heterologous
 PT to the vWF.
 XX
 PS Disclosure; SEQ ID NO 1; 64pp; English.
 XX
 CC The invention describes a fusion polypeptide comprising a von Willebrand
 CC factor A-like domain (vWF) amino acid sequence and an amino acid sequence
 CC heterologous to the vWF. Also described are: a method of preventing or
 CC ameliorating a symptom of anthrax in a subject thought to be at risk for
 CC exposure to or suspected of having been exposed to Bacillus anthracis;
 CC and a pharmaceutical composition comprising the novel fusion polypeptide.
 CC The composition and method are useful in preventing or ameliorating
 CC symptoms of cutaneous and/or inhalation anthrax. This sequence encodes
 CC human von Willebrand factor A-like domain (vWF) amino acid sequence
 CC TANGO197.
 CC
 SQ Sequence 2272 BP; 638 A; 554 C; 558 G; 522 T; 0 U; 0 Other:
 Query Match 74.4%; Score 1052.4; DB 11; Length 2272;
 Best Local Similarity 99.9%; Pred. No. 2e-250;
 Matches 1053; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AGGACCCGGAGGAAGGCGCCCGGAGTGGCGCTCCCTAGAGGTCTGGCGAGTTGCGG 60
 DB 110 AGGACCCGGAGGAAGGCGCCCGGAGTGGCGCTCCCTAGAGGTCTGGCGAGTTGCGG 169
 QY 61 AGCGTGGAGAGAGGAGCCCTGCTCTCCCGGGGCTGCGGAGCATGGCGAGGAGCG 120
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 QY 361 CACCCGAGAAACAACCTTAATGAATAGACAGAAAGACAGAAACAATCCGCAAGGCT 420
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 DB 530 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATGATGAAGATTGAAG 589
 QY 481 GGCAGTAGCAGATTTTATTTGAAAACAGACAAAGGTACAGGAACAGCCAGGCTCATCT 540
 DB 590 GGCAGTAGCAGATTTTATTTGAAAACAGACAAAGGTACAGGAACAGCCAGGCTCATCT 649
 QY 541 TGCTTTGACTGATGAGAACTCCATGAAGATCTTTTCTATTCAGAGAGGAGGCTTA 600
 DB 650 TGCTTTGACTGATGAGAACTCCATGAAGATCTTTTCTATTCAGAGAGGAGGCTTA 709
 QY 601 TAGGTCTGAGATCTTGGTGCAATTTGTTTACTGTGTGTGTAAGATTTCATGAGAC 660
 DB 710 TAGGTCTGAGATCTTGGTGCAATTTGTTTACTGTGTGTGTAAGATTTCATGAGAC 769
 QY 661 ACAGCTGGCCCGGATTTGGGAGACATGAAGATCATGTGTTCCCGAATGAGAGGCTTCA 720
 DB 770 ACAGCTGGCCCGGATTTGGGAGACATGAAGATCATGTGTTCCCGAATGAGAGGCTTCA 829
 QY 721 GGCTTGGCAAGCATATCATCACTCAATTTTGAAGATCTTCATGAAATTTAGACAGC 780
 DB 830 GGCTTGGCAAGCATATCATCACTCAATTTTGAAGATCTTCATGAAATTTAGACAGC 889
 QY 781 TGAACCATCCACATATGTGACAGAGAGTCATTTCAAGTTGTCTGAGAGGAAACGGCTT 840
 DB 890 TGAACCATCCACATATGTGACAGAGAGTCATTTCAAGTTGTCTGAGAGGAAACGGCTT 949
 QY 841 CCGAATATGCCCGCAACGTGACAGGGTCTCTGACGCTTCMAAGATCATGATCGGTCA 900
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 QY 901 ACTCAATGAGAAAGCCCTTTTCTGTGGAAGACACTTATTTACTGTGTCCAGGCTATCTT 960
 DB 1010 ACTCAATGAGAAAGCCCTTTTCTGTGGAAGATCTTATTTACTGTGTCCAGGCTATCTT 1069
 QY 961 AAAAGAACTGGCATGAAGAGCTGCACTCCAGGTGACATGAACGATGAGTGGCTCTTTTAT 1020
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RESULT 2
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LOCUS
DEFINITION

AK031465 3161 bp mRNA linear HTC 03-APR-2004
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:6030436P19 product:ANTLAX TOXIN RECEPTOR
PRECURSOR (TUMOR ENDOTHELIAL MARKER 8) homolog (Mus musculus), full
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AK031465
AK031465.1 GI:26082340
HTC, CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komori, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
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prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
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AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Saeki, N., Carninci, P.,
Komori, H., Akiyama, J., Nishi, K., Kikunishi, T., Ishihara, H., Itoh, M.,
Yamamoto, R., Matsunaga, S., Hazama, M., Nishibe, T., Harada, A.,
Sumi, N., Ishii, Y., Nakamura, S., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
Yoneda, Y., Iehikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system -384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861

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AUTHORS

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The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 689-690 (2001)

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REFERENCE
AUTHORS

5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
PUBMED
REFERENCE
AUTHORS

6 (bases 1 to 3161)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
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Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
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Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL

Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-ees@gscl.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT

cdna library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>

FEATURES

Source

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Location/Qualifiers
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/dev_stage="13 days embryo"
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/notes="ANTIRAX TOXIN RECEPTOR PRECURSOR (TUMOR ENDOTHELIAL
MARKER 8) homolog [Mus musculus] (SWISSPROT|Q9CZ52,
evidence: FASTA, 100%ID, 84.6%length, match=1428)"
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ORIGIN

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Query Match      60.4%; Score 853.4; DB 4; Length 3161;
Best Local Similarity 87.3%; Pred. No. 1e-196;
Matches 935; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

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RESULT 3
AL542724 1006 bp mRNA linear EST 24-MAR-2004
LOCUS AL542724 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE011YL09
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION AL542724
VERSION AL542724.3 GI:45718299
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1006)
REFERENCE 1. W.B., Gruber, C., Jessee, J., and Polayes, D.
JOURNAL Pull-length cDNA libraries and normalization
COMMENT Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:30548161.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Creteil, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1660.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?b=CS0DE011YL09&id=1660.f.
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FEATURES

Source

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Location/Qualifiers
1..1006
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon.9606"
/clone="CS0DE011YL09"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and EcoRV sites
of the pCMVSPORT 6 vector. Library was not normalized."
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ORIGIN

Query Match 55.0%; Score 778.2; DB 1; Length 1006;
Best Local Similarity 98.9%; Pred. No. 1.8e-178;
Matches 804; Conservative 1; Mismatches 4; Indels 4; Gaps 2;

1 AAGACCCGGAGGAGGAGGCGCGGATGCGGCTCCCTGAGGATGCTGGCGAGTTGCGCG 60
192 AAGACCCGGAGGAGGAGGCGCGGATGCGGCTCCCTGAGGATGCTGGCGAGTTGCGCG 251
61 ACCGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
252 A--GTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 309
121 GAGAGCCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
310 GAGAGCCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 369
181 CGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
370 CGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 429
241 CTTGATTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
430 CTTGATTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 489
301 GGAACGTTGGCTCACAATTCATCAACCCACAGTTGAGAGTCTCTTATTTGTTTCTC 360
490 GGAACGTTGGCTCACAATTCATCAACCCACAGTTGAGAGTCTCTTATTTGTTTCTC 549
361 CACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
550 CACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 609
421 AGAAGAACTCCAGAAAGTTCTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
610 AGAAGAACTCCAGAAAGTTCTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 669
481 GGCAGTGAAGCAGATTTATTTAGAAAACAGACAGAGGTAACAGAGGTAACAGAGGTAACAT 540
670 GGCAGTGAAGCAGATTTATTTAGAAAACAGACAGAGGTAACAGAGGTAACAT 729
541 TGGTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 600
730 TGGTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 789
601 TAGGTCTGAGATCTTGTCAGATTTGTTTACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 660
790 TAGGTCTGAGATCTTGTCAGATTTGTTTACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 849
661 ACAGCTGGCCCGGATTCGGAGCAGTAAGATCATGTTTCCCGTAATGACGGCTTCA 720
850 ACAGCTGGCCCGGATTCGGAGCAGTAAGATCATGTTTCCCGTAATGACGGCTTCA 909
721 GGCTCGCAAGGATATCATCTCAATTTTGAAGAAGTCTGATGGAATTTCTACACG 780
910 GGCTCGCAAGGATATCATCTCAATTTTGAAGAAGTCTGATGGAATTTCTACACG 967
781 TGAACATCCACCATATGTCAGAGAGTCATT 813
968 CTGAACATCCACCATATGTCAGAGAGTCATT 1000

RESULT 4
BM800898 1054 bp mRNA linear EST 05-MAR-2002
LOCUS BM800898
DEFINITION AGENCOURT_6420797 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5541228
5', mRNA sequence.
ACCESSION BM800898
VERSION BM800898.1 GI:19117721
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE Homidae; Homo.
1 (bases 1 to 1054)
AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapdb-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
<http://image.llnl.gov>
Place: LLM12238 row: j column: 13
High quality sequence stop: 595.
Location/Qualifiers
1..1054
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5541228"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NciI;
site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 52.9%; Score 748; DB 3; Length 1054;
Best Local Similarity 97.8%; Pred. No. 4.2e-171;
Matches 790; Conservative 0; Mismatches 15; Indels 3; Gaps 3;

18 GCCCGCGATGGCGGTCCTTGAAGGTCGTGGCGAGTTCCCGAGCGTGGAGGAGCGCG 77
11 GCCCGCGATGGCGGTCCTTGAAGGTCGTGGCGAGTTCCCGAGCGTGGAGGAGCGCG 70
78 ACCGTCTCTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 137
71 ACCGTCTCTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 130
138 GCTTCAGTGGCTCTCTTTGGCCACTGTGCTCATCTGCGCCCGGAGGAGGAGGAGGAGGAGGAG 197
131 GCTTCAGTGGCTCTCTTTGGCCACTGTGCTCATCTGCGCCCGGAGGAGGAGGAGGAGGAGGAG 190
198 GGAAGATGGGGGTCGAGCTGCTAGCGGAGATTGAACCTGATCTTATTTGAGCAAAAT 257
191 GGAAGATGGGGGTCGAGCTGCTAGCGGAGATTGAACCTGATCTTATTTGAGCAAAAT 250
258 CAGAAAGTGTGTCGACCACTGAATGAATCTATTAATTTGAGAAAGTTGGCTCACA 317
251 CAGAAAGTGTGTCGACCACTGAATGAATCTATTAATTTGAGAAAGTTGGCTCACA 310
318 AATTGATGACCCACAGTTGAGATGTCCTTATTTGTTTCTCCACCAGAGAAACAACCT 377
311 AATTGATGACCCACAGTTGAGATGTCCTTATTTGTTTCTCCACCAGAGAAACAACCT 370
378 TATGAAATGTCAGAAAGCAGAAACAATTCCTGCAAGGCTTGAAGAACTCCAGAAAG 437
371 TATGAAATGTCAGAAAGCAGAAACAATTCCTGCAAGGCTTGAAGAACTCCAGAAAG 430
438 TTCTGCGAGAGAGGAGCACTTCATGATGAGAGATTGAAAGGCGCAGTGAAGATTT 497
431 TTCTGCGAGAGAGGAGCACTTCATGATGAGAGATTGAAAGGCGCAGTGAAGATTT 490
498 ATTATGAAACAGACAGAGGTAACAGACAGCCAGGCTCATCTTGTGATGATGAG 557
491 ATTATGAAACAGACAGAGGTAACAGACAGCCAGGCTCATCTTGTGATGATGAG 550
558 AACTCATGAATCTCTTTTCTATTTCCAGAGGAGGCTAATAGTCTCGAGATCTTG 617

Dd	551	AACTCATGAAAGATCTCTTTTCTATTTCAGAGAGGGAGGCTTAATAAGCTCGAATCTTG	610			
Oy	618	GTCGAATTGTACTGTTGGTGGTGTGAAAAGATTTCATAGAGACAACAGTGGCCGGATTG	677			
Dd	611	GTGCAGATTGTTACTGTTGGTGGTGTGAAAAGATTTCATAGAGACAACAGTGGCCGGATTG	670			
Oy	678	CGAGACGTAGAAGATCATGTGTTTCCCCTGGAATGACGGCTTTCAGGCTTCGMAAGCATCA	737			
Dd	671	CGGACAGTAGAGATCATGTGTTTCCCCTGGAATGACGGCTTTCAGGCTTCG-AGGGATCA	729			
Oy	738	TCCACTCAATTTGGAAGAGTCCCGCATCGAAATTCAGACGCTGAACCATCCACCAT-A	796			
Dd	730	TCCACTCCAGTTTAAAGAGTCCCGCATCGAAATTCAGCGGTTGAACATCCCCCATGA	789			
Oy	797	TGTGCA-GGAGAGTCATTTCAAGTTGTC	823			
Dd	790	TGTGAGGAGAGACATTTCCACGGTGC	817			
RESULT 5	B1823853	878 bp	mRNA linear EST 04-OCT-2001			
LOCUS	B1823853					
DEFINITION	603039031P1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5179974 5', mRNA sequence.					
ACCESSION	B1823853					
VERSION	B1823853.1	GI:15935416				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 878) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMN at: http://image.llnl.gov Plate: L1AM11448 row: n column: 07 High quality sequence stop: 804. Location/Qualifiers					
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/db_xref="taxon:9606"						
/clone="IMAGE:5179974"						
/lab_host="DH10B"						
/clone_1lb="NIH MGC_115"						
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: This is a NIH_MGC Library."						
ORIGIN						
Query Match	52.4%	Score 740.6;	DB 3; Length 878;			
Best Local Similarity	95.4%;	Pred. No. 2.6e-169;				
Matches	839;	Mismatches 29;	Indels 11; Gaps 7;			
48	GGCAGATTGGCGAGCGTGGGAAGAGCGGACCTGCTCTCCCGGCGCTGCCGCGCCATGG		107			

Db	1	GGCAGATTCCGGAGCGCTGGGAAAGAGCGGAGCCCTGCTCTCCCGGCGCTCGGGCCATCG	60
QY	108	CCACGCGCGAGCGGAGAGCCCTCGGCATTCGGCTTCCAGTGGCTCTCTTTGGCCACTCTGG	167
Db	61	CCACGCGCGGAGCGGAGAGCCCTCGGCATTCGGCTTCCAGTGGCTCTCTTTGGCCACTCTGG	120
QY	168	TGCTCATCTCGCGCGGGCGAAGGGGAGCGAGGGAGAGTGGGGGGTCCAGCCGTCTACGGCG	227
Db	121	TGCTCATCTCGCGCGGGCGAAGGGGAGCGAGGGAGAGTGGGGGGTCCAGCCGTCTACGGCG	180
QY	228	GATTTCGACTGTACTTCAATTTTGGACAATTCAGGAGTGTGTCTGACCACTGTGAAATGAA	287
Db	181	GATTTCGACTGTACTTCAATTTTGGACAATTCAGGAGTGTGTCTGACCACTGTGAAATGAA	240
QY	288	TCTATTAATCTTGTGGAAACAGTTGGCTCAACAATTCATCAGCCCAAGTTGAAATGTCT	347
Db	241	TCTATTAATCTTGTGGAAACAGTTGGCTCAACAATTCATCAGCCCAAGTTGAAATGTCT	300
QY	348	TTATTTGTTTTCTCCACCCGAGAAACAACCTTAATGAAACTGACGAGAGACAGAGAACAA	407
Db	301	TTATTTGTTTTCTCCACCCGAGAAACAACCTTAATGAAACTGACGAGAGACAGAGAACAA	360
QY	408	TCCGTCAAGGCGCTTGAAGAAGCTCCAGAAAGTTCTGCAGAGAGAGACACTTACATGATG	467
Db	361	TCCGTCAAGGCGCTTGAAGAAGCTCCAGAAAGTTCTGCAGAGAGAGACACTTACATGATG	420
QY	468	AAGGATTTGAAAGGCGCAGTAGAGAGATTTATATGAAACAGACAAAGGTTACAGACAG	527
Db	421	AAGGATTTGAAAGGCGCAGTAGAGAGATTTATATGAAACAGACAAAGGTTACAGACAG	480
QY	528	CCAGCGTCATATTCGCTTTTGACTATGAGAACTCCCATGAAAGATCTTTTTCATATCAG	587
Db	481	CCAGCGTCATATTCGCTTTTGACTATGAGAACTCCCATGAAAGATCTTTTTCATATCAG	540
QY	588	AGAGGGAGGCGCTAATAGGCTCGAGATCTTGGTGCATTTGTTACTGTGTGTGTAAG	647
Db	541	AGAGGGAGGCGCTAATAGGCTCGAGATCTTGGTGCATTTGTTACTGTGTGTGTAAG	599
QY	648	ATTTCATATGAGACACAGCTGGCCCGGATTCGGGACAGTAAGATCATGTGTTTCCGTGA	707
Db	600	ATTTCATATGAGACACAGCTGGCCCGGATTCGGGACAGTAAGATCATGTGTTTCCGTGA	659
QY	708	ATGACGGCTTTCAAGGCTCTGCAAGGATCATTCCACTCAATTTTG-AAGAACTCCTGCATC	766
Db	660	ATGACGGCTTTCAAGGCTCTGCAAGGATCATTCCACTCAATTTTGAAAGAAAGATCCTGCATC	719
QY	767	-GAATTCACACACTGAAACCATCACCATATATGACAGAGAGATC-ATTTCAGATTGCG	824
Db	720	GGAATTCACACACTGAAACCATCACCATATATGACAGAGAGATCATTTCAGATTGCG	779
QY	825	TGAGAGG--AAACGGCTTCCGACATGCGCG--CAAGCTGACAGAGG--TCCTCTGCAGC	877
Db	780	TGAGAGGGAACCGGTTTCCGACATGCGCGGCAACGTCGACAGAGGTCCTTTGGAGGT	839
QY	878	TTCAAGATCAATGACTCGGTCACACTCAATGAGAACCC	916
Db	840	TTCCAGATCATGACTCGGTCACACTCAATGAGAACCC	878
RESULT 6			
LOCUS	CX872420	744 bp	linear
DEFINITION	HEBSC4.68.H01.g1.A037.NIH.MGC.262.Homo.sapiens.cDNA clone		EST 03-FEB-2005
ACCESSION	CX872420		
VERSION	CX872420.1	GI:58555594	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homnidae; Homo.		
REFERENCE	1 (bases 1 to 744)		

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NIH
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: BresaGen, Inc.
 cDNA Library Preparation: Express Genomics, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
 University of Georgia
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Place: LLNL5815 row: p column: 02
 Seq primer: JENREV (CAGGAACAGCTATGACC)
 High quality sequence stop: 744.
 Location/Qualifiers

FEATURES

source

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1..744
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7487092"
/sex="male"
/tissue_type="embryonic stem"
/cell_type="human embryonic stem cells"
/cell_line="BG01"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_1ib="NIH_MGC_262"
/notes="Vector: pExpress-1; Site 1: NotI; Site 2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos and
differentiated to an early neural progenitor cell type.
Cell line id and NIH Registry designation is BG01.
Positive for Nestin and Musashi expression. Passage number
18. cDNA primed using oligo-dT primer:
5'-pGACGTGCTTACATGCGCGAGCGCGCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. This primary library
is non-normalized (normalized primary library is
NIH_MGC_259). It was constructed by Express Genomics
(Federick, MD). Sequence ends have been trimmed to
exclude vector and regions below phred quality 16. Note:
this is a Mammalian Gene Collection library."

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ORIGIN

Query Match 50.7%; Score 717; DB 8; Length 744;
 Best Local Similarity 100.0%; Pred. No. 1.4e-163;
 Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AGGACCGGAGGAGAGGCGCGGATGCGGCTCCCTAGAGGTGCGGAGTTGGCGG 60
DB 28 AGGACCGGAGGAGAGGCGCGGATGCGGCTCCCTAGAGGTGCGGAGTTGGCGG 87
QY 61 AGCGTGGAGAGAGCGGAGCTCTCCCGGGGCTGCGGGCCATGCGCAGCGCGAGG 120
DB 88 AGCGTGGAGAGAGCGGAGCTCTCCCGGGGCTGCGGGCCATGCGCAGCGCGAGG 147
QY 121 GAGAGCCTCGGAGATCGGCTTCAGTGGCTCTTTGGCCACTCTGGTGCATCTGGCC 180
DB 148 GAGAGCCTCGGAGATCGGCTTCAGTGGCTCTTTGGCCACTCTGGTGCATCTGGCC 207
QY 181 CGGGCAAGGGGAGCGAGAGATGGGGTCCAGCTCTACGGGGATTGACCTGTA 240
DB 208 CGGGCAAGGGGAGCGAGAGATGGGGTCCAGCTCTACGGGGATTGACCTGTA 267
QY 241 CTTTCATTTTGGACAATTCAGAGAGTGTGTCACCACTGGAATGAATCTATTACTTTGT 300
DB 268 CTTTCATTTTGGACAATTCAGAGAGTGTGTCACCACTGGAATGAATCTATTACTTTGT 327
QY 301 GGAACAGTTGGCTCACAATTCATCAAGCCCAAGTTGAAGATGCTTTATGTTTTCTC 360

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DB 328 GGAACAGTTGGCTCACAATTCATCAAGCCCAAGTTGAAGATGCTTTATGTTTTCTC 387
QY 361 CACCCGAGGAACAACCTTAATGAAGTGAACAGAGAGAGAAACAATCCGTCAGAGCCT 420
DB 388 CACCCGAGGAACAACCTTAATGAAGTGAACAGAGAGAGAAACAATCCGTCAGAGCCT 447
QY 421 AGAAGACTCCAGAAAGTTTCCGAGAGAGACACTTAATCATGATGAGATTTGAAG 480
DB 448 AGAAGACTCCAGAAAGTTTCCGAGAGAGACACTTAATCATGATGAGATTTGAAG 507
QY 481 GGGCAGTACAGAGATTTTATGAACAAGAGAGAGTACAGAGCAGGTCATCAT 540
DB 508 GGGCAGTACAGAGATTTTATGAACAAGAGAGTACAGAGCAGGTCATCAT 567
QY 541 TGCTTTGACTGATGAGAGATTCATGAGATCTCTTTTCTTATTCAGAGAGGAGCTTAA 600
DB 568 TGCTTTGACTGATGAGAGATTCATGAGATCTCTTTTCTTATTCAGAGAGGAGCTTAA 627
QY 601 TAGGTCCTGAGATCTTGGTGCAATTTGTTTACTGTGTGTGTAAGATTTCAATGAGAC 660
DB 628 TAGGTCCTGAGATCTTGGTGCAATTTGTTTACTGTGTGTGTAAGATTTCAATGAGAC 687
QY 661 ACAAGTGGCCCGGAGATTTGGGACAGTAAGATCATGTTTCCCGAATGAGGCTT 717
DB 688 ACAAGTGGCCCGGAGATTTGGGACAGTAAGATCATGTTTCCCGAATGAGGCTT 744

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RESULT 7

CO245219

LOCUS CO245219 833 bp mRNA linear EST 23-JUN-2004
 DEFINITION AGENCOURT_26524177 NIH_MGC_212 Homo sapiens cDNA clone
 IMAGE:30924322 5', mRNA sequence.

ACCESSION

CO245219

VERSION CO245219.1 GI:49108057
 EST.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

Organism Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE

1 (bases 1 to 833)

NIH-MGC <http://mgc.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Daniela S. Gerhard, Ph.D.

COMMENT Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Mary Hendrix
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDAM1166 row: j column: 11
 High quality sequence start: 6
 High quality sequence stop: 688.
 Location/Qualifiers

FEATURES

source

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/clone="IMAGE:30924322"
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/lab_host="DH10B (T1 phage resistant)"
/clone_1ib="NIH_MGC_212"
/notes="Organ: Lung; Vector: pYX-Asc; Site 1: EcoR I;  

Site 2: Not I; The library was constructed according  

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  

1996. Denatured RNA was size fractionated on a 1% agarose  

gel. First strand cDNA synthesis was primed with oligo-dT

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Db 431 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGACCTTACATGATGAAGATTCCGAAG 490
Qy 481 GGCCAGTAGAGATTTATTATGAAGAAAGAGAGAGGTAACAGAGACGCCAGGTCATCAT 540
Db 491 GGCCAGTAGAGATTTATTATGAAGAAAGAGAGGTAACAGAGACGCCAGGTCATCAT 550
Qy 541 TCGCTTGAAGTGAAGAACTCCATGATCTCTTTTCTATTTCAGAGAGGAGGCTTA 600
Db 551 TCGTTTGAAGTGAAGAACTCCATGATCTCTTTTCTATTTCAGAGAGGAGGCTTA 610
Qy 601 TAGGCTTCAGATCTGGTGCAATTTGTTACTGTGTGGTGGAAGATTTCAATGAGC 660
Db 611 TAGGCTTCAGATCTGGTGCAATTTGTTACTGTGTGGTGGAAGATTTCAATGAGC 670
Qy 661 ACAGCTGAGCCGAGATTCGAGACAGTAAGATCATGTGTTCCGTAATGAGCGCTTCA 720
Db 671 AAGTTTGGCC--GGATCCGACAGTAAGATCATGTGTTCCGTAATGAGCG--TTTA 726
Qy 721 GGCTTCGAAGGATCATCTCACTCAATT 748
Db 727 AGATTCGAAGGATCATCTCACTCAATT 754

RESULT 9
Bg281561 820 bp mRNA linear EST 21-FEB-2001
LOCUS 602402412F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4544691 5',
DEFINITION mRNA sequence.

ACCESSION BG281561
VERSION BG281561.1 GI:13030486
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 820)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: ATCC/DC/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: LNCM1228 row: h column: 04
High quality sequence stop: 815.

FEATURES
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/clone="IMAGE:4544691"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 48.5%; Score 685.6; DB 2; Length 820;
Best Local Similarity 96.6%; Pred. No. 6.5e-156;
Matches 786; Conservative 0; Mismatches 19; Indels 9; Gaps 8;

Qy 1 AGAACCCGAGAGAAAGGCCCGAGTGGCGGCTCTGAGGGGTCTGGCGAGTTTCGCG 60
Db 9 AGAACCCGAGAGAAAGGCCCGAGTGGCGGCTCTCTGAGGGGTCTGGCGAGTTTCGCG 68
Qy 61 AGCGTGGAG 120
Db 69 AGCGTGGAG 128
Qy 121 GAGAGCCCTCGGATCGGCTTCCAGTGGCTCTCTTTGGGCACTCTGTGCTCATCTGCGC 180
Db 129 GAGAGCCCTCGGATCGGCTTCCAGTGGCTCTCTTTGGGCACTCTGTGCTCATCTGCGC 188
Qy 181 CGGGAG 240
Db 189 CGGGAG 248
Qy 241 CTTCAATTTTGAAGAAATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
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Qy 301 GGAACAGTT--GGCTCAAAATTCATCAGCCCAAGTTGAGATGCTCT--TTATTGTTT 357
Db 309 GGAACAGTTGGGTTCAATTTTCATCAGCCCAAGTTGAGATGCTCTCTTATATGCTTTT 368
Qy 358 CTCCACCCGAG 417
Db 369 CTCCACCCGAG 428
Qy 418 CTTAG 477
Db 429 CTTAG 488
Qy 478 AAGGCGCAGTGAAGAGATTTATT--ATGAAAACAGAGAGAGAGAGAGAGAGAGAGAGAG 536
Db 489 AAGGCGCAGTGAAGAGATTTATT--ATGAAAACAGAGAGAGAGAGAGAGAGAGAGAGAG 548
Qy 537 TCATTGCTTTGACTGATGAG 596
Db 549 TCATTGCTTTGACTGATGAG 608
Qy 597 CTAATAGGCTTCGAGATCTTGATGCAATTTGTTTACTGTCTTGGTGGA--AAATTCAT 655
Db 609 CTAATAGGCTTCGAGATCTTGATGCAATTTGTTTACTGTGTGTAAGAGAGAGAGAGAGAG 668
Qy 656 GAGACAG 714
Db 669 GAGACAG 728
Qy 715 CTTGAGGCTTCGAG 774
Db 729 TTTGAGGCTTCG--AGGATCATCATCAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAG 786
Qy 775 AGCAGTGAACCATCCACATATGTGCGAGAGAG 808
Db 787 AGCAGTGAACCATCA--CATATGTGCGAGAGAGAG 819

RESULT 10
AK013005 1614 bp mRNA linear HTC 03-APR-2004
LOCUS AK013005
DEFINITION Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2810405N18 product:ANTPAX TOXIN RECEPTOR
PRECURSOR (TUMOR ENDOTHELIAL MARKER 8) homolog [Mus musculus], full
insert sequence.
ACCESSION AK013005
VERSION AK013005.1 GI:12850099
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1

[illegible][illegible]

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Db      542 AAGCCCTTGTGTGGAGACACTTATTGTGTGCCAGACACCAATCTTGAAGAAGTT 601
Qy      971 GGCATGAAGCTGCACTCCAGGTCAGACATGAACGAGGGCTCTTTTATCCAGTTCT 1030
Db      602 GGCATGAAGCTGCACTCCAGGTCAGACATGAACGAGGGCTCTTTTATCCAGTTCT 661
Qy      1031 GTCATCATCAACCAACCACTGTTTGAAGGTTCCATCCATCCGCCCTGCTGATC 1090
Db      662 GTCATCATCAACCAACCACTGTTTGAAGGTTCCATCCATCCGCCCTGCTGATC 721
Qy      1091 CTGTTCTGCTCTAGCCCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1150
Db      722 CTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 781
Qy      1151 ATTATCAAGAGGTCCTCCACCCCTGCGCAGAGAGTGAAGGAAA 1197
Db      782 ATCATCAAGAGGTCCTCCACCCCTGCTGAGAGAGTGAAGGAGA 828

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RESULT 11
CP126791      780 bp      mRNA      linear      EST 05-AUG-2003
LOCUS      UI-HF-ET0-65V-O-15-0-UI.r1 NIH_MGC_214 Homo sapiens cDNA clone
DEFINITION      IMAGE:30560510 5', mRNA sequence.
ACCESSION      CP126791
VERSION      CP126791.1 GI:33204381
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 780)
Normalisation and subtractions: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Mary Hendrix
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/humanfl.html
Seq primer: pyx-5.

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Location/Qualifiers
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/clone="IMAGE:30560510"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/lab_host="DH10B (T1 phage resistant)"
/clone_1ib="NIH_MGC_214"
/notes="Organ: Lung; Vector: pyx-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction. ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATTAAGGCCA. Tissue was provided by Mary Hendrix."

```

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Tissue Procurement: Mary Hendrix
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/humanfl.html
Seq primer: pyx-5.

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ORIGIN

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Query Match      45.6%; Score 644.4; DB 6; Length 780;
Best Local Similarity 99.8%; Pred. No. 7.2e-146;
Matches 645; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      135 AGGACCCCGGAGAAAGGCGCGCGGATGCGGCTCCCTGAGGCTGTGCGAGTTGCGG 194
Qy      61 AGCCTGGAGAGAGAGGAGACCTGCTCTCCCGGGGCTGCGGGCCATGAGCCAGCGGAGG 120
Db      195 AGCCTGGAGAGAGAGGAGACCTGCTCTCCCGGGGCTGCGGGCCATGAGCCAGCGGAGG 254
Qy      121 GAGAGCCCTCGGCAATCGGCTTCAGTGGCTCTCTTGGCCACTGCTGCTCATCTGCGC 180
Db      255 GAGAGCCCTCGGCAATCGGCTTCAGTGGCTCTCTTGGCCACTGCTGCTCATCTGCGC 314
Qy      181 CGGGCAAGGGGAGCGCAGGAGGATGGGGGTCCAGCTGCTCAAGCGGATTTGACCTGTA 240
Db      315 CGGGCAAGGGGAGCGCAGGAGGATGGGGGTCCAGCTGCTCAAGCGGATTTGACCTGTA 374
Qy      241 CTTCAATTTTGGACAATCAGAAAGTGTGCTGACCACTGGAGTGAATCTATTAATCTTCT 300
Db      375 CTTCAATTTTGGACAATCAGAAAGTGTGCTGACCACTGGAGTGAATCTATTAATCTTCT 434
Qy      301 GGAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAATGTCCTTATTGTTTCTC 360
Db      435 GGAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAATGTCCTTATTGTTTCTC 494
Qy      361 CACCGAGAGAACACCTTAATGAAACCTGACAGAGACAGAGAACAAATCCGTCAAGCCT 420
Db      495 CACCGAGAGAACACCTTAATGAAACCTGACAGAGACAGAGAACAAATCCGTCAAGCCT 554
Qy      421 AGAAGAACTCCGAAAGTTCTGCGCAGAGAGAACCTTCATGCAATGAGATTTGAAG 480
Db      555 AGAAGAACTCCGAAAGTTCTGCGCAGAGAGAACCTTCATGCAATGAGATTTGAAG 614
Qy      481 GGCAGTAGAGCATTTATTATGAAACAGACAAAGGTCAGAGACAGCGGCTCATCAT 540
Db      615 GGCAGTAGAGCATTTATTATGAAACAGACAAAGGTCAGAGACAGCGGCTCATCAT 674
Qy      541 TCGTTGACTGATGAGAACTCCATGAGATCTTTTCTATTCAGAGGAGGCTTAA 600
Db      675 TCGTTGACTGATGAGAACTCCATGAGATCTTTTCTATTCAGAGGAGGCTTAA 734
Qy      601 TAGGTCGAGATCTTGGCAATGTTTACTGCTGTGTGTGAAA 646
Db      735 TAGGTCGAGATCTTGGCAATGTTTACTGCTGTGTGTGAAA 780

```

```

RESULT 12
BE741333      725 bp      mRNA      linear      EST 15-SEP-2000
LOCUS      601594179F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948114 5',
DEFINITION      mRNA sequence.
ACCESSION      BE741333
VERSION      BE741333.1 GI:10155125
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 725)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga@bhs-remail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

```


DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at: Image.lim.gov
 Plate: L1CMB10 row: n column: 19
 High quality sequence stop: 711.
 Location/Qualifiers

FEATURES

Source

1..725
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3948114"
 /issue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NIH_MGC_9"
 /note="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Size selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 45.1%; Score 637.8; DB 2; Length 725;
 Best Local Similarity 98.8%; Pred. No. 2.9e-144;
 Matches 653; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 395 GACGAGAGAACAAATCCGTCAGAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGAC 454
 1 GACGAGAGAACAAATCCGTCAGAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGAC 60
 QY 455 ACTTACATGATGAGAGATTGAAAAGGCCAGTGAAGATTTATTGAAAACAGACAA 514
 61 ACTTACATGATGAGAGATTGAAAAGGCCAGTGAAGATTTATTGAAAACAGACAA 120
 QY 515 GGGTACAGGACAGCAGCTCATGTTGCTTGAATGAGAACTCCATGAAGATCTC 574
 121 GGGTACAGGACAGCAGCTCATGTTGCTTGAATGAGAACTCCATGAAGATCTC 180
 QY 575 TTTTCTATTGAGAGAGAGGCTTAATAGTCTCGAATCTTGGTGAATTTGTTACTGT 634
 181 TTTTCTATTGAGAGAGAGGCTTAATAGTCTCGAATCTTGGTGAATTTGTTACTGT 240
 QY 635 GTTGTGTGAAGAATTTCAATGAGACACAGCTGCCGATGGGACAGTAAGATCAT 694
 241 GTTGTGTGAAGAATTTCAATGAGACACAGCTGCCGATGGGACAGTAAGATCAT 300
 QY 695 GTTGTTCCTGGATGAGCGCTTTCAGGCTTGAAGGATCATCCATTTTGAAG 754
 301 GTTGTTCCTGGATGAGCGCTTTCAGGCTTGAAGGATCATCCATTTTGAAG 360
 QY 755 AAGTCTGATCGAAATTTCTAGAGCTGAACCATTCACATATGTGACAGAGATCTT 814
 361 AAGTCTGATCGAAATTTCTAGAGCTGAACCATTCACATATGTGACAGAGATCTT 420
 QY 815 CAACTTGTGTGAGAGAAAGCGCTTCGACATCCCGCAAGTGAAGAGGCTCTTCG 874
 421 CAACTTGTGTGAGAGAAAGCGCTTCGACATCCCGCAAGTGAAGAGGCTCTTCG 480
 QY 875 AGCTTCAAGATCATGACTCGGTCACTCAATGAGAAAGCCCTTTTCTGTGGAAGACT 934
 481 AGCTTCAAGATCATGACTCGGTCACTCAATGAGAAAGCCCTTTTCTGTGGAAGACT 540
 QY 935 TATTACTGTGTCAGGCTCATCTTAA-AGAAGTTGGCATGAAGCTGCACTCCAGT 993
 541 TATTACTGTGTCAGGCTCATCTTAA-AGAAGTTGGCATGAAGCTGCACTCCAGT 600
 QY 994 CAGCATGAAGATGAGCTCTCTTTTATCTCAAGTTCTGTTCATCATCAACACACACTG 1053
 601 CAGCATGAAGATGAGCTCTCTTTTATCTCAAGTTCTGTTCATCATCAACACACACTG 660
 QY 1054 T 1054

Db 661 T 661

RESULT 13

CFI32432

641 bp mRNA 1line EST 05-AUG-2003

CFI32432

UI-HF-P00-two-m-16-0-UI.r1 NIH_MGC_215 Homo sapiens cDNA clone

LOCUS

IMAGE:30560079 5', mRNA sequence.

DEFINITION

CFI32432.1 GI:33215693

ACCESSION

CFI32432

VERSION

EST.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 641)
 Bonaldo, M.F., Lennon, G. and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 8889548
 PUBMED
 JOURNAL

COMMENT

Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 Tissue Procurement: Mary Hendrix
 Tissue Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/humanfl.html
 Seq primer: pyx-5.

FEATURES

1..641
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30560079"
 /issue_type="Chondrosarcoma Lung Metastasis cell lines"
 /lab_host="DH10B (T1 phage resistant)"
 /note="Organ: Lung; Vector: pYX-Asc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with Not I and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is GATTAAGCCA. Tissue was provided by Mary Hendrix."

ORIGIN

Query Match 44.6%; Score 630; DB 6; Length 641;
 Best Local Similarity 99.8%; Pred. No. 2.2e-142;
 Matches 641; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 26 ATGGCGGCTCTGAGGCTGTGGCGAGTTCGGAGACCTGGGAGAGAGGACCTGCT 85
 1 ATGGCGGCTCTGAGGCTGTGGCGAGTTCGGAGACCTGGGAGAGAGGACCTGCT 60
 QY 86 CTCCTCCGCGCTGGGCGATGCGCAGCGGAGGAGAGAGCCCTCGGATCGGCTTCAG 145
 61 CTCCTCCGCGCTGGGCGATGCGCAGCGGAGGAGAGAGCCCTCGGATCGGCTTCAG 120
 QY 146 TGGCTCTTTGGCACTGTGCTCATCTGCGCCCGGCAAGGGGAGCCAGGAGAT 205

Db 121 TGGCTCTCTTTGGCCACTGTGTCTCATCTGCGCGGGCAGGGGAGCGAGGAGAT 180
 QY 206 GGGGGTCCAGCCGTCTAGCGCGGATTGACCTGTACTTATTTTGGACAATATCAGGAAT 265
 Db 181 GGGGGTCCAGCCGTCTAGCGCGGATTGACCTGTACTTATTTTGGACAATATCAGGAAT 240
 QY 266 GTGCTGACACCTGGAATGAATCTATTACTTTTGGAAAGTTGGCTCACAATTCATC 325
 Db 241 GTGCTGACACCTGGAATGAATCTATTACTTTTGGAAAGTTGGCTCACAATTCATC 300
 QY 326 AGCCCACTAGTGAATGTCTTATTTTCTCCACCCCGAGAACACTTAAATGAA 385
 Db 301 ACCCCACAGTTGAGATGTCTTATTTTCTCCACCCCGAGAACACTTAAATGAA 360
 QY 386 CTGACAGAGACAGAGAACAAATCCGTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCCA 445
 Db 361 CTGACAGAGACAGAGAACAAATCCGTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCCA 420
 QY 446 GGAGGAGACACTTACATGATGAGAGATTTGAAAGGCGCAGTGAGAGATTTATATGAA 505
 Db 421 GGAGGAGACACTTACATGATGAGAGATTTGAAAGGCGCAGTGAGAGATTTATATGAA 480
 QY 506 AACAGACAGAGGATGACAGACAGCCATCATATTTGACTGATGAGAACTTCAT 565
 Db 481 AACAGACAGAGGATGACAGACAGCCATCATATTTGACTGATGAGAACTTCAT 540
 QY 566 GAAGATCTCTTTTCTTATTCAGAGAGGAGCTTATAGTCTGAGATCTTGGTGCAT 625
 Db 541 GAAGATCTCTTTTCTTATTCAGAGAGGAGCTTATAGTCTGAGATCTTGGTGCAT 600
 QY 626 GTTACTGTGTGTGTGAAAGATTTCAATGAGACACAGCTG 667
 Db 601 GTTACTGTGTGTGTGAAAGATTTCAATGAGACACAGCTG 641

RESULT 14
 BG281831 964 bp mRNA linear EST 21-FEB-2001
 LOCUS 602403057F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:454502 5',
 DEFINITION mRNA sequence.

ACCESSION BG281831
 VERSION BG281831.1 GI:13030757
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 964)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC/DCPD/DRP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: LNCM1230 row: a column: 15
 High quality sequence stop: 659.
 Location/Qualifiers

FEATURES
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 /db_xref="taxon:9606"
 /clone="IMAGE:454502"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_20"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 41.2%; Score 582; DB 2; Length 964;
 Best Local Similarity 98.3%; Pred. No. 1.2e-130;
 Matches 641; Conservative 0; Mismatches 5; Indels 6; Gaps 5;

ORIGIN
 1 AGACCCCGGAGGAAAGGCGCGGATGGCGCTCCGTGAGGCTGTGGCGAGTTGCCG 60
 Db 22 AGACCCCGGAGGAAAGGCGCGGATGGCGCTCCGTGAGGCTGTGGCGAGTTGCCG 81
 QY 61 AGCGTGGAGAGAGCGGAGACCTGCTCTCCCGGGCTGCGGGCCATGCGCAC- GCGGAGAC 119
 Db 82 AGCGTGGAGAGAGCGGAGACCTGCTCTCCCGGGCTGCGGGCCATGCGCGGAGC 141
 QY 120 GGAGAGCCCTCGGACATCGGCTTCCAGTGGCTCTTTTGGCCACTGTGCTCATCTGCG 179
 Db 142 GGAGAGCCCTCGGACATCGGCTTCCAGTGGCTCTTTTGGCCACTGTGCTCATCTGCG 201
 QY 180 CCGGCGAAGGAGGAGCGCAGAGAGATGAGGCTTCCAGCTGTCTTACCGCGGATTTGACTGT 239
 Db 202 CCGGCGAAGGAGGAGCGCAGAGAGATGAGGCTTCCAGCTGTCTTACCGCGGATTTGACTGT 261
 QY 240 ACTTCAATTTTGGACAAATCAGAGAGATGCTGCTCAGACATGAGATGAAATCTATTAC-TTT 298
 Db 262 ACTTCAATTTTGGACAAATCAGAGAGATGCTGCTCAGACATGAGATGAAATCTATTACTTTT 321
 QY 299 GTGGAACAG-TTGGCTCAAAATTCATGAGCCACAGTTGAGATGCTTATTGTTT 357
 Db 322 GTGGAACAGTTTGGCTCAAAATTCATGAGCCACAGTTGAGATGCTTATTGTTT 381
 QY 358 CTCACCCGAGGAGCAACTTAATGAACTGACAGAGACAGAGAACAAATCCGTCAAG 417
 Db 382 CTCACCCGAGGAGCAACTTAATGAACTGACAGAGACAGAGAACAAATCCGTCAAG 441
 QY 418 CCTAGAGAACTCCGAAAGTCTGCGAGAGAGACACTTCAATGAGAGATTTGA 477
 Db 442 CCTAGAGAACTCCGAAAGTCTGCGAGAGAGACACTTCAATGAGAGATTTGA 501
 QY 478 AAGGCGCAGTGAAGCATTTATGAAACAGACAGAGG--TACAGACAGCAGCGTC 535
 Db 502 AAGGCGCAGTGAAGCATTTATGAAACAGACAGAGGATGACAGACAGCAGCGTC 561
 QY 536 ATCATTTGCTTTGACTGATGAGAGAACTCCATGAGATCTTTTCTATTCAAG-AGGA 594
 Db 562 ATCATTTGCTTTGACTGATGAGAGAACTCCATGAGATCTTTTCTATTCAAGAGGAG 621
 QY 595 GCGTAATAGTCTCGAGATCTTGGCAATTTTACTGCTGTGTGTA 646
 Db 622 GCGTAATAGTCTCGAGATCTTGGCAATTTTACTGCTGTGTGTA 673

RESULT 15
 DN993680 672 bp mRNA linear EST 17-MAY-2005
 LOCUS TC113711 Human adult whole brain, large insert, PCNV expression
 DEFINITION library Homo sapiens cDNA clone TC113711 5' similar to Homo sapiens
 anthrax toxin receptor 1 (ANTXR1), transcript variant 3, mRNA
 sequence.

ACCESSION DN993680
 VERSION DN993680.1 GI:66253511
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 672)

AUTHORS

TITLE

JOURNAL

COMMENT

Birkett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L.,
 Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M.,
 Zhang, X., Zay, G., and He, W.
 High-throughput cloning of full-length human cDNAs directly from
 cDNA libraries optimized for large and rare transcripts
 Unpublished (2005)
 Contact: Kovacs, KP
 High Throughput cDNA Cloning
 Origene Technologies, Inc. (www.origene.com)
 6 Taft Court, Suite 100, Rockville, MD 20850, USA
 Tel: 301 340 3188
 Fax: 301 340 8606
 Email: cDNA@origene.com
 This EST submission is part of an on-going human full-length
 cloning project at Origene Technologies, Inc.
 Please contact Origene for access.
 Origene Technologies, Inc.
 6 Taft Ct. Suite 100
 Rockville, MD 20850
 Tel: (301) 340-3188
 http://www.origene.com
 Seq primer: PCMV6 5prime forward vector primer, Origene
 Technologies Inc.

FEATURES

SOURCE

Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="TC13711"
 /issue_type="Whole brain"
 /clone_lib="Human adult whole brain, large insert, pCMV
 expression library"
 /note="Organ: Brain; Vector: pCMV6-XL5; Site 1: EcoRI;
 Site 2: XhoI/SalI compatible end ligatio; Oligo-dT primed
 reverse transcription optimized for large and GC rich mRNA
 transcripts, cDNA size selection, optimized ligation for
 large inserts into mammalian expression vector, random
 clones selected for end sequence verification of
 full-length genes"

ORIGIN

Query Match 40.4%; Score 571; DB 8; Length 672;
 Best Local Similarity 100.0%; Pred. No. 5.5e-128; Indels 0; Gaps 0;
 Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGGACCCGCGAGAGAGGCGCGGATGCGCGTCCCTGAGGGTCTGTGGCAGTTTCGGCG 60
 DB 102 AGGACCCGCGAGAGAGGCGCGGATGCGCGTCCCTGAGGGTCTGTGGCAGTTTCGGCG 161
 QY 61 AGCGTGGAGAGAGCGGACCTCTCTCCCGGGCTGCGGCGCATGCGCACGCGAGCG 120
 DB 162 AGCGTGGAGAGAGCGGACCTCTCTCCCGGGCTGCGGCGCATGCGCACGCGAGCG 221
 QY 121 GAGAGCCCTCGGCACTCGGCTTCCAGTGGCTCTTTGGSCACTGCGTGCATCTGCGC 180
 DB 222 GAGAGCCCTCGGCACTCGGCTTCCAGTGGCTCTTTGGSCACTGCGTGCATCTGCGC 281
 QY 181 CGGCGAAGGGGAGCGACAGGAGATGGGGGTCCAGCCTGCTACGCGCGGATTTGACTGTA 240
 DB 282 CGGCGAAGGGGAGCGACAGGAGATGGGGGTCCAGCCTGCTACGCGCGGATTTGACTGTA 341
 QY 241 CTTCAATTTTGACAATATCAGGAAGTGTCTGCACCATCTGAAATGAATCTATTAATTTGT 300
 DB 342 CTTCAATTTTGACAATATCAGGAAGTGTCTGCACCATCTGAAATGAATCTATTAATTTGT 401
 QY 301 GGAACAGTTGGCTCACAATTCATCAGGCCACAGTTGGAATGTCCTTATTTGTTTCTC 360
 DB 402 GGAACAGTTGGCTCACAATTCATCAGGCCACAGTTGGAATGTCCTTATTTGTTTCTC 461
 QY 361 CACCGAGAGAACCTTAATGAACCTGACAGAGACAGAGAACAAATCCGTCAAGGCT 420
 DB 462 CACCGAGAGAACCTTAATGAACCTGACAGAGACAGAGAACAAATCCGTCAAGGCT 521

QY 421 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATCATGAAGATTTGAAG 480
 DB 522 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATCATGAAGATTTGAAG 581
 QY 481 GGCACGTGAGCAGATTTATTATGAACACAGACAAGGTACAGGACAGCCAGCTCATCAT 540
 DB 582 GGCACGTGAGCAGATTTATTATGAACACAGACAAGGTACAGGACAGCCAGCTCATCAT 641
 QY 541 TGCTTTGACTGATGAGAACTCCATGAAGAT 571
 DB 642 TGCTTTGACTGATGAGAACTCCATGAAGAT 672

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	906.8	64.1	1609	US-09-620-312D-8	Sequence 8, Appli
2	516.8	36.5	3981	US-09-799-451-250	Sequence 250, App
3	346.2	24.5	2234	US-10-104-047-669	Sequence 669, App
4	307.4	21.7	1492	US-09-774-528-297	Sequence 297, App
5	307.4	21.7	1492	US-10-120-988-297	Sequence 297, App
6	79.4	5.6	450	US-10-131-827-8330	Sequence 8330, Ap
7	55.2	3.9	612	US-09-902-540-1357	Sequence 1357, Ap
8	51.6	3.6	985	US-09-322-409-25	Sequence 25, Appl
9	51.6	3.6	985	US-09-322-409-27	Sequence 27, Appl
10	51.6	3.6	985	US-09-451-527-25	Sequence 25, Appl
11	51.6	3.6	985	US-09-451-527-27	Sequence 27, Appl
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13	51.6	3.6	2158	US-08-261-578-1	Sequence 1, Appli
14	51.4	3.6	1660	US-09-722-0971-9	Sequence 9, Appli
15	50.8	3.6	3829	US-08-631-097-8	Sequence 8, Appli
16	50.8	3.6	3829	US-08-810-712-6	Sequence 6, Appli
17	50.2	3.6	1412	US-09-614-912-197	Sequence 197, App
18	50.2	3.6	36311	US-09-949-016-13627	Sequence 13627, A
19	50	3.5	1013	US-09-322-409-6	Sequence 6, Appli
20	50	3.5	1013	US-09-322-409-8	Sequence 8, Appli
21	50	3.5	1013	US-09-451-527-6	Sequence 6, Appli
22	50	3.5	1013	US-09-451-527-8	Sequence 8, Appli
23	49.8	3.5	658	US-08-998-416-595	Sequence 595, App
24	49.8	3.5	2608	US-09-618-596A-1	Sequence 1, Appli

25	49.8	3.5	2609	US-09-437-568A-1	Sequence 1, Appli
26	49.4	3.5	194	US-09-621-976-801	Sequence 801, App
27	48.8	3.5	1039	US-09-902-540-1280	Sequence 1280, Ap
28	48.8	3.5	4167	US-09-973-278-700	Sequence 700, App
29	48.6	3.4	603	US-10-178-449A-11	Sequence 11, Appl
30	48.6	3.4	908	US-09-800-729-25	Sequence 25, Appl
31	48.6	3.4	2445	US-09-949-016-781	Sequence 781, App
32	48.6	3.4	2539	US-10-144-198-21	Sequence 21, Appl
33	48.4	3.4	396	US-09-640-173-53	Sequence 53, Appl
34	48.4	3.4	396	US-09-713-550-53	Sequence 53, Appl
35	48.4	3.4	396	US-09-825-294-53	Sequence 53, Appl
36	48.4	3.4	396	US-09-970-966-53	Sequence 53, Appl
37	48.4	3.4	1898	US-08-342-411A-1	Sequence 1, Appli
38	47.8	3.4	1766	US-10-142-835-27	Sequence 27, Appl
39	47.6	3.4	323	US-09-621-976-10374	Sequence 10374, A
40	47.6	3.4	530	US-09-461-325-28	Sequence 28, Appl
41	47.6	3.4	530	US-10-012-542-28	Sequence 28, Appl
42	47.6	3.4	530	US-10-115-123-28	Sequence 28, Appl
43	47.6	3.4	1378	US-09-149-476-208	Sequence 208, App
44	47.6	3.4	2323	US-09-149-476-24	Sequence 24, Appl
45	47.4	3.4	1248	US-09-489-847-101	Sequence 101, App

ALIGNMENTS

```
RESULT 1
US-09-620-312D-8
; Sequence 8, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Aunani, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aildong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunding
; APPLICANT: Wang, Duntui
; APPLICANT: Wang, Zhilwei
; APPLICANT: John Tillinghaast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP28
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 8
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (309)..(1202)
US-09-620-312D-8
Query Match 64.1%; Score 906.8; DB 3; Length 1609;
Best Local Similarity 99.8%; Pred. No. 5.4e-223;
Matches 908; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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206 AGGACCCGCGAGGAGGCGCCGCGATGCGCTCCCTGAGGATCGTGGCGAGTTGCGCG 265
61 AAGCGGGGAGGAGGCGGACCTGCTCTCCCGGGCTGCGGGCCATGCGCCAGCGGAGG 120
266 AAGCGGGGAGGAGGCGGACCTGCTCTCCCGGGCTGCGGGCCATGCGCCAGCGGAGG 325
121 GAGAGCCCTCGGCAATCGGCTTCAGTGGCTCTCTTTGGCCACTGTGCTCATCTGCGC 180
326 GAGAGCCCTCGGCAATCGGCTTCAGTGGCTCTCTTTGGCCACTGTGCTCATCTGCGC 385
181 CGGGGAGGAGGAGGCGGAGGAGTGGGGCTCCAGCTGCTCAAGCGGATTTGACCTGTA 240
386 CGGGGAGGAGGAGGCGGAGGAGTGGGGCTCCAGCTGCTCAAGCGGATTTGACCTGTA 445
241 CTTCAATTTTGGCAAAATCGAAGAGTGTGTCGACCACTGGAATGAAATATTACTTGT 300
446 CTTCAATTTTGGCAAAATCGAAGAGTGTGTCGACCACTGGAATGAAATATTACTTGT 505
301 GGAACGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAATGTCCTTATTGTTTCTC 360
506 GGAACGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAATGTCCTTATTGTTTCTC 565
361 CACCGGAGGAGCAACCTTAATGAACTGA CAGAGAGCAGAGAACAAATCCGTAAGGCTT 420
566 CACCGGAGGAGCAACCTTAATGAACTGA CAGAGAGCAGAGAACAAATCCGTAAGGCTT 625
421 AAGAGAACTCCGAAAGTTCTGCGAGAGAGACATTTACATGCAATGAGATTTGAAAG 480
626 AAGAGAACTCCGAAAGTTCTGCGAGAGAGACATTTACATGCAATGAGATTTGAAAG 685
481 GGCAGTGAAGCATTTATTAAGAAACAGACAAAGGATCAGAGACAGCGCTCATCAT 540
686 GGCAGTGAAGCATTTATTAAGAAACAGACAAAGGATCAGAGACAGCGCTCATCAT 745
541 TGCCTTGAATGAGAACTCCAGTAAGATCTCTTTTCTAATTCAGAGAGGAGGCTTAA 600
746 TGCCTTGAATGAGAACTCCAGTAAGATCTCTTTTCTAATTCAGAGAGGAGGCTTAA 805
601 TGGGTCGTGAGATCTTGGTGGCAATGTTTACTGTGTGTGTAAGAAATTTCAATGAGAC 660
806 TGGGTCGTGAGATCTTGGTGGCAATGTTTACTGTGTGTGTAAGAAATTTCAATGAGAC 865
661 AAGAGTGGCCCGGATTCGAGACAGTAAGATCATGTGTTCCCGTGAATGAGCGCTTCA 720
866 AAGAGTGGCCCGGATTCGAGACAGTAAGATCATGTGTTCCCGTGAATGAGCGCTTCA 925
721 GGCCTGCAAGGATCATCTCAATTTTGAAGAAATGTCGTGATGAAATTCATGACAC 780
926 GGCCTGCAAGGATCATCTCAATTTTGAAGAAATGTCGTGATGAAATTCATGACAC 985
781 TGAACCATCAACATATGTCAGAGAGATTTCAAGTGTGTCAGAGAGAAACGGCTT 840
986 TGAACCATCAACATATGTCAGAGAGATTTCAAGTGTGTCAGAGAGAAACGGCTT 1045
841 CCGACATGCGCCGCAAGTGAAGAGGATCTCTGACAGCTTCAAGATCAATGATCGGTGAC 900
1046 CCGACATGCGCCGCAAGTGAAGAGGATCTCTGACAGCTTCAAGATCAATGATCGGTGAC 1105
901 ACTCAATGAG 910
1106 ACTCAATGAG 1115

RESULT 2
US-09-799-451-250
; Sequence 250, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Aundt, Vinod

APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Xue, Aildong J.
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Ma, Yungqing
APPLICANT: Yamazaki, Victoria
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Dunrui
APPLICANT: Yang, Yonghong
APPLICANT: Weinman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pc_fl_genes Version 2.0
SEQ ID NO 250
LENGTH: 3981
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (297)..(1118)
US-09-799-451-250

Query Match 36.5%; Score 516.8; DB 3; Length 3981;
Best Local Similarity 99.6%; Pred. No. 1.6e-122;
Matches 518; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

678 CGGACAGTAAGATATGTTTCCCGGAATGAGAGGCTTTCAGGCTCGAAGGATCA 737
1 CGGACAGTAAGATATGTTTCCCGGAATGAGAGGCTTTCAGGCTCGAAGGATCA 60
738 TCCACTCAATTTTGAAGAGCTCGCATGGAATTCAGACAGTGAACCATCCATCAT 797
61 TCCACTCAATTTTGAAGAGCTCGCATGGAATTCAGACAGTGAACCATCCATCAT 120
798 GTGCAAGAGATCATTTCAAGTTGTGTGAGAGAAACGGCTTCCGACATGCGCCGACG 857
121 GTGCAAGAGATCATTTCAAGTTGTGTGAGAGAAACGGCTTCCGACATGCGCCGACG 180
858 TGGACAGGATCTCTGACGCTTCAAGATCAATGATCTCGTCACTCAATGAGAGCCCT 917
181 TGGACAGGATCTCTGACGCTTCAAGATCAATGATCTCGTCACTCAATGAGAGCCCT 240
918 TTTCTGTGAAGACACTTATTTACTGTGTCCAGCGCTTATCTTAAAGAAATGGCATGA 977
241 TTTCTGTGAAGACACTTATTTACTGTGTGTCCAGCGCTTATCTTAAAGAAATGGCATGA 300
978 AAGTGCATCTCAGGTCAGATGAACGATGGCTCTTTTATCTCCAGTTCTGTATCA 1037
301 AAGTGCATCTCAGGTCAGATGAACGATGGCTCTTTTATCTCCAGTTCTGTATCA 360
1038 TACCAACCAACACTGTTTGAACGGTTCATCTTGGCCATTCGCCCTGCTGATCCGTTCC 1097
361 TACCAACCAACACTGTTTGAACGGTTCATCTTGGCCATTCGCCCTGCTGATCCGTTCC 420
1098 TGCCTCTAGCCCTGAGCTCTCTGATGATTTGAGCCCTCTGCTGACATGATTAATCA 1157
421 TGCCTCTAGCCCTGAGCTCTCTGATGATTTGAGCCCTCTGCTGACATGATTAATCA 480
1158 AAGAGTCCCTCCACCCCTGCGAGAGAGTGAAGAAA 1197
481 AAGAGTCCCTCCACCCCTGCGAGAGAGTGAAGAAA 520

RESULT 3
US-10-104-047-669

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: Sequence 669, Application US/10104047
: Patent No. 6943241
:
: GENERAL INFORMATION:
: APPLICANT: HELIX RESEARCH INSTITUTE
: TITLE OF INVENTION: No. 6943241el full length cdna
: FILE REFERENCE: H1-A0105
: CURRENT APPLICATION NUMBER: US/10/104,047
: CURRENT FILING DATE: 2002-03-25
: PRIOR APPLICATION NUMBER:
: PRIOR FILING DATE:
: NUMBER OF SEQ ID NOS: 4096
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 669
: LENGTH: 2234
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-104-047-669

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Query Match	24.5%;	Score 346.2;	DB 3;	Length 2234;
Best Local Similarity	58.3%;	Pred. No. 9.2e-79;		
Matches 628; Conservative	0;	Mismatches 443;	Indels 6;	Gaps 1;

Oy	104	TTGGCAGAGGGGGAGCGGAGAGCCCTGGGATCGGGCTTCAAGTGGCTCTCTTTGGCCACT	163
Db	529	ATGGTGGGGAGCGGTCCCGGCCCCGAGCCCGGGAGCTGGCTGTTCCTCCGGGCTGTGG	588
Oy	164	CTGGTGTCTCATCTGCGCCCGGGCAAGGGGGGAGCGCAGGAGAGTGGGGGTTCAGCCTGTCTAC	223
Db	589	CTGTGTGTGCTCAGGGGTCCCGGGGGGGGTGTGTGGCGCCGAGGAGCAGCCCTCTTGAGA	648
Oy	224	GGCGGATTTGACCTGTACTTCAATTTTGGACAATACAGAACTGTGTGCACCACTGGAAAT	283
Db	649	AGAGCTTTGATCTCTACTTCTGTCTCTTGAGCAAGCTCTGGAGTGTGGCAAAATATACGTGATTT	708
Oy	284	GAATCTTATCTTGTGTGGACAAGTGGGCTCAAAATTCATCACCCCAAGTTGAGATG	343
Db	709	GAATATTTAATTTGTGACAGAACCTCGGAGAGATTTGTAGCCTGAAATAGATTTA	768
Oy	344	TCTTTATTTGTTTCTCCACCCGAGGAACAACTTATGAAACTGACAGAGACAGAGAA	403
Db	769	TCTTTCAATGTGTCTTCTTCTCAGCAACTATTTTGGCATTTATCTGGAGACAGAGGC	828
Oy	404	CAAAATCCGTCAAGGCTTAGAGAACTCCAGAAAGTTCTTGCCAGAGAGAGACATTACATG	463
Db	829	AAATCACTAAAGGCTTGGAGATTTAAACGTGTACTCCAGTAGGAGAGACATATATC	888
Oy	464	CATGAAGATTTGAAAGGGCCAGTAGAGAGATTTATTTGAAAACAGCAAGGGTACAGG	523
Db	889	CATGAAGACTAAACCTAGCCGATATACAAAT-----TCAGAAAGCAGAGGGCTTGAAA	942
Oy	524	ACAGCAGACGTCATCTATTGCTTTGACTGATGGAGAACTCCATGAAAGATCTCTTTTCTAT	583
Db	943	ACCTCAAGTATATAATTTGCTCTGTGCACATGGCAGAGTTGGACGGTCTGTGTCCATCATAT	1002
Oy	584	TCAGAGAGGAGGCTAATAGGTCTTCGAGATCTTGGTCAAATTTGTTACTGTGTGTGTGTG	643
Db	1003	GCAGAGAAAGAGCAAAAGATATCCAGGTCACTTGGGGGCTAAGTGTATTTAGTTGGTGTGTC	1062
Oy	644	AAAGATTTCAATGAGACACAGCTGGCCCCGGATTTGGGACAGTAAAGATCATGTGTTCCTC	703
Db	1063	CTTGTATTTTGAACAAGACACAGCTTAAAGAAATTTGTGATTCACAGAGACAAAGTTTCCCT	1122
Oy	704	GTTGAATGACGGCTTTCAAGGCTCTGCAGAGCATCATCCAATTTTAAAGAGTCTGTC	763
Db	1123	GTCMAAGGTGGAATTTTCAGGCTTTTAAAGGAATTAATTTCTATCTAGCTCAAGTCATGT	1182
Oy	764	ATCGAAATTTAGCAGCTGAACCATTCACCATATGTGCAGAGAGTCAATTTCAAGTTGTC	823
Db	1183	ACTGAAATCTTGAATTCGAGCCCTCAAGTGTCTGTGTGGGGAGAAATTTTCAGATGTCTC	1242
Oy	824	GTCAGAGAGAAAGGCTTCCGACATGCCCCGCAACGTGGACAGGGTCTCTGACAGCTTCAAG	883
Db	1243	TTTAAGTGAAGAGATTCATGTCTGGGCACTGTGGAAATGGCAAGTGTCTCTGCACTTACACT	1302

QY	884	ATCATAGACTGGTCACTCAATAGAAAGCCCTTTCTGTGGAAGACACTTAATTAACG	943
Db	1303	GTAATGGAACATATACACAGNGTATAAACGATAGTACAGCTTAATTCATGCTT	136
QY	944	TGTCAGGCGCTATCTTAAAGAAAGTTGCGATGAAGCTGCACCTCCAGGTACGATGAC	100
Db	1363	TGTCCTGACCACTATCTGAATTAAGAGCTGGAGAAACCTTGATGTTCACTGAGCTTAAAT	142
QY	1004	GATGCGCTCTCTTTATCTCCAGTTCTGTCATCATCACACACACACTGTTCTGACGAT	106
Db	1423	GGAGGAATCTGTATTTACAGATCATTAATTGTCACAGCCACAGAAATGTTCTAAGGG	148
QY	1064	TCCATCTCGGCATGCGCCCTGCTGATCCTGTTCTGCTCTTACGCCCTGACTCTCTCTGG	112
Db	1483	ATCGACAGCATATGTTATTTTGGTGTATCTGCTACCTCTGGGGAATCGGTTGAATGTGG	154
QY	1124	TGGTTCTGGCCCCCTGCTGTCGACCTGTGATATACAGAGGAGTCCCTTCACCCCTGCGC	1180
Db	1543	TGGTTTGGCCCCCTTGTCTGCACAAAGTGTTATTAAGATTCCTTCACACACACCCGCGC	1599

RESULT 4
US-09-774-528-297
; Sequence 297, Application US/09774528

```

? GENERAL INFORMATION:
? APPLICANT: Tang, Y. Tom
? APPLICANT: Zhou, Ping
? APPLICANT: Goodrich, Ryle
? APPLICANT: Liu, Chenghua
? APPLICANT: Asundi, Vinod
? APPLICANT: Ren, Feiyang
? APPLICANT: Zhang, Jie
? APPLICANT: Zhao, Qing A.
? APPLICANT: Yang, Yongchong
? APPLICANT: Xue, Aildong J.
? APPLICANT: Wehrman, Tom
? APPLICANT: Wang, Jian-Rui
? APPLICANT: Wang, Dunrui
? APPLICANT: Dimañac, Radoje T.
? TITLE OF INVENTION: No. 6743619e1 Nucleic Acids and
? TITLE OF INVENTION: Polypeptides
? FILE REFERENCE: 802
? CURRENT APPLICATION NUMBER: US/09/774,528
? CURRENT FILING DATE: 2001-01-30
? NUMBER OF SEQ ID NOS: 441
? SOFTWARE: pt_FL_genes Version 2.0
? SEQ ID NO 297
?
? LENGTH: 1492
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURES:
? NAME/KEY: CDS
? LOCATION: (79) .. (1434)
US-09-774,528-297

```

Query Match	21.7%	Score 307.4;	DB 3;	Length 1492;
Best Local Similarity	59.2%	Pred. No. 7.3e-69;		
Matches 546; Conservative	0;	Mismatches 371;	Indels 6;	Gaps 1;

QY	258	CAGGAAGTGTGCTGCACCACTGGAAATGAATCATTA	CTTGTTGGAAACAGTGGCTCACA	31.7
Db	2	CACGCCGCCGGCGAATTA	CTGGATTGAAATTATATAATTCGACAGCACTTGGCGGAGA	61
QY	318	AATTATCAGCCACAGTGGAGATGTCCTTATATGTTTCTC	CACCCGAGAACTT	377
Db	62	GATTTGTGACCCCTGAAATGAGATTATCTTCACTTGTG	TTTCTTCTCAAGCACTTATTTA	121
QY	378	TATGAAATGACAGAGA	CAGAGAACTATCCGTCAAGGCTAGAGAAGAACTCCAGAAAG	437
Db	122	TTTTTCATTAATCTGAGAGACAGAGCGAATATCGTAAGAGCTTGAAGAGATTTAAACGTG		181

Oy	438	TTCTGCCAGGAGGAGACATTACATGCATGAGTAAGATTTTGAAGGGCCAGTGAGCAAAATTT	497
Oy	438	TTCTGCCAGGAGGAGACATTACATGCATGAGTAAGATTTTGAAGGGCCAGTGAGCAAAATTT	497
Db	182	TTAGTCCAGTGGAGAGACATATATCATGAGAGCTAAAGCTAAGCGATGAACAAAT--	239
Oy	498	ATTATGAAAACAGACAAAGGATACAGACAGCCAGCGTCATCTTGTGACTGATGAG	557
Db	240	----TCAGAAAAGCAGGAGGCTTGAAAACTCCAGATCATTAATTGCTCTGACAGATGGCA	295
Oy	558	AACTCATGAAGAATCTCTTTTCTATTTCAAGAGAGGAGGCTAATATAGTCTCGAATCTTG	617
Db	296	AGTTGGAGCGCTGTGGTCATCATATGACAGAAAGAGCAAGATATCCAGGTCACTTG	355
Oy	618	GTGCAATTTGTTTACTGTGTGGTGGAAAGATTTCAATGAGACACAGCTGGCCGGATTTG	677
Db	356	GCGCTAGTGTATTTATTTGTGGGGTCTTGATTTTGAACACAGCAGCTTTAAAGAAATTG	415
Oy	678	CGGACAGTAAGGATCATGTGTTCCTCCGTGAATGACGCGCTTCAGGCTCTGCAGGACATCA	737
Db	416	CTGATTCAGAGGAGCAATTTTCCCTGTCAAAAGGTGAATTTCAAGCTTTTAAAGGAATA	475
Oy	738	TCCACTCAATTTTGAAGAATGCTTCGATCGAAATTTAGACAGCTGAACCATCAACATAT	797
Db	476	TTAATTTCTATCTAGCTCAGTCATGTACTGAAATCTGAAATTTGACGCGCTCAAGTGCT	535
Oy	798	GTGCAGAGAGATCATTTTCAAGTTGCTGGAGAGAAAGCGCTTCGACATGCCCCGCAAG	857
Db	536	GTGTGGGGGAGAAATTTCAAGTGTCTTAAGTGAAGAGAGATTCATGCTGGGCAGTGGGA	595
Oy	858	TGACACAGGATCCTCTGCAGCTTCAAGATCAATGACTCGGTCACTCAATGAGAACCCCT	917
Db	596	ATGGCAGTGTCTCTGCACATTACCTGTAATGAAACATATACACAGGTGTAAACCG	655
Oy	918	TTTCTGTGAAGACATTATTTACTGTGTCCAGCGCTATCTTTAAAGAAAGTTGGCATGA	977
Db	656	TAAGTGACAGCTTATTTCTATGCTTTGTCTGACACTATCTGTAATAAGCTGGAGAA	715
Oy	978	AAGCTGCACCTCAGGTCAGCATGAACGATGGCCTCTTTTATCTCCAGTTCTGTCACTA	1037
Db	716	CTCTTGATGTTTCACTGAGCTTTTATGAGGAAATCTGTCAATTCAGAGATCATTAATTTG	775
Oy	1038	TCACCACACACACACTGTTCTGACGGTTCATCTGGCCATCGCCCTGCTGATTCCTGTTCC	1097
Db	776	TCACAGCCACAGATGTTCTTACGAGGATCGACGCCATATTTTATTTGGTGTACTGC	835
Oy	1098	TGCTTCTAGCCCTGTGCTCTCTGTGGTATCTGTGGCCCTCTGTGTCACCTGTGATTATCA	1157
Db	836	TACTCTGGGGATCGGTTTGATGTGTGGTTTGGCCCTTTGTGCGAAAGGTATATTA	895
Oy	1158	AGGAGGTCCTTCACACCCCTGCG 1180	
Db	896	AGGATCTCTCACACACACCCCGC 918	
RESULT 5			
US-10-120-988-297			
; Sequence 297, Application US/10120988			
; Patent No. 6919193			
; GENERAL INFORMATION:			
; APPLICANT: Tang, Y. Tom			
; APPLICANT: Goodrich, Ryle			
; APPLICANT: Liu, Chenghua			
; APPLICANT: Ren, Feiyan			
; APPLICANT: Wang, Dunrui			
; APPLICANT: Drmanac, Radoje T.			
; TITLE OF INVENTION: No. 6919193el Nucleic Acids and			
; FILE REFERENCE: PolyPeptides			
; CURRENT APPLICATION NUMBER: US/10/120,988			
; CURRENT FILING DATE: 2002-04-11			
; PRIOR APPLICATION NUMBER: 09/774,528			
; PRIOR FILING DATE: 2001-01-30			
; NUMBER OF SEQ ID NOS: 441			
; SOFTWARE: pc.fl.genes Version 2.0			

```

; SEQ ID NO 297
; LENGTH: 1492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79)..(1434)
US-10-120-988-297

Query Match      21.7%; Score 307.4; DB 3; Length 1492;
Best Local Similarity 59.2%; Pred. No. 7.3e-69;
Matches 546; Conservative 0; Mismatches 371; Indels 6; Gaps 1.

Oy      258  CAGGAAGTGTCTCTGACCACTCGAATGAAATCTATTACTTTGTGGAACAGTTGCTCACA 317
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2    CACCCCGCCGCCGAATTAACGTGATTGAAATTTAATTATTTGATACAGCAACTTGGCGAGA 61

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Query Match	Similarity	21.7%	Score 307.4	DB 3	Length 1492	
Best Local	Similarity	59.2%	Pred. No. 7.3e-69			
Matches	546	Conservative	0	Mismatches	371	Indels 6; Gaps 1
QY	258	CAGGAAGTGTCTCACCACCTCGAATGAATCTATTACTTTGTGAAACGTTGGCTCACA	317			
Db	2	CAACCCGCGGGCGAATAACTGGAATGAAATTTTAATTGGTACAGCAACTGGGAGGA	61			
QY	318	AATTCATCAGCCACAGTGGAAATGTCCTTTATTTGTTTCTCCACCCGAGAACACCT	377			
Db	62	GATTTGTGAGCCCTGGAATGAGATTATCTTCAATGTGTTTCTTCAGACCACTAATTA	121			
QY	378	TAAATGAATCTGACGAAGAAGAGAACAAATCCGTCAGAGGCTGAAACATCCGGAAG	437			
Db	122	TTTGTCCATTAACTGAGAACAGAGCAAAATCAGTAAAGGCTTGAGGATTTAAACGTC	181			
QY	438	TTCTGCCAGAGAGACACTTACATGCATGAAGATTGAAAGGCGCAGTGCAGATTT	497			
Db	182	TTTAATCCAGTATGAGAGAGACATATATCATGAGAGACTAAAGCTAGCATGAACAAAT--	239			
QY	498	ATTATGAAGACAGACAGAGGTAACAGACAGCCAGCTCATCATTTGCTTTGACTGATGAG	557			
Db	240	----TCGAAAGCAGAGGCTTGAAACCTCAGATCATTAATGCTCTGACAGATGCA	295			
QY	558	AACTCATGAAGATCTCTTTTCAATTCAGAGAGGAGGACATTAATAGTCTGAGATCTTG	617			
Db	296	AGTTGAGAGGCTCTGGTGCATCATATGACAGAAAGGCAAGATATCAGGTCACTTG	355			
QY	618	GTGCATATGTTTACCTGTGTTGTGTGAAGAATTTCAATGAGACACAGCTGGCCGGAATG	677			
Db	356	GGGCTAAGTGTTAATGTCTTGGGGCTCTGATTTTGAACAAAGCACAGCTTGAAAGATTTG	415			
QY	678	CGACAGTAGAATCATGTGTTTCCCGTGAATGACGCTTTCAGGCTCTGCAAGCATCA	737			
Db	416	CTGATTCGAAGACCAAGTTTCCCTGTCGAAGGTGATTTTCAGGCTCTTAAAGGAATA	475			
QY	738	TCCACTCAATTTTGAAGAAGTCGCAATCGAAATCTTCAAGCTGAACATCATCAATAT	797			
Db	476	TTAATTTCAATCTAGCTCAGTCATGATGTACTGAATCTTGAATTCAGACCTCTCAATGTCT	535			
QY	798	GTGCAGAGAGTCAATTCATAGTTGTCTGAGAGGAACGGCTTCCGATGCCCCGAACG	857			
Db	536	GTGTGGGGAGGAATTTCAATGTGCTTAAAGTGAAGAGATTCATGTGGGCATCCGA	595			
QY	858	TGACAGGGTCTCTGACGCTTCAAGATCAATGACTCGGTACACTCACTGAAGAAGCCT	917			
Db	596	ATGCAAGTGTCTCTGCACTTACACTGTAATGAACATATACACGAGTGTAAAAACAG	655			
QY	918	TTTCTGTGAGAGACACTTATTAATGTGTCCAGGCGCCATCTTAAAGAAAGTGTGCACGA	977			
Db	656	TAAAGTACACTTAATTTATGTGTTGTCTGCACTCATCTGTAATAAAGTGGAGAAA	715			
QY	978	AAGCTGCACTCAGGTACAGATGAACGATGCGCTCTCTTTATCTCCAGTTCTGTCAATCA	103			
Db	716	CTCTTGAATGTTCACTGAGCTTTTAAATGAGAGAAATCTGTCAATTCAGAGTCAATTAATG	775			
QY	1038	TCACCAACACACACTGTTCTGACGGTTCATCTGGCCATGCGCCTGTGTAATCTGTTCC	109			
Db	776	TCACAGCCACAGAAATGTTCTAAACGGGATCGCAGCCATATGTTATTTTGGGTATCATGC	835			
QY	1098	TGCTTCCTAGCCCTGGCTCTCTCTGTGTGAGTCTGGCCCTCTGCTGCACTGATTAATCA	115			
Db	836	TACTCTGTGGGATCGGTGATGTGTGTGTTTGGCCCTTGTGCTGCAAGATGTTAATTA	895			

Patent No. 6471957
GENERAL INFORMATION:
APPLICANT: Sim, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/09/322,409
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 985
TYPE: DNA
ORGANISM: Canis familiaris
US-09-322-409-27

Query Match 3.6%; Score 51.6; DB 3; Length 985;
Best Local Similarity 65.8%; Pred. No. 0.0037;
Matches 75; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 1301 CTCATCTAGACAGCTTTTCTCTAGTCCCTGTATTCAAATCCAGTGTCAACATTC 1360
Db 122 CCTCTGTACAAAGTCTTGCCCCCAAGAAATTGTATATATATCATCCTTTCTACACG 63

Qy 1361 AATTAATGCTATATGAAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1414
Db 62 AA 9

RESULT 10
US-09-451-527-25
Sequence 25, Application US/09451527
Patent No. 6482403
GENERAL INFORMATION:
APPLICANT: Sim, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/09/451,527
CURRENT FILING DATE: 1999-12-01
EARLIER APPLICATION NUMBER: 09/322,409
EARLIER FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 174
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 985
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (74)..(901)
US-09-451-527-25

Query Match 3.6%; Score 51.6; DB 3; Length 985;
Best Local Similarity 65.8%; Pred. No. 0.0037;
Matches 75; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 1301 CTCATCTAGACAGCTTTTCTCTAGTCCCTGTATTCAAATCCAGTGTCAACATTC 1360
Db 864 CCTCTGTACAAAGTCTTGCCCCCAAGAAATTGTATATATATCATCCTTTCTACACG 923

Qy 1361 AATTAATGCTATATGAAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1414
Db 62 AA 9

Db 924 AA 977

RESULT 11
US-09-451-527-27/C
Sequence 27, Application US/09451527
Patent No. 6482403
GENERAL INFORMATION:
APPLICANT: Sim, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/09/451,527
CURRENT FILING DATE: 1999-12-01
EARLIER APPLICATION NUMBER: 09/322,409
EARLIER FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 174
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 985
TYPE: DNA
ORGANISM: Canis familiaris
US-09-451-527-27

Query Match 3.6%; Score 51.6; DB 3; Length 985;
Best Local Similarity 65.8%; Pred. No. 0.0037;
Matches 75; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 1301 CTCATCTAGACAGCTTTTCTCTAGTCCCTGTATTCAAATCCAGTGTCAACATTC 1360
Db 122 CCTCTGTACAAAGTCTTGCCCCCAAGAAATTGTATATATATCATCCTTTCTACACG 63

Qy 1361 AATTAATGCTATATGAAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1414
Db 62 AA 9

RESULT 12
US-07-602-608-1
Sequence 1, Application US/07602608
Patent No. 5382524
GENERAL INFORMATION:
APPLICANT: Desnick, Robert J.
APPLICANT: Bishop, David F.
APPLICANT: Ioannou, Yiannis A.
APPLICANT: Wang, Anne M.
TITLE OF INVENTION: CLONING AND EXPRESSION OF BIOLOGICALLY
TITLE OF INVENTION: ACTIVE ALPHA-N-ACETYL GALACTOSAMINIDASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/602,608
FILING DATE: 24-OCT-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742

Query Match 3.6%; Score 51.6; DB 3; Length 985;
Best Local Similarity 65.8%; Pred. No. 0.0037;
Matches 75; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

RESULT 15
US-08-631-097-8
; Sequence 8, Application US/08631097

Patent No. 5968816
GENERAL INFORMATION:
APPLICANT: Kimchi, Adi
TITLE OF INVENTION: Tumor Suppressor Genes, and Use of Said Genes and Protein
TITLE OF INVENTION: Tumor Suppressor Genes, and Use of Said Genes and Protein
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wigman, Cohen, Leitner, & Myers, P.C.
STREET: 900 17th Street, N.W., Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/631,097
FILING DATE: 12-Apr-96
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11598
FILING DATE: 12-Oct-94
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Herbert
REGISTRATION NUMBER: 25,109
REFERENCE/DOCKET NUMBER: 0744.057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)473-7700
TELEFAX: (202)473-6915
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3829 base pair
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: not applicable
ORIGINAL SOURCE:
ORGANISM: homo sapiens
STRAIN: not applicable
INDIVIDUAL ISOLATE: not applicable
DEVELOPMENTAL STAGE: not applicable
HAPLOTYPE: not applicable
TISSUE TYPE: blood
CELL TYPE: leucocyte
CELL LINE: HeLa
ORGANELLE: not applicable
IMMEDIATE SOURCE:
LIBRARY: not applicable
CLONE: not applicable
POSITION IN GENOME:
CHROMOSOME/SEGMENT: not applicable
MAP POSITION: not applicable
UNITS: not applicable
FEATURE:
NAME/KEY: SEQ ID. NO:8 is the sequence
NAME/KEY: in claim 1(vi) starting at triplet in position 201-203
NAME/KEY: and ending at the triplet 3018-3020
LOCATION: not available
IDENTIFICATION METHOD: experiment-
IDENTIFICATION METHOD: in specification
OTHER INFORMATION: prevention of IFN- γ -induced
OTHER INFORMATION: programmed cell death
PUBLICATION INFORMATION: not available
US-08-631-097-8

Query Match 3.6%; Score 50.8; DB 2; Length 3829;
Best Local Similarity 74.4%; Pred. No. 0.011;

Matches 64; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
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Db 3736 TTCCCTGATTTTTATATATCTGATCTATCAATTAATCAATTTGATGATCTGAAAAA 3795
Qy 1388 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1413
Db 3796 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3821
Search completed: December 17, 2005, 13:37:32
Job time : 269.178 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 17, 2005, 13:22:55 ; Search time 1300.57 Seconds
(without alignments)
8990.628 Million cell updates/sec

Title: US-09-970-076-1

Perfect score: 1414
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Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/ptodaca/1/pubpna/us09_PUBCOMB.seq:*
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- 9: /cgn2_6/ptodaca/1/pubpna/us10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodaca/1/pubpna/us11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1414	100.0	1414	10	US-11-047-278-1 Sequence 1, Appl1
2	1414	100.0	1454	6	US-10-133-937-58 Sequence 58, Appl1
3	1414	100.0	1454	6	US-10-159-563-58 Sequence 58, Appl1
4	1193.8	84.4	5540	3	US-09-918-715-176 Sequence 176, Appl1
5	1193.8	84.4	5540	3	US-09-918-715-231 Sequence 231, Appl1
6	1193.8	84.4	5540	6	US-10-301-822-198 Sequence 198, Appl1
7	1193.8	84.4	5540	8	US-10-474-794-176 Sequence 176, Appl1
8	1193.8	84.4	5540	9	US-10-474-794-231 Sequence 231, Appl1
9	1193.8	84.4	5540	9	US-10-979-159-176 Sequence 176, Appl1
10	1193.8	84.4	5540	9	US-10-979-159-231 Sequence 231, Appl1
11	1193.8	84.4	5540	10	US-11-047-278-5 Sequence 5, Appl1
12	1052.4	74.4	2272	3	US-09-796-753-11 Sequence 11, Appl1
13	1052.4	74.4	2272	6	US-10-038-307-1 Sequence 1, Appl1
14	1052.4	74.4	2272	6	US-10-038-307-11 Sequence 11, Appl1
15	1052.4	74.4	2272	6	US-10-201-292-1 Sequence 957, Appl1
16	1052.4	74.4	2353	5	US-10-198-846-9957 Sequence 957, Appl1
17	963	68.1	2397	6	US-10-062-674-1757 Sequence 1757, Appl1
18	962.8	68.1	1674	6	US-10-038-307-17 Sequence 17, Appl1
19	962.8	68.1	1674	6	US-10-201-292-17 Sequence 17, Appl1
20	952.4	67.4	1650	6	US-10-038-307-13 Sequence 13, Appl1
21	952.4	67.4	1650	6	US-10-038-307-15 Sequence 15, Appl1
22	952.4	67.4	1650	6	US-10-201-292-13 Sequence 13, Appl1
23	952.4	67.4	1650	6	US-10-201-292-13 Sequence 15, Appl1

24	951.4	67.3	1056	6	US-10-038-307-23 Sequence 23, Appl1
25	951.4	67.3	1056	6	US-10-201-292-23 Sequence 23, Appl1
26	951.4	67.3	1713	6	US-10-038-307-19 Sequence 19, Appl1
27	951.4	67.3	1713	6	US-10-201-292-19 Sequence 19, Appl1
28	951	67.3	1008	6	US-10-038-307-25 Sequence 25, Appl1
29	951	67.3	1008	6	US-10-201-292-25 Sequence 25, Appl1
30	950.8	67.2	1650	6	US-10-038-307-9 Sequence 9, Appl1
31	950.8	67.2	1650	6	US-10-201-292-9 Sequence 9, Appl1
32	914.4	64.7	1047	6	US-10-038-307-21 Sequence 21, Appl1
33	914.4	64.7	1047	6	US-10-201-292-21 Sequence 21, Appl1
34	906.8	64.1	1609	5	US-10-037-270-8 Sequence 8, Appl1
35	906.8	64.1	1609	5	US-10-117-722-8 Sequence 8, Appl1
36	906.8	64.1	1609	9	US-10-122-851-8 Sequence 8, Appl1
37	905.2	64.0	1718	8	US-10-357-930-30300 Sequence 30300, A
38	894.6	63.3	1608	6	US-10-201-292-35 Sequence 35, Appl1
39	890	62.9	1436	10	US-11-047-278-9 Sequence 9, Appl1
40	867.6	61.4	1623	6	US-10-038-307-11 Sequence 11, Appl1
41	867.6	61.4	1623	6	US-10-201-292-11 Sequence 11, Appl1
42	853.4	60.4	5220	3	US-09-918-715-186 Sequence 186, Appl1
43	853.4	60.4	5220	3	US-09-918-715-300 Sequence 300, Appl1
44	853.4	60.4	5220	8	US-10-474-794-186 Sequence 186, Appl1
45	853.4	60.4	5220	8	US-10-474-794-300 Sequence 300, Appl1

ALIGNMENTS

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RESULT 1
US-11-047-278-1
; Sequence 1, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296, 97745
; CURRENT APPLICATION NUMBER: US/11/047, 278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970, 076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251, 481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)..(1207)
US-11-047-278-1
Query Match 100.0%; Score 1414; DB 10; Length 1414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB	1	AGACCCGCGAGGAAGGCGCGAGTGGCGCTCCCTGAGGCTGCTGCGAGTTCGCGG	60
QY	61	AGCGTGGAGAGAGCGGACCTGCTCTCCCGGAGCTGCGGCGCATGCGCGAGCGG	120
DB	61	AGCGTGGAGAGAGCGGACCTGCTCTCCCGGAGCTGCGGCGCATGCGCGAGCGG	120
QY	121	GAGAGCCCTTGGCATGCGCTTCCAGTGGCGCTCTTTGGCACTGCTGCTCATCTGCGG	180
DB	121	GAGAGCCCTTGGCATGCGCTTCCAGTGGCGCTCTTTGGCACTGCTGCTCATCTGCGG	180
QY	181	CGGCGAGGCGGAGCGAGGAGGATGGGGGCTCCAGCTGCTAAGCGCGGATTTGA	240
DB	181	CGGCGAGGCGGAGCGAGGAGGATGGGGGCTCCAGCTGCTAAGCGCGGATTTGA	240

Db 181 CGGGCAAGGGGACGCGAGGAGATGGGGGTCCAGCTCTACGCGGATTTGACCTGTA 240
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Db 241 CTTCAATTTTGAACAATCAGAAAGTGTGTGCAACAATGAAATCTATTAATCTTGT 300
Qy 301 GGAAGAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATGTCCTTTATGTTTCTC 360
Db 301 GGAAGAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATGTCCTTTATGTTTCTC 360
Qy 361 CACCCGAGAGAACCTTATGAAAATGACAGAAAGCAGAAACAAATCCGTCAGGCT 420
Db 361 CACCCGAGAGAACCTTATGAAAATGACAGAAAGCAGAAACAAATCCGTCAGGCT 420
Qy 421 AGAAGAACTCCAGAAAGTCTGCGAGAGAGACCTTACATGATGAAAGATTGAAAG 480
Db 421 AGAAGAACTCCAGAAAGTCTGCGAGAGAGACCTTACATGATGAAAGATTGAAAG 480
Qy 481 GGCAGTGAAGATTTATGAAAACAGAGGGTACAGGACAGCCAGCTCATCAT 540
Db 481 GGCAGTGAAGATTTATGAAAACAGAGGGTACAGGACAGCCAGCTCATCAT 540
Qy 541 TCGCTTGAATGAGAACTCCATGAAATCTTTTCTATTCAGAGAGGAGCTTA 600
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Qy 601 TAGGTCGAGATCTTGTGCAATGTTTACTGTGTGTGTAAGAAATTTCAATGAGAC 660
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Qy 721 GCGCTGCAAGGATATCACTCAATTTTGAAGAGTCTGATGAAATCTAGACAC 780
Db 721 GCGCTGCAAGGATATCACTCAATTTTGAAGAGTCTGATGAAATCTAGACAC 780
Qy 781 TGAACCATCAACATATGTCAGAGAGTCAATTTCAAGTTGTGTCAGAGAGAAACGGCT 840
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Qy 841 CGGACATGCGCGCAAGTGTGAGAGAGGCTCTGACAGCTTCAAGATCAATGACCTGCTAC 900
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Qy 901 ACTCAATGAGAAACCTTTTCTGTGAGAGACATTTAATGTCGTGACAGCCCTATCTT 960
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Qy 961 AAAAGAAAGTTGGATGAAAGCTGCACTCCAGGTCAGATGAAAGGAGCTCTTTTAT 1020
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Qy 1021 CTCGATTTGTCATCATCAACAACAACATGTTTGAAGGTCATCTGAGCATCTG 1080
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Qy 1081 CCTGCTGATCTGTTCTGCTCTGAGCCCTGCTCTCTCTGTTGTTCTGAGCTCTG 1140
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Db 1141 CTGCACTGATTTATCAAGAGGTCCTCAACCCCTGCGAGAGAGTGAAGAAATTA 1200
Qy 1201 AATTAATTAACAAGAAAGAAAGAAATCCCAAGAAACAGATTAACCAACAC 1260
Db 1201 AATTAATTAACAAGAAAGAAAGAAATCCCAAGAAACAGATTAACCAACAC 1260
Qy 1261 CGGTGCAAGATTTATTAATGATGCTGTAAGTCTCAATCTGACAGCTTTT 1320
Db 1261 CGGTGCAAGATTTATTAATGATGCTGTAAGTCTCAATCTGACAGCTTTT 1320

Qy 1321 CCTTATTTTCCCTGATTAATCCAGTGTCTAAATTAATAGCTATGAAAT 1380
Db 1321 CCTTATTTTCCCTGATTAATCCAGTGTCTAAATTAATAGCTATGAAAT 1380
Qy 1381 CAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1414
Db 1381 CAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1414

RESULT 2
US-10-133-937-58
; Sequence 58, Application US/10133937
; Publication No. US20030207278A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringer, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Melzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; FILE REFERENCE: 11613.56US01
; CURRENT APPLICATION NUMBER: US/10/133,937
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-937-58

Query Match 100.0%; Score 1414; DB 6; Length 1454;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGACCCGCGAGAGAGGCGCGGATGCGCGTCTGAGGCTGTGCGAGTTGCGG 60
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Db 101 AGCGTGGAGAGAGGCGCGCTGCTCCCGGGCTGCGGGCCATGCGCGGAGG 160
Qy 121 GAGAGCCCTCGGATCGGCTTCAGTGGCTCTTTGACACTGTGTCTATCTGCGC 180
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Qy 181 CGGCAAGGGGAGCGCAGAGAGATGGGGTTCAGCTGCTAAGCGGATTTGACCTGTA 240
Db 221 CGGCAAGGGGAGCGCAGAGAGATGGGGTTCAGCTGCTAAGCGGATTTGACCTGTA 280
Qy 241 CTTCAATTTTGAACAATCAGAAAGTGTGTGCAACAATGAAATCTATTAATCTTGT 300
Db 281 CTTCAATTTTGAACAATCAGAAAGTGTGTGCAACAATGAAATCTATTAATCTTGT 340
Qy 301 GGAAGAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATGTCCTTTATGTTTCTC 360
Db 341 GGAAGAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATGTCCTTTATGTTTCTC 400
Qy 361 CACCCGAGAGAACCTTATGAAAATGACAGAAAGCAGAAACAAATCCGTCAGGCT 420
Db 401 CACCCGAGAGAACCTTATGAAAATGACAGAAAGCAGAAACAAATCCGTCAGGCT 460
Qy 421 AGAAGAACTCCAGAAAGTCTGCGAGAGAGACCTTACATGATGAAAGATTGAAAG 480
Db 461 AGAAGAACTCCAGAAAGTCTGCGAGAGAGACCTTACATGATGAAAGATTGAAAG 520
Qy 481 GGCAGTGAAGATTTATGAAAACAGAGGGTACAGGACAGCCAGCTCATCAT 540
Db 521 GGCAGTGAAGATTTATGAAAACAGAGGGTACAGGACAGCCAGCTCATCAT 580

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Qy 901 ACTCAATGGAAGCCCTTTTCTGTGGAACAACATTATTACTGTGTCCAGCCCTATCTT 960
Db 941 ACTCAATGGAAGCCCTTTTCTGTGGAACAACATTATTACTGTGTCCAGCCCTATCTT 1000
Qy 961 AAAAGAGTTGGCATGAAGCTGCACTCCAGGTCAAGATGAAGATGAGCTCTTTTAT 1020
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Db 1061 CTCGAGTTCTGTATCATATCAACACACACTGTTCTGACGGTTCATCTTGCCATGCG 1120
Qy 1081 CCTGCTGATCCCTGCTCTGCTCTGAGCCCTGCTCTGCTCTGCTCTGCTCTGCTCTG 1140
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Qy 1201 AATTAATAATCAAG 1260
Db 1241 AATTAATAATCAAG 1300
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Db 1301 CCGTGCAAGTATTTTATCAATGCTCTGAAATCTATCTCAATCTGAGACGCTTTT 1360
Qy 1321 CCTCTAGTCCCTGATTTTCAATCCAGTGTCTAATCAATTAATAGCTATGTAAT 1380
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Db 1421 CAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1454

RESULT 4
US-09-918-715-176
; Sequence 176, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-176

Query Match 84.4%; Score 1193.8; DB 3; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AGGACCCGCGAGAGAGGCGCCGCGATGCGCTCCCTGAGGTCGTGCGAGTTCGCG 60
Db 41 AGGACCCGCGAGAGAGGCGCCGCGATGCGCTCCCTGAGGTCGTGCGAGTTCGCG 100

Qy 61 AGCGTGGAGAGAGCGGACCCCTGCTCTCCCGGAGCTGCGGAGCATAGGCGAGCGAGCG 120
Db 101 AGCGTGGAGAGAGCGGAGCCCTGCTCTCCCGGAGCTGCGGAGCATAGGCGAGCGAGCG 160
Qy 121 GAGAGCCCTCGGATGCGCTTCAAGTGTCTCTTTGGCACTGTGTGTCTATCTGTGCG 180
Db 161 GAGAGCCCTCGGATGCGCTTCAAGTGTCTCTTTGGCACTGTGTGTCTATCTGTGCG 220
Qy 181 CGGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGTCTAGCGGAGTTGAACCTGTA 240
Db 221 CGGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGTCTAGCGGAGTTGAACCTGTA 280
Qy 241 CTTCAATTTTGAACAATGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
Db 281 CTTCAATTTTGAACAATGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 340
Qy 301 GGAACAGTTGGCTCAAAATTCATGAGCCACAGTTGAGATGTCTTTATGTTTCTC 360
Db 341 GGAACAGTTGGCTCAAAATTCATGAGCCACAGTTGAGATGTCTTTATGTTTCTC 400
Qy 361 CACCGAGAGAACACTTAATGAATCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 401 CACCGAGAGAACACTTAATGAATCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460
Qy 421 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGACATTACATGCAATGAAGATTTGAAG 480
Db 461 AGAAGAACTCCAGAAAGTTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 520
Qy 481 GGCAGTGAAGCATTTATTAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 521 GGCAGTGAAGCATTTATTAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 580
Qy 541 TGCTTGAATGAAG 600
Db 581 TGCTTGAATGAAG 640
Qy 601 TAGGCTGAGATCTTGTGCAATGTTTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
Db 641 TAGGCTGAGATCTTGTGCAATGTTTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 700
Qy 661 ACAGCTGCGCGGATTCGAGACAGTAAAGATATGTTCCTCCGTAATGAGCGCTTGA 720
Db 701 ACAGCTGCGCGGATTCGAGACAGTAAAGATATGTTCCTCCGTAATGAGCGCTTGA 760
Qy 721 GGCTGCAAGGCAATCAATCAATCAATTTGAAGAGCTGTGAGAGAGAGAGAGAGAG 780
Db 761 GGCTGCAAGGCAATCAATCAATCAATTTGAAGAGCTGTGAGAGAGAGAGAGAGAG 820
Qy 781 TGAACCATCAACATATGTGAGAGAGTCAATTTCAAGTTGTCTGAGAGAGAGAGAGAG 840
Db 821 TGAACCATCAACATATGTGAGAGAGTCAATTTCAAGTTGTCTGAGAGAGAGAGAGAG 880
Qy 841 CCGACATGCGCGCAACGTGAGAGAGTCTGTGAGCTTCAAGATCAATGATCTGGTCA 900
Db 881 CCGACATGCGCGCAACGTGAGAGAGTCTGTGAGCTTCAAGATCAATGATCTGGTCA 940
Qy 901 ACTCAATGAGAGCCCTTTCTGTGGAAGACATTATTAATGATGATGATGATGATGAT 960
Db 941 ACTCAATGAGAGCCCTTTCTGTGGAAGATTAATTAATGATGATGATGATGATGAT 1000
Qy 961 AAAAGAGTTGGCATGAAGCTGCACTCCAGGTCAAGATGAAGATGAGCTCTTTTAT 1020
Db 1001 AAAAGAGTTGGCATGAAGCTGCACTCCAGGTCAAGATGAAGATGAGCTCTTTTAT 1060
Qy 1021 CTCGAGTTCTGTATCATATCAACACACACTGTTCTGACGGTTCATCTTGCCATGCG 1080
Db 1061 CTCGAGTTCTGTATCATATCAACACACACTGTTCTGACGGTTCATCTTGCCATGCG 1120
Qy 1081 CCTGCTGATCCCTGCTCTGCTCTGAGCCCTGCTCTGCTCTGCTCTGCTCTGCTCTG 1140
Db 1121 CCTGCTGATCCCTGCTCTGCTCTGAGCCCTGCTCTGCTCTGCTCTGCTCTGCTCTG 1180


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; ORGANISM: Homo Sapiens
;
; FEATURE:
;
; NAME/KEY: CDS
; LOCATION: (144) ... (1838)
;
US-10-301-822-198
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Query Match	84.4%	Score 1193.8	DB 6	Length 5540
Best Local Similarity	99.8%	Pred. No. 0		
Matches 1195; Conservative	0	Mismatches 2	Indels 0	Gaps 0

OY	1	AGGACCCCGGAGGAAGGCGCCCGGATGGCGGCTCCCTGAGGGATGCTGGCAGATTGCGG	60
Db	41	AGGACCCCGGAGGAAGGCGCCCGGATGGCGGCTCCCTGAGGGATGCTGGCAGATTGCGG	100
OY	61	AGCGTGGGAAGGAGCGGACCTGCTCTCCCGGGCTGCGGACATGGCCACGGCGGAGCG	120
Db	101	AGCGTGGGAAGGAGCGGACCTGCTCTCCCGGGCTGCGGACATGGCCACGGCGGAGCG	160
OY	121	GAGAGCCTCGGCATTCGGCTTCATGAGGCTCTCTTTGGCCACTCTGGTGTCTATCTGGCC	180
Db	161	GAGAGCCTCGGCATTCGGCTTCATGAGGCTCTCTTTGGCCACTCTGGTGTCTATCTGGCC	220
OY	181	CGGGCAAGGGGGAGCCGAGGGAGATGGGGGTCCAGCTGTCTGCGGCAATTGGACCTGTG	240
Db	221	CGGGCAAGGGGGAGCCGAGGGAGATGGGGGTCCAGCTGTCTGCGGCAATTGGACCTGTG	280
OY	241	CTTCAATTTTGGACAAATCAGGAAGTGTGTGCAACACTGGAAATGAAATCTATTAATTGT	300
Db	281	CTTCAATTTTGGACAAATCAGGAAGTGTGTGCAACACTGGAAATGAAATCTATTAATTGT	340
OY	301	GGAACTGTTGGCTCACAATTCATCAGCCACAGTTGAGATGTCTTTATTTGTTTCTC	360
Db	341	GGAACTGTTGGCTCACAATTCATCAGCCACAGTTGAGATGTCTTTATTTGTTTCTC	400
OY	361	CACCCGAGGAAACAACCTTAATGAACTGACAGAAAGACAGAAACAATTCGTCAGGCGCT	420
Db	401	CACCCGAGGAAACAACCTTAATGAACTGACAGAAAGACAGAAACAATTCGTCAGGCGCT	460
OY	421	AGAAAGACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGCATGAAAGATTTGAAAG	480
Db	461	AGAAAGACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGCAATGAAAGATTTGAAAG	520
OY	481	GGCCAGTGAAGATTTATATGAAAACAGACAGGGGTACAGGACAGCCAGCTCATAT	540
Db	521	GGCCAGTGAAGATTTATATGAAAACAGACAGGGGTACAGGACAGCCAGCTCATAT	580
OY	541	TGCTTGACTGATGAGAACTCCATGAAATCTCTTTTCTATTCAGAGAGGAGGCTTA	600
Db	581	TGCTTGACTGATGAGAACTCCATGAAATCTCTTTTCTATTCAGAGAGGAGGCTTA	640
OY	601	TAGGTCTGAGATCTTGGTGAATGTTACTGTGTGTGTGAAGATTTTCATAGAC	660
Db	641	TAGGTCTGAGATCTTGGTGAATGTTACTGTGTGTGTGAAGATTTTCATAGAC	700
OY	661	ACAGCTGGCCCGGATTCGGAACGTBAAGATCATGTGTTCCCGTGAATGACGGCTTTCA	720
Db	701	ACAGCTGGCCCGGATTCGGAACGTBAAGATCATGTGTTCCCGTGAATGACGGCTTTCA	760
OY	721	GGCTCTGCAAGGCATCATCCATCTAAATTTTGAAGAGTCTCTGCATGCAATTTCTAGAC	780
Db	761	GGCTCTGCAAGGCATCATCCATCTAAATTTTGAAGAGTCTCTGCATGCAATTTCTAGAC	820
OY	781	TGAACCATCCACCATATGTGACAGAGATCATTTCAAGTGTGCTGAGAGAAACGGCTT	840
Db	821	TGAACCATCCACCATATGTGACAGAGATCATTTCAAGTGTGCTGAGAGAAACGGCTT	880
OY	841	CCGACATGCCCGCAACGTGACAGGGTCTCTTGACCTTCAGATCAATGACTCGGTCA	900
Db	881	CCGACATGCCCGCAACGTGACAGGGTCTCTTGACCTTCAGATCAATGACTCGGTCA	940
OY	901	ACTCAATGAAAGCCCTTTCTGTGGAAGACATTTACTGTGTGCAAGCGCTATCTT	960
Db	941	ACTCAATGAAAGCCCTTTCTGTGGAAGATCTTATTTACTGTGTGCAAGCGCTATCTT	1000

QY	961	AAAGAAGTTGGCATGAAAGTGTGATCTCCAGGTCCAGATGAAGATGGCCCTCTCTTTAT	1020
Db	1001	AAAAGAAGTGGCAGTGAAGCTGACATCCAGGTCCAGATGAAGATGAAGATGGCCCTCTCTTTAT	1060
QY	1021	CTCCAGTTCTGTCAATCATCAACCAACACACTGTTTGAAGGTTCCATCCGCGCATGCG	1080
Db	1061	CTCCAGTTCTGTCAATCATCAACCAACACACTGTTTGAAGGTTCCATCCGCGCATGCG	1120
QY	1081	CTGTGTGATTCCTGTTCTGTGCTCTGAAGCCGTGGCTCTCTCTGTGTGTGTCTGGCCCTCTG	1140
Db	1121	CTGTGTGATTCCTGTTCTGTGCTCTGAAGCCGTGGCTCTCTCTGTGTGTGTCTGGCCCTCTG	1180
QY	1141	CTGCACGTGTATTATCAAGAGAGTCCCTCCACCCCTGCGGAGAGATGAGAGAAA	1197
Db	1181	CTGCACGTGTATTATCAAGAGAGTCCCTCCACCCCTGCGGAGAGATGAGAGAAA	1237

RESULT 7
US-10-474-794-176

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1      : Sequence 176, Application US/10474794
2      : Publication No. US20040213799A1
3      :
4      : GENERAL INFORMATION:
5      :
6      : APPLICANT: Carson-Walter, Eleanor
7      : APPLICANT: St. Croix, Brad
8      : APPLICANT: Vogelstein, Bert
9      : APPLICANT: Kinzler, Kenneth
10     :
11     : TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
12     :
13     : FILE REFERENCE: 1107.00179
14     :
15     : CURRENT APPLICATION NUMBER: US/10/474.794
16     :
17     : CURRENT FILING DATE: 2003-10-14
18     :
19     : PRIOR APPLICATION NUMBER: 60/282,850
20     :
21     : PRIOR FILING DATE: 2001-04-11
22     :
23     : PRIOR APPLICATION NUMBER: 60/308,829
24     :
25     : PRIOR FILING DATE: 2001-08-01
26     :
27     : NUMBER OF SEQ ID NOS: 359
28     :
29     : SOFTWARE: FastSeq for Windows Version 4.0
30     :
31     : SEQ ID NO 176
32     :
33     : LENGTH: 5540
34     :
35     : TYPE: DNA
36     :
37     : ORGANISM: Homo sapiens
38     :
39     : US-10-474-794-176

```

Query Match	84.4%	Score	1193.8	DB	8	Length	5540
Best Local Similarity	99.8%	Pred. No.	0				
Match 1195; Conservative	0	Mismatches	2	Indels	0	Gaps	0

QY	1	AGGACCCGCGAGAAAGGAGCCCGCGAGATGAGCGCGTCCCTGAGAGGCGTGGTGGCGAGTTCCGCGG	60
Db	41	AGGACCCGCGAGAAAGGAGCCCGCGAGATGAGCGCGTCCCTGAGAGGTCGTGGCGAGTTCCGCGG	100
QY	61	AGCGTGGGAAAGAGACGGACCGTGTCTTCCCGGAGCTGCGGAGCCATGAGCCAGCGGAGCG	120
Db	101	AGCGTGGGAAAGAGACGGACCGTGTCTTCCCGGAGCTGCGGAGCCATGAGCCAGCGGAGCG	160
QY	121	GAGAGCCCTCGGCAATCGGCTTCCAGTGGCTCTCTTTGGCCACTCTGTGTCATCTGCGC	180
Db	161	GAGAGCCCTCGGCAATCGGCTTCCAGTGGCTCTCTTTGGCCACTCTGTGTCATCTGCGC	220
QY	181	CGGCGAAGGGGAGACGACAGGAGATGAGGGGTCCAGCCTGTACGCGGAGTTGACGTGA	240
Db	221	CGGCGAAGGGGAGACGACAGGAGATGAGGGGTCCAGCCTGTCTACGCGGAGTTGACGTGA	280
QY	241	CTTCATTTTGGACAACATCAGGAATGTGCTGCACACTGGAAATGAATCTTATCTTGT	300
Db	281	CTTCATTTTGGACAACATCAGGAATGTGCTGCACACTGGAAATGAATCTTATCTTGT	340
QY	301	GGAACAGTTGGCTCACAATTCATCAGCCCAAGTTGAGATGTCCTTATTTGTTTTCTC	360
Db	341	GGAACAGTTGGCTCACAATTCATCAGCCCAAGTTGAGATGTCCTTATTTGTTTTCTC	400
QY	361	CACCCGAGGAACAACCTTATGAACTGACAGGAAGACAGGAACAACATCCGTCAAGGCTT	420

Db 401 CACCCGAGAACACTTAATGAACTGACAGAAAGACAGAAACAAATCCGTCAAGGCT 460
Qy 421 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTAATGATGATTAAGATTTGAAAG 480
Db 461 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTAATGATGATTAAGATTTGAAAG 520
Qy 481 GGCAGAGAGACAGATTTATGAAACAGACAGAGGTACAGAGACAGCCGATCATCAT 540
Db 521 GGCAGAGAGACAGATTTATGAAACAGACAGAGGTACAGAGACAGCCGATCATCAT 580
Qy 541 TGCTTGAATGATGAGAACTCCATGAAAGATCTCTTTTCTATTGACAGAGAGGCTTAA 600
Db 581 TGCTTGAATGATGAGAACTCCATGAAAGATCTCTTTTCTATTGACAGAGAGGCTTAA 640
Qy 601 TAGGCTGAGAGATTTGGTGCATTTGTTTACTGTGTGTGTGTGAAAGATTTCAATGAGAC 660
Db 641 TAGGCTGAGAGATTTGGTGCATTTGTTTACTGTGTGTGTGTGAAAGATTTCAATGAGAC 700
Qy 661 ACAGCTGGCCGGGATTTGGGACAGTAAAGATCATGTGTTCCGGTGAATGACGGCTTTCA 720
Db 701 ACAGCTGGCCGGGATTTGGGACAGTAAAGATCATGTGTTCCGGTGAATGACGGCTTTCA 760
Qy 721 GGCCTGCAAGGACATCCATCACTCAATTTTGAAGAGTCCATGCAATTCAGACAGC 780
Db 761 GGCCTGCAAGGACATCCATCACTCAATTTTGAAGAGTCCATGCAATTCAGACAGC 820
Qy 781 TGAACATCCACATATGTGACAGAGATCATTTCAAGTTGTCTGTGAGAGAAAGGCTT 840
Db 821 TGAACATCCACATATGTGACAGAGATCATTTCAAGTTGTCTGTGAGAGAAAGGCTT 880
Qy 841 CCGACATGCCCGGACAGTGGACAGAGGTCTCTGACGCTCAAGATCAATGACCTCGGCTAC 900
Db 881 CCGACATGCCCGGACAGTGGACAGAGGTCTCTGACGCTCAAGATCAATGACCTCGGCTAC 940
Qy 901 ACTCAATGAGAAAGCCCTTTTCTGTGAAAGACATTTATTACTGTGTGACAGGCTCATCTT 960
Db 941 ACTCAATGAGAAAGCCCTTTTCTGTGAAAGATTTATTACTGTGTGACAGGCTCATCTT 1000
Qy 961 AAAAGAGTGGCATGAAAGCTGCACTCCAGCTCAGATGAAAGATGAGGCTCTCTTTTAT 1020
Db 1001 AAAAGAGTGGCATGAAAGCTGCACTCCAGCTCAGATGAAAGATGAGGCTCTCTTTTAT 1060
Qy 1021 CTCAGTTCTGTCAATCAACACACACACACTGTTTCAAGAGTTCATCCGAGGCTATGCG 1080
Db 1061 CTCAGTTCTGTCAATCAACACACACACACTGTTTCAAGAGTTCATCCGAGGCTATGCG 1120
Qy 1081 CCTGCTGATCTGTCTCTGCTCTGAGCCCTGCTCTCTCTGTGTGTGTGTGAGGCTCTCTG 1140
Db 1121 CCTGCTGATCTGTCTCTGCTCTGAGCCCTGCTCTCTCTGTGTGTGTGTGAGGCTCTCTG 1180
Qy 1141 CTGCACTGTGATTTATCAAGAGAGTCCCTCAACCCCTGCGAGAGAGTGAAGAAA 1197
Db 1181 CTGCACTGTGATTTATCAAGAGAGTCCCTCAACCCCTGCGAGAGAGTGAAGAAA 1237

RESULT 8

US-10-474-794-231
; Sequence 231, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Voelkelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107, 00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; PRIORITY FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-474-794-231
Query Match 84.4%; Score 1193.8; DB 8; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AGGACCCGCGAGAGAGGCGCCGCGATGCGGCTGCTGAGGCTGTGGAGTTCGCG 60
Db 41 AGGACCCGCGAGAGAGGCGCCGCGATGCGGCTGCTGAGGCTGTGGAGTTCGCG 100
Qy 61 AGCTGGAGAGAGGCGGACCTCTCTCCCGGGCTGCGGCGCATGCGCACGCGGAGCG 120
Db 101 AGCTGGAGAGAGGCGGACCTCTCTCCCGGGCTGCGGCGCATGCGCACGCGGAGCG 160
Qy 121 GAGAGCCCTGGGATGGGCTTCAGTGGCTCTTTGGCACTGTGATGCTCATGCGC 180
Db 161 GAGAGCCCTGGGATGGGCTTCAGTGGCTCTTTGGCACTGTGATGCTCATGCGC 220
Qy 181 CCGGCAAGGGGAGCGAGAGAGATGGGGTCCAGCTGCTACGCGGATTTGACCTGTA 240
Db 221 CCGGCAAGGGGAGCGAGAGAGATGGGGTCCAGCTGCTACGCGGATTTGACCTGTA 280
Qy 241 CTTCATTTTGGACAAATCAGAAAGTGTGTGACCACTGGAATGAAATCTAATCTTGT 300
Db 281 CTTCATTTTGGACAAATCAGAAAGTGTGTGACCACTGGAATGAAATCTAATCTTGT 340
Qy 301 GGAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATGCTTTATGTTTCTC 360
Db 341 GGAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATGCTTTATGTTTCTC 400
Qy 361 CACCCGAGAAACAACCTTAATGAACTGACAGAAAGACAGAAACAAATCCGTCAAGGCT 420
Db 401 CACCCGAGAAACAACCTTAATGAACTGACAGAAAGACAGAAACAAATCCGTCAAGGCT 460
Qy 421 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTAATGATGATTAAGATTTGAAAG 480
Db 461 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTAATGATGATTAAGATTTGAAAG 520
Qy 481 GGCAGAGAGACAGATTTATGAAACAGACAGAGGTACAGAGACAGCCGATCATCAT 540
Db 521 GGCAGAGAGACAGATTTATGAAACAGACAGAGGTACAGAGACAGCCGATCATCAT 580
Qy 541 TGCTTGAATGATGAGAACTCCATGAAAGATCTCTTTTCTATTGACAGAGAGGCTTAA 600
Db 581 TGCTTGAATGATGAGAACTCCATGAAAGATCTCTTTTCTATTGACAGAGAGGCTTAA 640
Qy 601 TAGGCTGAGAGATTTGGTGCATTTGTTTACTGTGTGTGTGTGAAAGATTTCAATGAGAC 660
Db 641 TAGGCTGAGAGATTTGGTGCATTTGTTTACTGTGTGTGTGTGAAAGATTTCAATGAGAC 700
Qy 661 ACAGCTGGCCGGGATTTGGGACAGTAAAGATCATGTGTTCCGGTGAATGACGGCTTTCA 720
Db 701 ACAGCTGGCCGGGATTTGGGACAGTAAAGATCATGTGTTCCGGTGAATGACGGCTTTCA 760
Qy 721 GGCCTGCAAGGACATCCATCACTCAATTTTGAAGAGTCCATGCAATTCAGACAGC 780
Db 761 GGCCTGCAAGGACATCCATCACTCAATTTTGAAGAGTCCATGCAATTCAGACAGC 820
Qy 781 TGAACATCCACATATGTGACAGAGATCATTTCAAGTTGTGTGTGAGAGAAAGGCTT 840
Db 821 TGAACATCCACATATGTGACAGAGATCATTTCAAGTTGTGTGTGAGAGAAAGGCTT 880
Qy 841 CCGACATGCCCGGACAGTGGACAGAGGTCTCTGACGCTCAAGATCAATGACCTCGGCTAC 900
Db 881 CCGACATGCCCGGACAGTGGACAGAGGTCTCTGACGCTCAAGATCAATGACCTCGGCTAC 940
Qy 901 ACTCAATGAGAAAGCCCTTTTCTGTGAAAGACATTTATTACTGTGTGACAGGCTCATCTT 960

Db 941 ACTCAATGAGAAAGCCCTTTCTGTGAGAGATACTATTACTGTGTCCAGCCCTATCTT 1000
Qy 961 AAAAGAGTTGGCATGAAGCTGACCTCCAGGTACAGATGAAGATGAGCTCTTTTAT 1020
Db 1001 AAAAGAGTTGGCATGAAGCTGACCTCCAGGTACAGATGAAGATGAGCTCTTTTAT 1060
Qy 1021 CTCGAGTTCTGTATCATCAACCAACACACTGTTCTGAAGGTTCCATCTTGCCATGCG 1080
Db 1061 CTCGAGTTCTGTATCATCAACCAACACACTGTTCTGAAGGTTCCATCTTGCCATGCG 1120
Qy 1081 CTCGCTGATCCCTGTCTCTCTCTCTAGCCCTGCTCTCTCTCTCTCTCTCTCTCTG 1140
Db 1121 CTCGCTGATCCCTGTCTCTCTCTCTAGCCCTGCTCTCTCTCTCTCTCTCTCTCTG 1180
Qy 1141 CTCGACTGTGATTAATCAAGAGAGTCCCTCCACCCCTGCGAGAGAGTGAAGAAA 1197
Db 1181 CTCGACTGTGATTAATCAAGAGAGTCCCTCCACCCCTGCGAGAGAGTGAAGAAA 1237

RESULT 9
US-10-979-159-176
Sequence 176, Application US/10979159
Publication No. US20050142138A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/10/979,159
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US/09/918,715
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 176
LENGTH: 5540
TYPE: DNA
ORGANISM: Homo sapiens
US-10-979-159-176

Query Match 84.4%; Score 1193.8; DB 9; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGACCCGGAGGAGAGGCGCCGCGATGGCGGCTCCCTGAGGGTCTGAGGATTTGGGG 60
Db 41 AGGACCCGGAGGAGAGGCGCCGCGATGGCGGCTCCCTGAGGGTCTGAGGATTTGGGG 100
Qy 61 AGCGTGGAGAGAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGCGACGCGGAGCG 120
Db 101 AGCGTGGAGAGAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGCGACGCGGAGCG 160
Qy 121 GAGAGCCCTCGGATCGGCTTCCAGTGGCTCTTTTGGCCACTCTGCTGCTCATCTGCGC 180
Db 161 GAGAGCCCTCGGATCGGCTTCCAGTGGCTCTTTTGGCCACTCTGCTGCTCATCTGCGC 220
Qy 181 CGGGCAAGGGGGAGCGAGGGAGGATGGGGGTCCAGGCTGTAAGGGGATTTGACCTGTA 240
Db 221 CGGGCAAGGGGGAGCGAGGGAGGATGGGGGTCCAGGCTGTAAGGGGATTTGACCTGTA 280
Qy 241 CTTTCATTTTGGACAATTCAGAGAGTGTGTGACCACTGGAATGAATCTATTACTTTGT 300
Db 281 CTTTCATTTTGGACAATTCAGAGAGTGTGTGACCACTGGAATGAATCTATTACTTTGT 340
Qy 301 GGAACGTTGGCTCACAAATTCATGAGCCCAAGTTGAGAGTCTCTTATGTTTCTC 360

Db 341 GGAACGTTGGCTCACAAATTCATGAGCCCAAGTTGAGAGTCTCTTATGTTTCTC 400
Qy 361 CACCCGAGGAACAACCTTAATGAATGAACAGAGAGAGAGAAATTCGTCAGAGCCCT 420
Db 401 CACCCGAGGAACAACCTTAATGAATGAACAGAGAGAGAGAAATTCGTCAGAGCCCT 460
Qy 421 AGAAGACTCCAGAAAGTTCTGCGAGAGAGAGACCTTACATGCAITGAAGATTTGAAG 480
Db 461 AGAAGACTCCAGAAAGTTCTGCGAGAGAGAGACCTTACATGCAITGAAGATTTGAAG 520
Qy 481 GGGCGAGTGAAGATTTTATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 521 GGGCGAGTGAAGATTTTATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 580
Qy 541 TGCTTTGACTGATGAGAGAACTCCATGAAGATCTCTTTTCTTATTCAGAGAGAGAGCTAA 600
Db 581 TGCTTTGACTGATGAGAGAACTCCATGAAGATCTCTTTTCTTATTCAGAGAGAGAGCTAA 640
Qy 601 TAGGTCGAGATCTTGTGCAATTGTTTACTGTGTGAGTGAAGATTTCAATGAGAC 660
Db 641 TAGGTCGAGATCTTGTGCAATTGTTTACTGTGTGAGTGAAGATTTCAATGAGAC 700
Qy 661 AGAGTCGCGCGGATTTGGGAGAGATGATGATTTCCCGTAATGAGAGGCTTTTA 720
Db 701 AGAGTCGCGCGGATTTGGGAGAGATGATGATTTCCCGTAATGAGAGGCTTTTA 760
Qy 721 GGGCTGCAAGGATCATCTCACTCAATTTTGAAGAGTCCCTCATGAAATTTAGACAG 780
Db 761 GGGCTGCAAGGATCATCTCACTCAATTTTGAAGAGTCCCTCATGAAATTTAGACAG 820
Qy 781 TGAACATTCACCATATGTGACAGAGAGTCAATTTCAAGTTGTCGTGAGAGAGAGCGCTT 840
Db 821 TGAACATTCACCATATGTGACAGAGAGTCAATTTCAAGTTGTCGTGAGAGAGAGCGCTT 880
Qy 841 CCGACATGCGCGCAAGTGAAGAGGCTCTCGACGCTTCAAGATCAATGATCGGCTAC 900
Db 881 CCGACATGCGCGCAAGTGAAGAGGCTCTCGACGCTTCAAGATCAATGATCGGCTAC 940
Qy 901 ACTCAATGAGAAAGCCCTTTCTGTGGAAGACACTTATTACTGTGTCCAGCCCTATCTT 960
Db 941 ACTCAATGAGAAAGCCCTTTCTGTGGAAGATCTTATTACTGTGTCCAGCCCTATCTT 1000
Qy 961 AAAAGAGTTGGCATGAAGGCTGCACTCCAGGTCAAGATGAAGATGAGCTCTTTTAT 1020
Db 1001 AAAAGAGTTGGCATGAAGGCTGCACTCCAGGTCAAGATGAAGATGAGCTCTTTTAT 1060
Qy 1021 CTCGAGTTCTGTATCATCAACCAACACACTGTTCTGAAGGTTCCATCTTGCCATGCG 1080
Db 1061 CTCGAGTTCTGTATCATCAACCAACACACTGTTCTGAAGGTTCCATCTTGCCATGCG 1120
Qy 1081 CTCGCTGATCCCTGTCTCTCTCTCTAGCCCTGCTCTCTCTCTCTCTCTCTCTCTG 1140
Db 1121 CTCGCTGATCCCTGTCTCTCTCTCTAGCCCTGCTCTCTCTCTCTCTCTCTCTCTG 1180
Qy 1141 CTCGACTGTGATTAATCAAGAGAGTCCCTCCACCCCTGCGAGAGAGTGAAGAAA 1197
Db 1181 CTCGACTGTGATTAATCAAGAGAGTCCCTCCACCCCTGCGAGAGAGTGAAGAAA 1237

RESULT 10
US-10-979-159-231
Sequence 231, Application US/10979159
Publication No. US20050142138A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/10/979,159
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US/09/918,715

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; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 231
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-979-159-231

Query Match      84.4%; Score 1193.8; DB 9; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 AGGACCCGCGAGAGAGGCGCGGAGTGGGCGCTCCCTGAGGGTCCGTGGGAGTTGCGCG 60
DB      41 AGGACCCGCGAGAGAGGCGCGGAGTGGGCGCTCCCTGAGGGTCCGTGGGAGTTGCGCG 100
QY      61 AGCGTGGAGAGAGAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGGCCACGCGCGAGCG 120
DB      101 AGCGTGGAGAGAGAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGGCCACGCGCGAGCG 160
QY      121 GAGAGCCCTCGGAGTCGGCTTCCAGTGGCTCTTTGGCCACTCTGTGCTCATCTGCGC 180
DB      161 GAGAGCCCTCGGAGTCGGCTTCCAGTGGCTCTTTGGCCACTCTGTGCTCATCTGCGC 220
QY      181 CGGGCAAGGGGAGCGGAGAGATGGGGGTCCAGCCTGCTAGCGCGGATTTGACCTGTA 240
DB      221 CGGGCAAGGGGAGCGGAGAGATGGGGGTCCAGCCTGCTAGCGCGGATTTGACCTGTA 280
QY      241 CTTCATTTTGGACAATCAGGAAGTGTGCTGCACTGAGATGAATCTATTACTTTGT 300
DB      281 CTTCATTTTGGACAATCAGGAAGTGTGCTGCACTGAGATGAATCTATTACTTTGT 340
QY      301 GGAACAGTTGGCTCACAAAATTCATCAGCCCAAGTTGAGAATGCTTTATTTGTTTCTC 360
DB      341 GGAACAGTTGGCTCACAAAATTCATCAGCCCAAGTTGAGAATGCTTTATTTGTTTCTC 400
QY      361 CACCCGAGGAAACAACCTTAATGAACAGAGAGAGAGAGAGAAATCCGTCAAGGCT 420
DB      401 CACCCGAGGAAACAACCTTAATGAACAGAGAGAGAGAGAAATCCGTCAAGGCT 460
QY      421 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTAATGATGATGAAGATTGTAAG 480
DB      461 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTAATGATGATGAAGATTGTAAG 520
QY      481 GGGCAGTGAACAGATTTTATATGAAAACAAGAGGTACAGACAGCCAGCTCATCAT 540
DB      521 GGGCAGTGAACAGATTTTATATGAAAACAAGAGGTACAGACAGCCAGCTCATCAT 580
QY      541 TGCCTTACCTGATGAGAAATCTCCATGAAAGTCTTTTCTATTCAAGAGGGAGGTTAA 600
DB      581 TGCCTTACCTGATGAGAAATCTCCATGAAAGTCTTTTCTATTCAAGAGGGAGGTTAA 640
QY      601 TAGGCTCGAGATCTTGATGCAATTTGTTACTGATGTTGGTGTGAAGAATTTCAATGAGAC 660
DB      641 TAGGCTCGAGATCTTGATGCAATTTGTTACTGATGTTGGTGTGAAGAATTTCAATGAGAC 700
QY      661 ACAAGTGGCCCGGATTTGCGGACAGTAAAGATCATGTGTTTCCCGTGAATGACGGCTTTCA 720
DB      701 ACAAGTGGCCCGGATTTGCGGACAGTAAAGATCATGTGTTTCCCGTGAATGACGGCTTTCA 760
QY      721 GGGCTTCAGAGAGATCATCTCAATTTTGAAGAAGATCCGTCATTCGAATTTCCAGAGC 780
DB      761 GGGCTTCAGAGAGATCATCTCAATTTTGAAGAAGATCCGTCATTCGAATTTCCAGAGC 820
QY      781 TGAACCATCCACCATATGTGAGAGAGATCATTTCAAGTTGTCGTGAGAGAAACGGCTT 840
DB      821 TGAACCATCCACCATATGTGAGAGAGATCATTTCAAGTTGTCGTGAGAGAAACGGCTT 880
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QY      841 CGGACATGCGCCGCAACGTGAGACAGGCTCCTGACACTTCAAGATCATGACTCGGTAC 900
DB      881 CGGACATGCGCCGCAACGTGAGACAGGCTCCTGACACTTCAAGATCATGACTCGGTAC 940
QY      901 ACTCAATGAGAGACCTTTTCTGTGTGAGAGACATTATTACTGTGTCCAGCGCTATCTT 960
DB      941 ACTCAATGAGAGACCTTTTCTGTGTGAGAGACTTATTACTGTGTCCAGCGCTATCTT 1000
QY      961 AAAAGAGTTGGCATTAAGCTGACATCCAGGTCCAGATGAAGAGATGGCTCTCTTTTAT 1020
DB      1001 AAAAGAGTTGGCATTAAGCTGACATCCAGGTCCAGATGAAGAGATGGCTCTCTTTTAT 1060
QY      1021 CTCGACTGCTGATCATATACACACACACACTGTTTGAAGGTTCCATCCTGGCCATGCG 1080
DB      1061 CTCGACTGCTGATCATATACACACACACTGTTTGAAGGTTCCATCCTGGCCATGCG 1120
QY      1081 CCGTGTGATCTGTTCTGCTGCTCTAGCCCTGAGCTCTCTGTGTGTTCTGAGCCCTCTG 1140
DB      1121 CCGTGTGATCTGTTCTGCTGCTCTAGCCCTGAGCTCTCTGTGTGTTCTGAGCCCTCTG 1180
QY      1141 CTGCACTGTGATTAATCAAGAGAGTCCCTCACCCCTGCCAGAGAGATGAGAGAA 1197
DB      1181 CTGCACTGTGATTAATCAAGAGAGTCCCTCACCCCTGCCAGAGAGATGAGAGAA 1237

RESULT 11
US-11-047-278-5
; Sequence 5, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A. T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296, 97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; PRIOR FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144)..(1835)
US-11-047-278-5

Query Match      84.4%; Score 1193.8; DB 10; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 AGGACCCGCGAGAGAGGCGCGGATGGGCGCTCCCTGAGGGTCCGTGGGAGTTGCGCG 60
DB      41 AGGACCCGCGAGAGAGGCGCGGATGGGCGCTCCCTGAGGGTCCGTGGGAGTTGCGCG 100
QY      61 AGCGTGGAGAGAGAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGGCCACGCGCGAGCG 120
DB      101 AGCGTGGAGAGAGAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGGCCACGCGCGAGCG 160
QY      121 GAGAGCCCTCGGAGTCGGCTTCCAGTGGCTCTTTGGCCACTCTGTGCTCATCTGCGC 180
DB      161 GAGAGCCCTCGGAGTCGGCTTCCAGTGGCTCTTTGGCCACTCTGTGCTCATCTGCGC 220
QY      181 CGGGCAAGGGGAGCGGAGAGATGGGGGTCCAGCCTGCTAGCGCGGATTTGACCTGTA 240
DB      221 CGGGCAAGGGGAGCGGAGAGATGGGGGTCCAGCCTGCTAGCGCGGATTTGACCTGTA 280
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OY 241 CTTCAATTTTGA CAAATCAGAAAGTGTGTCACCACTGAAATGAATCTATTACTTGT 300
| | | | |
DB 281 CTTCAATTTTGA CAAATCAGAAAGTGTGTCACCACTGAAATGAATCTATTACTTGT 340
OY 301 GGAACAGTTGGCTCACAATTTCACTGACCCACAGTTGAGAATGCTTTATTGTTTTC 360
| | | | |
DB 341 GGAACAGTTGGCTCACAATTTCACTGACCCACAGTTGAGAATGCTTTATTGTTTTC 400
OY 361 CACCCGAGGAACAACCTTAATGAACTGACAGAAAGCAGAAACAATCCGCAAGGCT 420
| | | | |
DB 401 CACCCGAGGAACAACCTTAATGAACTGACAGAAAGCAGAAACAATCCGCAAGGCT 460
OY 421 AGAAGAACTCCAGAAAGTCTGCGAGAGAGACATCTACATGATGAAGATTTGAAAG 480
| | | | |
DB 461 AGAAGAACTCCAGAAAGTCTGCGAGAGAGACATCTACATGATGAAGATTTGAAAG 520
OY 481 GGCACAGTACAGATTTATTATGAAACAGACAGAGGTA CAGGACGCCATCAT 540
| | | | |
DB 521 GGCACAGTACAGATTTATTATGAAACAGACAGAGGTA CAGGACGCCATCAT 580
OY 541 TGCCTTGAAGTGAAGTCCATGAAGATCTCTTTCTATTCTAGAGAGGAGCTTA 600
| | | | |
DB 581 TGCCTTGAAGTGAAGTCCATGAAGATCTCTTTCTATTCTAGAGAGGAGCTTA 640
OY 601 TAGGTCTGAGATCTTGTCAGATTTGTTTAACTGTGTGTAAGAAAGATTTCAATTGAGAC 660
| | | | |
DB 641 TAGGTCTGAGATCTTGTCAGATTTGTTTAACTGTGTGTAAGAAAGATTTCAATTGAGAC 700
OY 661 ACAAGTGGCCCGGATTCGCGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTTCA 720
| | | | |
DB 701 ACAAGTGGCCCGGATTCGCGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTTCA 760
OY 721 GGCTCGAAGGATCATCACTCAATTTTGAAGAACTCTGATGAAGATTTAGCAGC 780
| | | | |
DB 761 GGCTCGAAGGATCATCACTCAATTTTGAAGAACTCTGATGAAGATTTAGCAGC 820
OY 781 TGAACCATCCACCATATGTGACAGAGAGTCAATTTCAAGTTGTCGTGAGAGAAACGGCTT 840
| | | | |
DB 821 TGAACCATCCACCATATGTGACAGAGAGTCAATTTCAAGTTGTCGTGAGAGAAACGGCTT 880
OY 841 CCGACATGCCCGGACAGTGA CAGGGTCTCTGACGCTTCAGATCAATGACTCGGTCAAC 900
| | | | |
DB 881 CCGACATGCCCGGACAGTGA CAGGGTCTCTGACGCTTCAGATCAATGACTCGGTCAAC 940
OY 901 ACTCAATGAAAGCCCTTTTCTGTGAAAGCACTTAATTTACTGTGCAAGCCGCTATCTT 960
| | | | |
DB 941 ACTCAATGAAAGCCCTTTTCTGTGAAAGCACTTAATTTACTGTGCAAGCCGCTATCTT 1000
OY 961 AAAAAGATTGGCATGAAAGCTGCACTCCAGGTCAAGATGAACGATGGCTCTCTTTTAT 1020
| | | | |
DB 1001 AAAAAGATTGGCATGAAAGCTGCACTCCAGGTCAAGATGAACGATGGCTCTCTTTTAT 1060
OY 1021 CTCACATTTCTGATCATCA CCAACA CACTGTTTGAAGGTTCCATCTCTGCAATCCG 1080
| | | | |
DB 1061 CTCACATTTCTGATCATCA CCAACA CACTGTTTGAAGGTTCCATCTCTGCAATCCG 1120
OY 1081 CCGTCGATGCTGTTCTGCTGCTAGCCCTGAGCTCTCTCTGAGTTCTGAGCCCTCTG 1140
| | | | |
DB 1121 CCGTCGATGCTGTTCTGCTGCTAGCCCTGAGCTCTCTCTGAGTTCTGAGCCCTCTG 1180
OY 1141 CTGCACTGATTAATCAAGAGGTCCCTCAACCCCTGCGAGAGAGTGAAGAAA 1197
| | | | |
DB 1181 CTGCACTGATTAATCAAGAGGTCCCTCAACCCCTGCGAGAGAGTGAAGAAA 1237
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RESULT 12

US-11-047-278-7

; Sequence 7, Application US/11047278

; Publication No. US20050196407A1

; GENERAL INFORMATION:

; APPLICANT: Young, John A.T.

; APPLICANT: Bradley, Kenneth A.

```
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296, 97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (113) .. (1111)
US-11-047-278-7
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Query Match 74.4%; Score 1052.4; DB 10; Length 2112;
Best Local Similarity 99.9%; Pred. No. 1.6e-279;
Matches 1053; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 AGAAGCCGAGAGAGAGGCGCCGAGATGCGCGCTCGTAGGGGTCGTGCGAGTTGCGCG 60
| | | | |
DB 10 AGAAGCCGAGAGAGAGGCGCCGAGATGCGCGCTCGTAGGGGTCGTGCGAGTTGCGCG 69
OY 61 AGCGTGGAGAGAGAGGAGCCCTGCTCTCCCGGGCTGCGGGCCATGAGCCAGCGGAGG 120
| | | | |
DB 70 AGCGTGGAGAGAGAGGAGCCCTGCTCTCCCGGGCTGCGGGCCATGAGCCAGCGGAGG 129
OY 121 GAGAGCCCTCGGATCGGCTTCAGTGGCTCTTTGAGCACTGTGAGTCTATCTGCGC 180
| | | | |
DB 130 GAGAGCCCTCGGATCGGCTTCAGTGGCTCTTTGAGCACTGTGAGTCTATCTGCGC 189
OY 181 CCGGAGAGGAGGAGCGAGAGAGATGGGGTCAAGCTGCTACCGGATTTGACCTGTA 240
| | | | |
DB 190 CCGGAGAGGAGGAGCGAGAGAGATGGGGTCAAGCTGCTACCGGATTTGACCTGTA 249
OY 241 CTTCAATTTTGA CAAATCAGAAAGTGTGTCACCACTGGAATGAATCTATTACTTGT 300
| | | | |
DB 250 CTTCAATTTTGA CAAATCAGAAAGTGTGTCACCACTGGAATGAATCTATTACTTGT 309
OY 301 GGAACAGTTGGCTCACAATTTATCATAGCCCAAGTTGAGAATGCTTATTGTTTCTC 360
| | | | |
DB 310 GGAACAGTTGGCTCACAATTTATCATAGCCCAAGTTGAGAATGCTTATTGTTTCTC 369
OY 361 CACCGAGAGAACACTTAATGAACTGACAGAAAGCAGAGAACAAATCCGCAAGGCT 420
| | | | |
DB 370 CACCGAGAGAACACTTAATGAACTGACAGAAAGCAGAGAACAAATCCGCAAGGCT 429
OY 421 AGAAGAACTCCAGAAAGTCTGCGAGAGAGACACTTACATGATGAAGATTTGAAAG 480
| | | | |
DB 430 AGAAGAACTCCAGAAAGTCTGCGAGAGAGACACTTACATGATGAAGATTTGAAAG 489
OY 481 GGCACAGTACAGATTTATTATGAAACAGACAGAGGTA CAGGACGCCATCAT 540
| | | | |
DB 490 GGCACAGTACAGATTTATTATGAAACAGACAGAGGTA CAGGACGCCATCAT 549
OY 541 TGCCTTGAAGTGAAGATCTCAATGAAGATCTTTTCTATTCTAGAGAGGAGCTTA 600
| | | | |
DB 550 TGCCTTGAAGTGAAGATCTCAATGAAGATCTTTTCTATTCTAGAGAGGAGCTTA 609
OY 601 TAGGTCTGAGATCTTGTCAGATTTGTTTAACTGTGTGTAAGAAAGATTTCAATTGAGAC 660
| | | | |
DB 610 TAGGTCTGAGATCTTGTCAGATTTGTTTAACTGTGTGTAAGAAAGATTTCAATTGAGAC 669
OY 661 ACAAGTGGCCCGGATTCGCGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTTCA 720
| | | | |
DB 670 ACAAGTGGCCCGGATTCGCGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTTCA 729
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Db 770 AAGCTGGGCGCGATGCGAGACGTAGATCATGTGTTCCCTGAAATGACGGCTTTTCA 829
Qy 721 GGCTGCAAGGATCATCACTCAATTTGAAAGATCCTGATCGAAATCTAGCAGC 780
Db 830 GGCTGCAAGGATCATCACTCAATTTGAAAGATCCTGATCGAAATCTAGCAGC 889
Qy 781 TGAACCATCACCATTATGTGACAGAGAGTCAATTTCAAGTTGTCTGAGAGAAAGCGCTT 840
Db 890 TGAACCATCACCATTATGTGACAGAGAGTCAATTTCAAGTTGTCTGAGAGAAAGCGCTT 949
Qy 841 CCGACATGCGCCGACAGTGAAGAGTCTCTGACAGCTTCAAGATGAATGACTCGGTAC 900
Db 950 CCGACATGCGCCGACAGTGAAGAGTCTCTGACAGCTTCAAGATGAATGACTCGGTAC 1009
Qy 901 ACTCAATGAGAAGCCCTTTTCTGTGGAAGACATTATTAAGTGTCCAGCGCTATCTT 960
Db 1010 ACTCAATGAGAAGCCCTTTTCTGTGGAAGATCTTATTAAGTGTCTCCAGCGCTATCTT 1069
Qy 961 AAAAGAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAAGATGAGCCTCTTTTAT 1020
Db 1070 AAAAGAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAAGATGAGCCTCTTTTAT 1129
Qy 1021 CTCAGTTCTGTCTATCATCAACCAACCAACTGT 1054
Db 1130 CTCAGTTCTGTCTATCATCAACCAACCAACTGT 1163

RESULT 14
US-10-038-307-1
/ Sequence 1, Application US/10038307
/ Publication No. US20030134786A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Englin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/038,307
/ CURRENT FILING DATE: 2002-06-28
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 2272
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ NAME/KEY: CDS
/ LOCATION: (213) ..(1211)
US-10-038-307-1

Query Match 74.4%; Score 1052.4; DB 6; Length 2272;
Best Local Similarity 99.9%; Pred. No. 1,7e-279;
Matches 1053; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGAAGCCGCGAGGAAGGCGCCGCGATGGCGCTCCCTGAGGATCGTGGAGATTGCGCG 60
Db 110 AGAAGCCGCGAGGAAGGCGCCGCGATGGCGCTCCCTGAGGATCGTGGAGATTGCGCG 169
Qy 61 AGCGTGGAGAGAGCGGACCTGTCTCCCGGGCTGCGGGCCATGAGCCAGCGCGAGCG 120
Db 170 AGCGTGGAGAGAGCGGACCTGTCTCCCGGGCTGCGGGCCATGAGCCAGCGCGAGCG 229
Qy 121 GAGAGCCCTCGGATGAGTGGCTTCCAGTGGCTCTTTTGGCACTCTGTGTCTATTCGCC 180
Db 230 GAGAGCCCTCGGATGAGTGGCTTCCAGTGGCTCTTTTGGCACTCTGTGTCTATTCGCC 289
Qy 181 CCGGCAAGGGGAGCGAGGAGAGATGGGGTCCAGGCTGTAAGGCGAATTTGAACTGTGA 240
Db 290 CCGGCAAGGGGAGCGAGGAGAGATGGGGTCCAGGCTGTAAGGCGAATTTGAACTGTGA 349
Qy 241 CTTCAATTTTGAACAAATCAGAAATGTGTGTGCAACACTGAAATGAATCTATTAATTTGT 300
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Db 350 CTTCAATTTTGAACAAATCAGAAATGTGTGTGCAACACTGAAATGAATCTATTAATTTGT 409
Qy 301 GGAAGATTGGCTCAAAATTCATCAGCCCAAGTTGGAATGTCTTATTTGTTTCTC 360
Db 410 GGAAGATTGGCTCAAAATTCATCAGCCCAAGTTGGAATGTCTTATTTGTTTCTC 469
Qy 361 CACCCGAGGAACAACTTTAATGAAATCTGACAGAGACAGAGAACAAATCCGTAAGGCT 420
Db 470 CACCCGAGGAACAACTTTAATGAAATCTGACAGAGACAGAGAACAAATCCGTAAGGCT 529
Qy 421 AGAAGAACTCCGAAAGTTTCCGAGAGAGACCTTAACATGATGAAGATTTGAAAG 480
Db 530 AGAAGAACTCCGAAAGTTTCCGAGAGAGACCTTAACATGATGAAGATTTGAAAG 589
Qy 481 GGCAGTGAAGATTTTATGAAAGACAGCAAGGATACAGAGACAGCAGGCTCATCAT 540
Db 590 GGCAGTGAAGATTTTATGAAAGACAGCAAGGATACAGAGACAGCAGGCTCATCAT 649
Qy 541 TGCTTTGACTGATGAGAACTTCATGAAGATCTTTTCTATTCTATTCAGAGAGGAGCTTA 600
Db 650 TGCTTTGACTGATGAGAACTTCATGAAGATCTTTTCTATTCTATTCAGAGAGGAGCTTA 709
Qy 601 TAGGTCTGAGATCTTTGGTGCATTTGTTTACTGTGTGTGTGAAAGATTTCAATGAGAC 660
Db 710 TAGGTCTGAGATCTTTGGTGCATTTGTTTACTGTGTGTGAAAGATTTCAATGAGAC 769
Qy 661 ACAGCTGGCCGGATTTGGGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTTCA 720
Db 770 ACAGCTGGCCGGATTTGGGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTTCA 829
Qy 721 GGCTGCAAGGATCATCACTCAATTTTGAAGATCTGATCGAAATTTCTAGCAGC 780
Db 830 GGCTGCAAGGATCATCACTCAATTTTGAAGATCTGATCGAAATTTCTAGCAGC 889
Qy 781 TGAACCATCACCATTATGTGACAGAGAGTCAATTTCAAGTTGTCTGAGAGAAAGCGCTT 840
Db 890 TGAACCATCACCATTATGTGACAGAGAGTCAATTTCAAGTTGTCTGAGAGAAAGCGCTT 949
Qy 841 CCGACATGCGCCGACAGTGAAGAGTCTCTGACAGCTTCAAGATGAATGAGCCTGTCAC 900
Db 950 CCGACATGCGCCGACAGTGAAGAGTCTCTGACAGCTTCAAGATGAATGAGCCTGTCAC 1009
Qy 901 ACTCAATGAGAAGCCCTTTTCTGTGGAAGACATTATTAAGTGTCTCCAGCGCTATCTT 960
Db 1010 ACTCAATGAGAAGCCCTTTTCTGTGGAAGATCTTATTAAGTGTCTCCAGCGCTATCTT 1069
Qy 961 AAAAGAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAAGATGAGCCTCTTTTAT 1020
Db 1070 AAAAGAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAAGATGAGCCTCTTTTAT 1129
Qy 1021 CTCAGTTCTGTCTATCATCAACCAACCAACTGT 1054
Db 1130 CTCAGTTCTGTCTATCATCAACCAACCAACTGT 1163

RESULT 15
US-10-201-292-1
/ Sequence 1, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Englin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 2272
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (213)...(1211)
US-10-201-292-1

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Query Match      74.4%; Score 1052.4; DB 6; Length 2272;
Best Local Similarity 99.9%; Pred. No. 1.7e-279;
Matches 1053; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 AGGACCCGCGAGGAGGCGCGCGATGCGCGCTCCCTGAGGCTCGGCGACTTGCGCG 60
DB 110 AGGACCCGCGAGGAGGCGCGCGATGCGCGCTCCCTGAGGCTCGGCGACTTGCGCG 169
QY 61 AGCGTGGGAGAGAGCGGACCCTGCTCTCCCGGGCTGCGGGCCATGGCCACGCGAGCG 120
DB 170 AGCGTGGGAGAGAGCGGACCCTGCTCTCCCGGGCTGCGGGCCATGGCCACGCGAGCG 229
QY 121 GAGAGCCCTTGGGATCGGCTTCCAGTGGCTCTCTTTGGCCACTCTGGTGTCTATCTGGCG 180
DB 230 GAGAGCCCTTGGGATCGGCTTCCAGTGGCTCTCTTTGGCCACTCTGGTGTCTATCTGGCG 289
QY 181 CGGGCAAGGGGGAAGCGAGGAGATGGGGGTCCAGCCTGCTACGCGGATTTGACCTGTA 240
DB 290 CGGGCAAGGGGGAAGCGAGGAGATGGGGGTCCAGCCTGCTACGCGGATTTGACCTGTA 349
QY 241 CTTCAATTTTGGACAATCAGGAAGTGTGCTGCAACACTGGAATGAAATCTATTACTTTGT 300
DB 350 CTTCAATTTTGGACAATCAGGAAGTGTGCTGCAACACTGGAATGAAATCTATTACTTTGT 409
QY 301 GGAACAGTTGGCTCACAATTTCAACGCCACAGTTGAGAATGTCCTTTATTTGTTTCTC 360
DB 410 GGAACAGTTGGCTCACAATTTCAACGCCACAGTTGAGAATGTCCTTTATTTGTTTCTC 469
QY 361 CACCCGAGGAACAACCTTAATGAACTGACAGAAAGACAGAAACAATCCGTCAGGCT 420
DB 470 CACCCGAGGAACAACCTTAATGAACTGACAGAAAGACAGAAACAATCCGTCAGGCT 529
QY 421 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGATGATGAGATTGAAAG 480
DB 530 AGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGATGATGAGATTGAAAG 589
QY 481 GGGCAGTGAAGCAATTTATTATGAAAACAGCAAGGTAAGGACAGCCGCTCATCAT 540
DB 590 GGGCAGTGAAGCAATTTATTATGAAAACAGCAAGGTAAGGACAGCCGCTCATCAT 649
QY 541 TGCTTTGACTGATGAGAACTCCATGAAAGTCTTTTCTATTCAAGAGGGAGGCTAA 600
DB 650 TGCTTTGACTGATGAGAACTCCATGAAAGTCTTTTCTATTCAAGAGGGAGGCTAA 709
QY 601 TAGGCTCGAGATCTTGGTGAATTTTACTGTGTGTGTGTAAGATTTCATATGAGAC 660
DB 710 TAGGCTCGAGATCTTGGTGAATTTTACTGTGTGTGTGTAAGATTTCATATGAGAC 769
QY 661 ACAAGCTGGCCGGAATTCGGAACAGTAAGATCATGTGTTCCGCTGAATGACGGCTTCA 720
DB 770 ACAAGCTGGCCGGAATTCGGAACAGTAAGATCATGTGTTCCGCTGAATGACGGCTTCA 829
QY 721 GGCTCTGCAAGGCAATCCACTCAATTTTGAAGAAGTCCGTCATCGAAATTCATAGAGC 780
DB 830 GGCTCTGCAAGGCAATCCACTCAATTTTGAAGAAGTCCGTCATCGAAATTCATAGAGC 889
QY 781 TGAACCATCCACATATGTGACAGAGATCATTTCAAGTTGTCTGAGAGGAAACGGCTT 840
DB 890 TGAACCATCCACATATGTGACAGAGATCATTTCAAGTTGTCTGAGAGGAAACGGCTT 949
QY 841 CCGACATGCCCGCAACGTGACAGGGTCTCTGCAAGCTTCAAGATCAATGACTGGTAC 900
DB 950 CCGACATGCCCGCAACGTGACAGGGTCTCTGCAAGCTTCAAGATCAATGACTGGTAC 1009
QY 901 ACTCAATGAGAAAGCCTTTTCTGTGAAAGACATTAATTTACTGTGCAGGCGCTATCTT 960

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DB 1010 ACTCAATGAGAAAGCCTTTTCTGTGAAAGATTAATTAATTTACTGTGTCCAGCGCTATCTT 1069
QY 961 AAAAGAGTTGGCATGAAGCTGCACTCCAGGTGACATGAAGAGTGGCTCTCTTTTAT 1020
DB 1070 AAAAGAGTTGGCATGAAGCTGCACTCCAGGTGACATGAAGAGTGGCTCTCTTTTAT 1129
QY 1021 CTCAGTTCTGTCAATCATCACCAACCACTGT 1054
DB 1130 CTCAGTTCTGTCAATCATCACCAACCACTGT 1163

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GenCore version 5.1.6
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OW nucleic - nucleic search, using BW model

Run on: December 17, 2005, 13:29:40 ; Search time 256.631 Seconds
(without alignments)
2700.811 Million cell updates/sec

Title: US-09-970-076-1
Perfect score: 1414
Sequence: 1 aggaccgcgcgaggaaggcc.....aaaaaaaaaaaaaaaaaaaa 1414

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1193.8	84.4	5540	US-11-186-284-198	Sequence 198, App
2	61.4	2765	6	US-10-750-185-25275	Sequence 25275, A
3	54	2126	6	US-10-909-125-809	Sequence 809, App
4	49.2	3.5	2773	US-10-689-742-43	Sequence 43, App1
5	48.6	3.4	2276	US-10-131-826A-9	Sequence 9, App1
6	48.6	3.4	2487	US-10-689-742-165	Sequence 165, App
7	47.2	3.3	894	US-10-689-742-5	Sequence 5, App1
8	46.8	3.3	1672	US-11-102-240-17	Sequence 17, App1
9	46.6	3.3	588	US-10-689-742-41	Sequence 41, App1
10	46.4	3.3	305312	US-10-995-561-13236	Sequence 13236, A
11	45.8	3.2	644	US-11-102-240-55	Sequence 55, App1
12	45.6	3.2	2463	US-11-108-528-3	Sequence 3, App1
13	45.6	3.2	4339	US-10-909-125-801	Sequence 801, App
14	45.2	3.2	2036	US-10-996-217A-8	Sequence 8, App1
15	45	3.2	6094	US-11-077-386-7	Sequence 7, App1
16	45	3.2	2092	US-10-689-742-137	Sequence 137, App
17	45	3.2	2933	US-10-131-826A-345	Sequence 345, App
18	44.8	3.2	1626	US-11-025-834A-12	Sequence 12, App1
19	44.8	3.2	1941	US-10-131-826A-165	Sequence 165, App
20	44.6	3.2	3265	US-11-102-240-69	Sequence 69, App1
21	44.4	3.1	961	US-11-102-240-143	Sequence 143, App1
22	44.4	3.1	1073	US-11-053-185-15	Sequence 15, App1
23	44	3.1	1883	US-10-131-826A-501	Sequence 501, App

24	43.8	3.1	1234	US-11-102-240-63	Sequence 63, App1
25	43.8	3.1	1904	US-10-131-826A-59	Sequence 59, App1
26	43.6	3.1	485	US-11-102-240-43	Sequence 43, App1
27	43.6	3.1	1073	US-11-102-240-95	Sequence 95, App1
28	43.6	3.1	1573	US-10-689-742-187	Sequence 187, App
29	43.6	3.1	2131	US-10-750-185-58717	Sequence 58717, A
30	43.6	3.1	2476	US-10-131-826A-489	Sequence 489, App
31	43.6	3.1	2479	US-10-955-054A-50	Sequence 50, App1
32	43.2	3.1	1690	US-11-090-439-43	Sequence 43, App1
33	43.2	3.1	2668	US-10-131-826A-511	Sequence 511, App
34	43.2	3.1	157224	US-11-112-908-51	Sequence 51, App1
35	43.2	3.1	170189	US-11-112-908-50	Sequence 50, App1
36	43	3.0	496	US-10-131-826A-533	Sequence 533, App1
37	43	3.0	1510	US-10-131-826A-533	Sequence 399, App
38	43	3.0	1674	US-10-131-826A-453	Sequence 453, App
39	43	3.0	169047	US-11-121-086-15	Sequence 15, App1
40	42.8	3.0	201	US-10-995-561-46434	Sequence 46434, A
41	42.8	3.0	311	US-11-123-896-361	Sequence 361, App
42	42.8	3.0	1204	US-10-131-826A-505	Sequence 505, App
43	42.8	3.0	1519	US-10-955-054A-181	Sequence 181, App
44	42.8	3.0	1624	US-10-131-826A-181	Sequence 181, App
45	42.8	3.0	645179	US-10-995-561-13293	Sequence 13293, A

ALIGNMENTS

RESULT 1
US-11-186-284-198
Sequence 198, Application US/1186284
Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhang
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
TITLE OF INVENTION: BURGART, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MP001-029P2RM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 198
LENGTH: 5540
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (144)...(1838)
US-11-186-284-198

Query Match 84.4%; Score 1193.8; DB 7; Length 5540;
Best Local Similarity 99.8%; Pred. No. 3.3e-294;
Matches 1195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGACCCGCGAGAGAGGCGCGCGATGCGCTCCCTGAGGCTCTGCGAGATTGCGG 60
DB 41 AGACCCGCGAGAGAGGCGCGCGATGCGCTCCCTGAGGCTCTGCGAGATTGCGG 100

QY 61 AGCGTGGAGGAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGAGCCACGCGGAGCG 120
 DB 101 AGCGTGGAGGAGCGGACCTGCTCTCCCGGGCTGCGGGCCATGAGCCACGCGGAGCG 160
 QY 121 GAGAGCCCTCGGCGATGCGCTTCCAGTGGCTCTTTGGGCACTCTGGTCTCATCTGGCG 180
 DB 161 GAGAGCCCTCGGCGATGCGCTTCCAGTGGCTCTTTGGGCACTCTGGTCTCATCTGGCG 220
 QY 181 CGGGCAAGGGGAGCGGAGGAGATGGGGATCCAGGCTCTCAAGCGGATTTGACCTGTA 240
 DB 221 CGGGCAAGGGGAGCGGAGGAGATGGGGATCCAGGCTCTCAAGCGGATTTGACCTGTA 280
 QY 241 CTTCAATTTTGGACAAATCAGGAAGTGTCTGCAACAATGAAATGAAATCTTATTA 300
 DB 281 CTTCAATTTTGGACAAATCAGGAAGTGTCTGCAACAATGAAATGAAATCTTATTA 340
 QY 301 GGAAACGTTGGCTCACAATTTATCAGCCCAAGTTGAAATGCTTATTTATTTCTC 360
 DB 341 GGAAACGTTGGCTCACAATTTATCAGCCCAAGTTGAAATGCTTATTTATTTCTC 400
 QY 361 CACCCGAGGAGCAACCTTAATGAACTGACAGAAAGACAGAAACAAATCCGTCAGGCGCT 420
 DB 401 CACCCGAGGAGCAACCTTAATGAACTGACAGAAAGACAGAAACAAATCCGTCAGGCGCT 460
 QY 421 AGAAGAACTCCAGAAAGTTCTGCGCAGAGAGAGACACTTAATGATGAAAGATTGAAAG 480
 DB 461 AGAAGAACTCCAGAAAGTTCTGCGCAGAGAGAGACACTTAATGATGAAAGATTGAAAG 520
 QY 481 GGCCAGTGGAGCATTTATTTAGAAAACAGCAAGGGTACAGAGACGCCAGGCTCATCT 540
 DB 521 GGCCAGTGGAGCATTTATTTAGAAAACAGCAAGGGTACAGAGACGCCAGGCTCATCT 580
 QY 541 TGGCTTGAATGAGAGATCTCATGAAAGTCTCTTTTCTATTGAGAGGAGGCTTA 600
 DB 581 TGGCTTGAATGAGAGATCTCATGAAAGTCTCTTTTCTATTGAGAGGAGGCTTA 640
 QY 601 TAGGCTCGAGATCTTGTGCAATTTGTTAATGTTGTGTGTAAGAAATTTCAATGAGAC 660
 DB 641 TAGGCTCGAGATCTTGTGCAATTTGTTAATGTTGTGTGTAAGAAATTTCAATGAGAC 700
 QY 661 AAGAGTGGCCGGATTTGGCGACAGTAAAGATCTGTGTTCCCGTGAATGAGCGGCTTGA 720
 DB 701 AAGAGTGGCCGGATTTGGCGACAGTAAAGATCTGTGTTCCCGTGAATGAGCGGCTTGA 760
 QY 721 GGCTCGAAGGCGATCATCTCAATTTTGAAGAGTCTGTCATGAAATTTAGACAGC 780
 DB 761 GGCTCGAAGGCGATCATCTCAATTTTGAAGAGTCTGTCATGAAATTTAGACAGC 820
 QY 781 TGAACCATCCACCATATGTGCAAGAGATCAATTTCAAGTTGTCTGAGAGAAACGGCTT 840
 DB 821 TGAACCATCCACCATATGTGCAAGAGATCAATTTCAAGTTGTCTGAGAGAAACGGCTT 880
 QY 841 CGGACATGCGCGGACAGTGAAGGGTCTCTGACGCTTCAAGATCAATGACTCGGTGAC 900
 DB 881 CGGACATGCGCGGACAGTGAAGGGTCTCTGACGCTTCAAGATCAATGACTCGGTGAC 940
 QY 901 ACTCAATGAAGACCTTTTCTGTGGAAGACCTTATTTAATGTTGTGCAAGCGCTATCTT 960
 DB 941 ACTCAATGAAGACCTTTTCTGTGGAAGATCTTATTTAATGTTGTGCAAGCGCTATCTT 1000
 QY 961 AAAAAGAGTTGGATGAAGCTGCACTCAGAGTCAAGATGAAGATGAGCTCTCTTTTAT 1020
 DB 1001 AAAAAGAGTTGGATGAAGCTGCACTCAGAGTCAAGATGAAGATGAGCTCTCTTTTAT 1060
 QY 1021 CTCGATTTCTGTATATATCAACCAACAATCTGTTCTGACGGTTCATCTGGCCATCGC 1080
 DB 1061 CTCGATTTCTGTATATATCAACCAACAATCTGTTCTGACGGTTCATCTGGCCATCGC 1120
 QY 1081 CCGGATGATCGTTTCTGCTCTAGCCGCTGCTCTCTGTTGTTGTTGCGCCCTCTG 1140
 DB 1121 CCGGATGATCGTTTCTGCTCTAGCCGCTGCTCTCTGTTGTTGTTGCGCCCTCTG 1180
 QY 1141 CTGCACTGTGATATATCAAGAGGTCCCTCCACCCCTGCGAGAGAGTGAAGAAA 1197

DB 1181 CTGCACTGTGATATATCAAGAGGTCTCTCCACCCCTCGAGAGAGTGAAGAGA 1237
 RESULT 2
 US-10-750-185-25275/c
 ; Sequence 25275, Application US/10750185
 ; Publication No. US2005026063A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MW1100-2
 ; CURRENT APPLICATION NUMBER: US/10/750,185
 ; PRIOR FILING DATE: 2003-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: Patencin version 3.1
 ; SEQ ID NO 25275
 ; LENGTH: 2765
 ; TYPE: DNA
 ; ORGANISM: Bovine 1986881163262
 US-10-750-185-25275
 Query Match 4.3%; Score 61.4; DB 6; Length 2765;
 Best Local Similarity 77.9%; Pred. No. 8,1e-06;
 Matches 74; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
 QY 733 CATATCCATCAATTTTGAAGAGTCTGATGAAATTTGAGAGCTGAACCATCCAC 792
 DB 211 CTTCTCCCTCTAGATATTTGAAGAAATCTGATGAAATTTCTAGAGCTGAACCATCCAC 152
 QY 793 CATATGCGAGAGAGTCAATTTCAAGTTGTGCTGA 827
 DB 151 CATATGCGAGAGGTAAATTTGAACCTAAGGTGA 117
 RESULT 3
 US-10-909-125-809
 ; Sequence 809, Application US/10909125
 ; Publication No. US20050261218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Beau, Christine
 ; APPLICANT: Lollo, Bridget
 ; APPLICANT: Bennett, C. Frank
 ; APPLICANT: Preiser, Susan M.
 ; APPLICANT: Grifley, Richard H.
 ; APPLICANT: Baker, Brenda F.
 ; APPLICANT: Vickers, Timothy
 ; APPLICANT: Marcussen, Eric G.
 ; APPLICANT: Koller, Eric
 ; APPLICANT: Swayze, Eric
 ; APPLICANT: Uain, Ravi
 ; APPLICANT: Bhat, Balkrishen
 ; APPLICANT: Peralta, Egen
 ; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
 ; FILE REFERENCE: ISI50080-100 (CORE0016US)
 ; CURRENT APPLICATION NUMBER: US/10/909,125
 ; PRIOR FILING DATE: 2004-07-30
 ; PRIOR APPLICATION NUMBER: US 60/492,056
 ; PRIOR FILING DATE: 2003-07-31
 ; PRIOR APPLICATION NUMBER: US 60/516,303
 ; PRIOR FILING DATE: 2003-10-31
 ; PRIOR APPLICATION NUMBER: US 60/531,596
 ; PRIOR FILING DATE: 2003-12-19
 ; PRIOR APPLICATION NUMBER: US 60/562,417

```

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 9
LENGTH: 2276
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-826A-9

Query Match 3.4%; Score 48.6; DB 6; Length 2276;
Best Local Similarity 67.0%; Pred. No. 0.013;
Matches 69; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1312 CAGCTTTTCTTCCTAGTTCCTGATTCGAATCCGAGGCTGAACATTCATTAAATACT 137
DB 2170 CTGGTTTATCTCTAGTGAATAATTAAGTCAAAAGTTATTATTCCTCGTCACAAAAA 222
OY 1372 ATATGAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1414
DB 2230 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2272

RESULT 6
US-10-689-742-165
Sequence 165, Application us/10689742
Publication No. US20050250180A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M
APPLICANT: Lavallee, Edward R
APPLICANT: Racie, Lisa A
APPLICANT: Evans, Cheryl
APPLICANT: Werberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 00766, 000091.10
CURRENT APPLICATION NUMBER: US/10/689,742

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/ CURRENT FILING DATE: 2003-10-22
/ PRIOR APPLICATION NUMBER: 09/746,783
/ PRIOR FILING DATE: 2000-12-21
/ NUMBER OF SEQ ID NOS: 231
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 165
/ LENGTH: 2487
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-689-742-165

Query Match
Best Local Similarity 58.7%; Pred. No. 0.014;
Matches 84; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1272 ATTTATACATGCTGTGAATTCATGCTCAATGCTAGTCTTTCTCTAGTCC 1331
DB 2291 ATGTTTAAATGCGCATTAATACTCTGCTGTAATAGTATTGTAATATTGG 2350
QY 1332 CTGTATTCAAATCCAGTGTCTACATTCATTAATAGCTAATGAAATCAAAAAA 1391
DB 2351 CAATAAATCTGCCCCGCAATTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2410
QY 1392 AAAAAAAAAAAAAAAAAAAAAA 1414
DB 2411 AAAAAAAAAAAAAAAAAAAAAA 2433

RESULT 7
US-10-689-742-5
/ Sequence 5, Application US/10689742
/ Publication No. US20050250180A1
/ GENERAL INFORMATION:
/ APPLICANT: Jacobs, Kenneth
/ APPLICANT: McCoy, John M
/ APPLICANT: Lavalie, Edward R
/ APPLICANT: Racie, Lisa A
/ APPLICANT: Evans, Cheryl
/ APPLICANT: Merberg, David
/ APPLICANT: Treacy, Maurice
/ APPLICANT: Spaulding, Vikki
/ TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
/ FILE REFERENCE: 00766.000091.10
/ CURRENT APPLICATION NUMBER: US/10/689,742
/ CURRENT FILING DATE: 2003-10-22
/ PRIOR APPLICATION NUMBER: 09/746,783
/ PRIOR FILING DATE: 2000-12-21
/ NUMBER OF SEQ ID NOS: 231
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 5
/ LENGTH: 894
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-689-742-5

Query Match
Best Local Similarity 3.3%; Score 47.2; DB 6; Length 894;
Matches 55; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1347 AGTGTTAATCAATTAATGCTATGAAATCAAAAAAAAAAAAAAAAAAAAA 1406
DB 819 AATCCCTAAATGCAATAAACTAGTATGTTTCAAAAAAAAAAAAAAAAAA 878
QY 1407 AAAAAAA 1414
DB 879 AAAAAAA 886

RESULT 8
US-11-102-240-17
/ Sequence 17, Application US/11102240
/ Publication No. US20050260647A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Wood, William L.
/ TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESSION
/ FILE REFERENCE: P3230R1C106C
/ CURRENT APPLICATION NUMBER: US/11/102,240
/ CURRENT FILING DATE: 2005-04-08
/ PRIOR APPLICATION NUMBER: 10/063662
/ PRIOR FILING DATE: 2002-05-07
/ PRIOR APPLICATION NUMBER: 10/068667
/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: PCT/US00/23328
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR APPLICATION NUMBER: 60/170262
/ PRIOR FILING DATE: 199-12-09
/ NUMBER OF SEQ ID NOS: 170
/ SEQ ID NO: 17
/ LENGTH: 1672
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-11-102-240-17

Query Match
Best Local Similarity 3.3%; Score 46.8; DB 7; Length 1672;
Matches 54; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1349 TGCTTAACATTCATTAATAGCTATATGAAATCAAAAAAAAAAAAAAAAAA 1408
DB 1588 TGCTTAACATTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1647
QY 1409 AAAAAA 1414
DB 1648 AAAAAA 1653

RESULT 9
US-10-689-742-41
/ Sequence 41, Application US/10689742
/ Publication No. US20050250180A1
/ GENERAL INFORMATION:
/ APPLICANT: Jacobs, Kenneth
/ APPLICANT: McCoy, John M
/ APPLICANT: Lavalie, Edward R
/ APPLICANT: Racie, Lisa A
/ APPLICANT: Evans, Cheryl
/ APPLICANT: Merberg, David
/ APPLICANT: Treacy, Maurice
/ APPLICANT: Spaulding, Vikki
/ TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
/ FILE REFERENCE: 00766.000091.10
/ CURRENT APPLICATION NUMBER: US/10/689,742
/ CURRENT FILING DATE: 2003-10-22
/ PRIOR APPLICATION NUMBER: 09/746,783
/ PRIOR FILING DATE: 2000-12-21
/ NUMBER OF SEQ ID NOS: 231
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 41
/ LENGTH: 588
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-689-742-41

Query Match
Best Local Similarity 3.3%; Score 46.6; DB 6; Length 588;
Matches 112; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 1194 AAAATTAATAAATAACAGAGAGAAAGAAAGAAATCCAGAAACAGATTAACCTA 1253
DB 337 AATCTAGTTGAGAAAAGAAAGAAACCAAGAGGCTTAATCACAAGGTTCTGAAATTA 396
```



```
/ GENERAL INFORMATION:
/ APPLICANT: Eseau, Christine
/ APPLICANT: Lollo, Bridget
/ APPLICANT: Bennett, C. Frank
/ APPLICANT: Freiler, Susan M.
/ APPLICANT: Grilley, Richard H.
/ APPLICANT: Baker, Brenda F.
/ APPLICANT: Vickers, Timothy
/ APPLICANT: Marcuseon, Eric G.
/ APPLICANT: Koller, Erich
/ APPLICANT: Swayze, Eric
/ APPLICANT: Jain, Ravi
/ APPLICANT: Bhat, Balkrishen
/ APPLICANT: Peralta, Eileen
/ TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
/ TITLE OF INVENTION: Of Small Non-Coding RNAs
/ FILE REFERENCE: ISIS0080-100 (CORE001.6US)
/ CURRENT APPLICATION NUMBER: US/10/909,125
/ PRIOR FILING DATE: 2004-07-30
/ PRIOR APPLICATION NUMBER: US 60/492,056
/ PRIOR FILING DATE: 2003-07-31
/ PRIOR APPLICATION NUMBER: US 60/516,303
/ PRIOR FILING DATE: 2003-10-31
/ PRIOR APPLICATION NUMBER: US 60/531,596
/ PRIOR FILING DATE: 2003-12-19
/ PRIOR APPLICATION NUMBER: US 60/562,417
/ PRIOR FILING DATE: 2004-04-14
/ NUMBER OF SEQ ID NOS: 2184
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 801
/ LENGTH: 4339
/ TYPE: DNA
/ ORGANISM: H. sapiens
US-10-909-125-801
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Query Match 3.2%; Score 45.6; DB 6; Length 4339;
Best Local Similarity 66.0%; Pred. No. 0.11;
Matches 66; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
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```
QY 1315 TCTTTCCCTAGTCCGTAATCCAGTCTCAATCAATTAATAGCTATA 1374
DB 4155 TCTTTACACGTTTAAACCTCTTAAGCAGCTCTTAATATATATTAATGCTCCC 4214
QY 1375 TCAAAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1414
DB 4215 TTTTATTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4254
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RESULT 14
US-10-996-217A-8/c
/ Sequence 8, Application US/10996217A
/ Publication No. US2005026651A1
/ GENERAL INFORMATION:
/ APPLICANT: Revivicor, Inc.
/ APPLICANT: Wells, Kevin
/ TITLE OF INVENTION: Use of Interfering RNA in the Production of Transgenic Animals
/ FILE REFERENCE: 10785.105070 REV 1015 US
/ CURRENT APPLICATION NUMBER: US/10/996,217A
/ CURRENT FILING DATE: 2004-11-22
/ PRIOR APPLICATION NUMBER: 60/523,938
/ PRIOR FILING DATE: 2003-11-21
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 8
/ LENGTH: 2036
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Construct
US-10-996-217A-8
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Query Match 3.2%; Score 45.2; DB 6; Length 2036;
Best Local Similarity 66.3%; Pred. No. 0.093;
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Matches 65; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 1317 TTTTCCCTAGTCCGTAATCCAGTCTCAATCAATTAATAGCTATAG 1376
DB 656 TTTTAGATATTTTCTTGTTCCCTTCTCACTGAACCTATTTTAGTATCTAAAA 597
QY 1377 AAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1414
DB 596 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 559
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```
RESULT 15
US-11-077-386-7
/ Sequence 7, Application US/11077386
/ Publication No. US20050272067A1
/ GENERAL INFORMATION:
/ APPLICANT: Macina, Roberto
/ APPLICANT: Turner, Leah R.
/ APPLICANT: Chen, Huel-Mei
/ APPLICANT: Rodriguez, Maria
/ APPLICANT: Liu, Shu-Hui
/ TITLE OF INVENTION: Compositions, Splice Variants and Methods Relating to Cancer Spec
/ TITLE OF INVENTION: Genes and Proteins
/ FILE REFERENCE: DEX-0537
/ CURRENT APPLICATION NUMBER: US/11/077,386
/ CURRENT FILING DATE: 2005-03-10
/ PRIOR APPLICATION NUMBER: US 60/566,706
/ PRIOR FILING DATE: 2004-04-30
/ PRIOR APPLICATION NUMBER: US 60/565,144
/ PRIOR FILING DATE: 2004-04-23
/ PRIOR APPLICATION NUMBER: US 60/551,911
/ PRIOR FILING DATE: 2004-03-10
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 7
/ LENGTH: 602
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-077-386-7
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```
Query Match 3.2%; Score 45; DB 7; Length 602;
Best Local Similarity 70.6%; Pred. No. 0.056;
Matches 60; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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```
QY 1330 CCGTGTATCAATCCAGTGTCTAATCAATTAATAGCTATGAATCAAAAA 1389
DB 447 CCATGTACTAATTAAGAAAGCTTTGAGCTAAAAA 506
QY 1390 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1414
DB 507 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 531
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Search completed: December 17, 2005, 18:54:52
Job time : 259.631 secs
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GenCore version 5.1.6
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OM nucleic - protein search, using 'frame_plus_n2p' model

Run on: December 14, 2005, 11:21:18, Search time 46.6092 Seconds
(without alignments)
5016.322 Million cell updates/sec

Title: US-09-970-076-1

Perfect score: 2540

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Ygapop	10.0	Ygapext	0.5
Egapop	6.0	Egapext	7.0
Delop	6.0	Delext	7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents AA -QFMT=faetan -SUFFIX=ra1 -MINMATCH=0.1 -LOOPCT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Issued Patents AA.*

- 1: /cgcn2_6/ptodata/1/1aa/5.COMB.pep.*
- 2: /cgcn2_6/ptodata/1/1aa/6.COMB.pep.*
- 3: /cgcn2_6/ptodata/1/1aa/H.COMB.pep.*
- 4: /cgcn2_6/ptodata/1/1aa/PCUS.COMB.pep.*
- 5: /cgcn2_6/ptodata/1/1aa/RE.COMB.pep.*
- 6: /cgcn2_6/ptodata/1/1aa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	965	38.0	488	2	US-10-104-047-2639
2	167	6.6	1155	1	US-08-286-889-46
3	167	6.6	1155	1	US-08-485-618-46
4	167	6.6	1155	1	US-08-362-652-46
5	167	6.6	1155	1	US-08-605-672-46
6	167	6.6	1155	1	US-08-482-293A-46
7	167	6.6	1155	1	US-08-943-363-46
8	167	6.6	1155	2	US-09-193-043-46
9	167	6.6	1155	2	US-09-688-307A-46
10	167	6.6	1155	2	US-09-350-259-46
11	167	6.6	1161	1	US-08-485-618-53
12	167	6.6	1161	1	US-08-362-652-53

13	167	6.6	1161	1	US-08-605-672-53	Sequence 53, Appl
14	167	6.6	1161	1	US-08-482-293A-53	Sequence 53, Appl
15	167	6.6	1161	1	US-08-943-363-53	Sequence 53, Appl
16	167	6.6	1161	2	US-09-193-043-53	Sequence 53, Appl
17	167	6.6	1161	2	US-09-688-307A-53	Sequence 53, Appl
18	167	6.6	1161	2	US-09-350-259-53	Sequence 53, Appl
19	167	6.6	1161	2	US-08-173-497-2	Sequence 2, Appl1
20	163.5	6.4	1161	1	US-08-286-889-2	Sequence 2, Appl1
21	163.5	6.4	1161	1	US-08-485-618-2	Sequence 2, Appl1
22	163.5	6.4	1161	1	US-08-485-618-99	Sequence 2, Appl1
23	163.5	6.4	1161	1	US-08-362-652-99	Sequence 2, Appl1
24	163.5	6.4	1161	1	US-08-605-672-99	Sequence 2, Appl1
25	163.5	6.4	1161	1	US-08-605-672-99	Sequence 2, Appl1
26	163.5	6.4	1161	1	US-08-482-293A-99	Sequence 2, Appl1
27	163.5	6.4	1161	1	US-08-482-293A-99	Sequence 2, Appl1
28	163.5	6.4	1161	1	US-08-943-363-2	Sequence 2, Appl1
29	163.5	6.4	1161	1	US-08-943-363-99	Sequence 2, Appl1
30	163.5	6.4	1161	2	US-09-193-043-2	Sequence 2, Appl1
31	163.5	6.4	1161	2	US-09-193-043-99	Sequence 2, Appl1
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33	163.5	6.4	1161	2	US-09-688-307A-99	Sequence 2, Appl1
34	163.5	6.4	1161	2	US-09-350-259-2	Sequence 2, Appl1
35	163.5	6.4	1161	2	US-09-350-259-99	Sequence 2, Appl1
36	162.5	6.4	1151	1	US-08-286-889-37	Sequence 37, Appl
37	162.5	6.4	1151	1	US-08-485-618-37	Sequence 37, Appl
38	162.5	6.4	1151	1	US-08-362-652-37	Sequence 37, Appl
39	162.5	6.4	1151	1	US-08-605-672-37	Sequence 37, Appl
40	162.5	6.4	1151	1	US-08-482-293A-37	Sequence 37, Appl
41	162.5	6.4	1151	1	US-08-943-363-37	Sequence 37, Appl
42	162.5	6.4	1151	2	US-09-193-043-37	Sequence 37, Appl
43	162.5	6.4	1151	2	US-09-688-307A-37	Sequence 37, Appl
44	162.5	6.4	1151	2	US-09-350-259-37	Sequence 37, Appl
45	162.5	6.4	1161	1	US-08-485-618-55	Sequence 55, Appl

ALIGNMENTS

RESULT 1
US-10-104-047-2639
; Sequence 2639, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OR INVENTION: No. 6943241el full length CDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2639
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2639

Alignment Scores:
Pred. No.: 2.22e-93
Score: 965.00
Percent Similarity: 64.34%
Best Local Similarity: 48.38%
Query Match: 37.99%

DB:	2	Gaps:	5
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US-09-970-076-1 (1-1414) x US-10-104-047-2639 (1-488)

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Db 3 AlGdInUrGserPro-----AlArGserProGlySerTrpLeuPneProGlyLeuTrp 20
QY 68 GAAGAGCGGAGCCCTGCTCTCCCGGCGCTGCGGCGCATGCGCGCGGAGAGGCC 127

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QY 128 CTCGGCATCGGCTTCAGTGGCTCTCTTGGCCACTGTGATGTCATCTGCGCGGGCAA 187
Db 21 -----LeuLeuValLeuSerGlyPro 27
QY 188 GGGGGA---CGCAGGAGGATGGGGGTCCAGCTGTGACGGCGGATTTGACCTGTACCTTC 244
Db 28 GlyGlyLeuLeuArgLagIngluInProSerCysArgAlaPheAspLeuTyrPhe 47
QY 245 ATTTGGCAAAATCAGGAAGTGTGTCGACCACTGGAATGAATCTACTTCTTGGA 304
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QY 365 CGAGCAACAACTTAAATGAACTGACAGAAACAGAAACAAATCCGTAGGCGCTTAGAA 424
Db 88 GlnAlaThrIleIleLeuProLeuThrGlyAspArgGlyLysIleSerLysGlyLeuGln 107
QY 425 GAATCTCAAAAAGTTTGTCCAGAGAGAGACCTTACTGATGCAAGATTTGAAAGGCC 484
Db 108 AspLeuLysArgValSerProValGlyGluThrTyrIleHisGluGlyLeuLysLeuAla 127
QY 485 AGTGAACAGATTTATATGAAACAGACAAAGGCTACAGGACCGCATCATTTGCT 544
Db 128 AsnGluGlnIle-----GlnLysAlaGlyGlyLeuLysThrSerSerIleIleIleAla 145
QY 545 TTGACTGATGAGAACTCCATGAAAGTCTCTTTTCTATTTCAGAGAGGAGGCTTATAG 604
Db 146 LeuThrAspGlyLysLeuAspGlyLysLeuValProSerTyrAlaGluLysGluAlaLysIle 165
QY 605 TCTCGAGATCTTGTCGCAATGTTTACTGTGTGTGTGTAAGATTTCAATGAGACAG 664
Db 166 SerArgSerLeuGlyAlaSerValTyrCysValGlyValLeuAspPheGluGlnAlaGln 185
QY 665 CTGGCCCGGATTCGCGACAGTAAAGATGATGTTTCCCGTGAATGACGCGCTTCAGGCT 724
Db 186 LeuGluArgIleAlaAspSerLysGluGlnValPheProValLysGlyLysPheGlnAla 205
QY 725 CTGCAAGGATCATTCACCTCAATTTTGAAGAAAGTCTGATCGAAATTCATGACGTGAA 784
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QY 845 CATGCCCGCAACGTGACAGAGGTCCTGTGACGCTTCAGATCATGATCGGCATCATC 904
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Db 346 LysValValIleLysAspProProProProAlaProAlaProLysGluGluGln 365
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QY 1193 GAA 1195
Db 366 Glu 366

RESULT 2
US-08-286-889-46
/ Sequence 46, Application US/08286889
/ Patent No. 5470953
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Mich
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 51
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/286,889
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: P38,659
/ REFERENCE/DOCKET NUMBER: 27866/32168
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 46:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1155 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-286-889-46

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Score: 167.00 Matches: 77
Percent Similarity: 42.47% Conservative: 50
Best Local Similarity: 25.75% Mismatches: 125
Query Match: 6.57% Indels: 47
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US-09-970-076-1 (1-1414) x US-08-286-889-46 (1-1155)
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Db 113 GlnArgAlaCysAlaLysAsnMetTyrAlaLysGlySerCys-LeuLeuLeuGlySer 132
QY 139 CTTCAGTGTGCTCTCTTTGGCCACTCTGTGTCATCTGCGCGGCAAGGGGAGCGAG 198
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Db 144 -----ProGluCyProGlyInGluMetAsp1Leu1aPheLeu1leAsp1 159
Qy 256 ATGAGAGAGTGTG---CTGCACACCTGGAAATGAATCTATTCTTGTGGAACGTTGGC 312
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Db 179 tGlyGlnLeuAlaSerThrSerThrSerPheSerLeuMetGlnTySerAsn1leuLys 199
Qy 373 AACCTTAATGAACCTGACAGAGACAGA-----GAACAAATCCGTCAGAG 417
Db 199 sThrHisPheThrPheThrGlnPheLysSerSerLeuSerProGlnSerLeuValAsp1 219
Qy 418 CCTAGAGAACTCCAGAAAGTTCTCCGAGAGACACTTACATGATGATAGATTGA 477
Db 219 a1leValGlnLeuGln-----GlyLeuThrTyThrAlaSerGly1leG1 234
Qy 478 AAGGGCCAGTACAGATTATTATGAAAACAGACAAAGGTACAGGACAGC---AGCGT 534
Db 234 nLysValValLysGlnLeuPheHisSerLysAsnGlyAlaArgLysSerAlaLysLys1 254
Qy 535 CATCATTTGCTTTGACTGATGAGAACTGCATGAAGATCTCTTTTCTATTCAAG- 589
Db 254 eleu1leVal1leThrAspGlyGlnLysPheArgAspProLeuGlnLysTrArgHisVal1 274
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Db 291 pAlaPheArgGlnProThrAlaLeuGlnGlnLeuAsnThr1leGlySerAlaProSerG1 311
Qy 688 GATCATGATGTTTCCCTGATGATGACGGCTTTCAGGCTCTCGAAGCATCATCACTCAAT 747
Db 311 nAspHisValPheLysValGlnLys---PheValAlaLeuArgSer1leGlnArgGln1 330
Qy 748 TTGAGAGAGCTCTGATCGAATTTAGACAGCTGAACCATCCACCTATGTCAGAGAG 807
Db 330 eGlnGlnLys-----1lePheAla1leGlnGlyThrGlnSerArgSerSer 346
Qy 808 GTATTTCAAGTGTCTGCGAGAGAGAAAGGCTTCCAGATGCCCGGACCGTGGAC 862
Db 346 rSerPheGlnHisGlnMetSerGlnGlnLysPheSerSerAlaLeuSerMetAsp 364

RESULT 3
US-08-485-618-46
Sequence 46, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497

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FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-46

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Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
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Percent Similarity:	42.47%					
Best Local Similarity:	25.75%					
Query Match:	6.57%					

US-09-970-076-1 (1-1414) x US-08-485-618-46 (1-1155)

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Db 93 GlyLeuSerLeuValAlaAspThrAsnAsnSerGlnLeuLeuAlaCysGlyProThrAla 112
Qy 88 CCGCGGGCTGGCGGC-----CATGGCACGCGCGAGAGCGGAGCCCTCGGACATCGG 138
Db 113 GlnArgAlaLysAlaLysAsnMetTyAlaLysGlySerCys-LeuLeuLeuLysSer 132
Qy 139 CTTCAGATGAGCTCTTTTGGCCACTGTGCTCATCTGCGCGGCGGACAGGAGCGACAG 198
Db 132 rLeuGlnPheHisGlnAla1leProAlaThrMet----- 143
Qy 199 GAGAGATGGGGGTCCAGCTGCTACGCGC---GGATTGACCTTACTTATTGGACAA 255
Db 144 -----ProGluCyProGlyInGluMetAsp1Leu1aPheLeu1leAsp1 159
Qy 256 ATGAGAGAGTGTG---CTGCACACCTGGAAATGAATCTATTCTTGTGGAACGTTGGC 312
Db 159 ySerGlySer1leAspGlnSerAspPheThrGlnMetLysAspPheValLysAlaLeuMe 179
Qy 313 TCACAAATTCATGACGCCACAGTTGAGATGATGCTCTTATGTTGTTTCCACCGAGAGAC 372
Db 179 tGlyGlnLeuAlaSerThrSerThrSerPheSerLeuMetGlnTySerAsn1leuLys 199
Qy 373 AACCTTAATGAACCTGACAGAGACAGA-----GAACAAATCCGTCAGAG 417
Db 199 sThrHisPheThrPheThrGlnPheLysSerSerLeuSerProGlnSerLeuValAsp1 219
Qy 418 CCTAGAGAACTCCAGAAAGTTCTCCGAGAGACACTTACATGATGATAGATTGA 477
Db 219 a1leValGlnLeuGln-----GlyLeuThrTyThrAlaSerGly1leG1 234
Qy 478 AAGGGCCAGTACAGATTATTATGAAAACAGACAAAGGTACAGGACAGC---AGCGT 534
Db 234 nLysValValLysGlnLeuPheHisSerLysAsnGlyAlaArgLysSerAlaLysLys1 254
Qy 535 CATCATTTGCTTTGACTGATGAGAACTGCATGAAGATCTCTTTTCTATTCAAG- 589
Db 254 eleu1leVal1leThrAspGlyGlnLysPheArgAspProLeuGlnLysTrArgHisVal1 274

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QY 590 -AGGAGCTAATAGCTCGAGATCTGTGCAATTTTACTGTGTGTGAGAGA 648
    ||||| :||| ||| ||| :||| |||
Db 274 eprogluaiaagiulysala-----glylelleagtyrallaileglyvalglyas 291
QY 649 T---TTCAATGAG---ACACAGCTGCCCGGATTT-----GCCGACAGTAA 687
    ||||| :||| ||| ||| :||| |||
Db 291 palapheargluProThrAlaLeuIngluLeuAenThrIleGlySerAlaProSerGI 311
QY 688 GATCATGTGTTTCCCGTGAATGACGGCTTTCAGGCTTCGACAGGATCATCATCAAT 747
    :||||| :||| :||| :||| :||| :|||
Db 311 naphsvalPheIysValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnI 330
QY 748 TTGAAGAAGTCTGCATCGAATTTCTAGCAGCTGAACCATCCACCATATGTGACAGA 807
    :||| :||| :||| :||| :||| :|||
Db 330 eglngluys-----IlePheAlaIleGlnGluThrGluSerArgSerSerse 346
QY 808 GTCAATTTCAGTTGTGTGAGAGAAACGGCTTCCACATGCCCGGACAGTGCAG 862
    :||| :||| :||| :||| :||| :|||
Db 346 rserPheGlnHISgluMetSerGlnGluIlyPheSerSerAlaLeuSerMetAsp 364

RESULT 4
US-08-362-652-46
; Sequence 46, Application US/08362652
; Patent No. 5766850
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,652
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-362-652-46

Alignment Scores:
Pred. No.: 2,08e-08 Length: 1155
Score: 167.00 Matches: 77
Percent Similarity: 42.47% Conservative: 50
Best Local Similarity: 25.75% Mismatches: 125
Query Match: 6.57% Indels: 47

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DB: 1 Gaps: 14
US-09-970-076-1 (1-1414) x US-08-362-652-46 (1-1155)
QY 28 GCGGCGTCCCTGAGAGGTGCTGGCGAGTCCGAGACGTGGAGAGACGCGACCTGCTCT 87
    ||||| :||| :||| :||| :||| :|||
Db 93 GlyLeuSerLeuValAlaAspThrAsnSerGlnLeuValAlaCysGlyProThrAla 112
QY 88 CCCCGGCTGGCGGG-----CATGGCCACGGCGGAGCGGAGACCTCGGCGATCGG 138
    :||||| :||| :||| :||| :||| :|||
Db 113 GlnArgAlaCysAlaIlyAsnMetYrAlaIysGlySerCys-LeuLeuLeuGlySerse 132
QY 139 CTTCAGTGGCTCTCTTGGCCACTCTGGTGTCTATCTGCGCGGAGGAGGAGCGAG 198
    :||| :||| :||| :||| :||| :|||
Db 132 rleuGlnPheIleGlnAlaIleProAlaThrMet----- 143
QY 199 GGAGAGTGGGGTCCAGCTGCTAGGC---GGATTGACCTGTACTTGTGACAA 255
    :||| :||| :||| :||| :||| :|||
Db 144 -----ProGluCysProGlyGlnGluMetAspIleAlaPheLeuIleAspGI 159
QY 256 ATCAGGAAGTGTG---CTGCACACCTGGAAATGAAATCTATTACTTTGGAACAGTTGAG 312
    :||||| :||| :||| :||| :||| :|||
Db 159 yserGlySerIleAspGlnSerAspPheThrGlnMetIysAspPheValIlyAlaLeuI 179
QY 313 TCACAAATTCATCAGCCCAACAGTTGAGATGTCCTTATTTGTTTCTCCACCGAGAAC 372
    :||| :||| :||| :||| :||| :|||
Db 179 cGlyGlnLeuAlaSerThrSerThrSerPheSerLeuMetGlnIlyrSerAsnIleuIy 199
QY 373 AACCTTAATGAACAGACGAAAGACGA-----GAACAATCCGTCAAG 417
    :||| :||| :||| :||| :||| :|||
Db 199 vThrIAspThrPheThrGlnPheIysSerSerLeuSerProGlnSerLeuValAspAl 219
QY 418 CCTAAGAACTCCAGAAAGTTCTGCAGAGAGACACTTCATGATCATGAAGATTGGA 477
    :||| :||| :||| :||| :||| :|||
Db 219 alIeValGlnLeuGln-----GlyLeuThrYrThrAlaSerGlyIleGI 234
QY 478 AAGGCCAGTGAAGAGATTATTATGAAGAACAGACAGAGGTACAGACAGCC---AGCGT 534
    :||| :||| :||| :||| :||| :|||
Db 234 nlyserValIlySgluLeuPheHISerIysAsnGlyAlaArgIlySerAlaIlyAs 254
QY 535 CATCATGTGTTGATGATGAGAACTCATGAAGATCTTTTCTATTATTCAGC----- 589
    :||| :||| :||| :||| :||| :|||
Db 254 eleuIleValIleThrAspGlyGlnIysPheArgAspProLeuGluIlyrAspHisValI 274
QY 590 -AGGAGCTAATAGCTCGAGATCTGTGCAATTTTACTGTGTGTGAGAGA 648
    ||||| :||| ||| ||| :||| |||
Db 274 eprogluaiaagiulysala-----glylelleagtyrallaileglyvalglyas 291
QY 649 T---TTCAATGAG---ACACAGCTGCCCGGATTT-----GCCGACAGTAA 687
    ||||| :||| ||| ||| :||| |||
Db 291 palapheargluProThrAlaLeuIngluLeuAenThrIleGlySerAlaProSerGI 311
QY 688 GATCATGTGTTTCCCGTGAATGACGGCTTTCAGGCTTCGACAGGATCATCATCAAT 747
    :||||| :||| :||| :||| :||| :|||
Db 311 naphsvalPheIysValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnI 330
QY 748 TTGAAGAAGTCTGCATCGAATTTCTAGCAGCTGAACCATCCACCATATGTGACAGA 807
    :||| :||| :||| :||| :||| :|||
Db 330 eglngluys-----IlePheAlaIleGlnGluThrGluSerArgSerSerse 346
QY 808 GTCAATTTCAGTTGTGTGAGAGAAACGGCTTCCACATGCCCGGACAGTGCAG 862
    :||| :||| :||| :||| :||| :|||
Db 346 rserPheGlnHISgluMetSerGlnGluIlyPheSerSerAlaLeuSerMetAsp 364

RESULT 5
US-08-605-672-46
; Sequence 46, Application US/08605672
; Patent No. 5817515
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103

```


NAME: Williams Jr., Joseph A.
 REGISTRATION NUMBER: 38,659
 REFERENCE/DOCKET NUMBER: 27866/32684
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1155 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-482-293A-46

Alignment Scores:

Pred. No.:	2,086-08	Length:	1155
Score:	167.00	Matches:	77
Percent Similarity:	42.47%	Conservative:	50
Best Local Similarity:	25.75%	Mismatches:	125
Query Match:	6.57%	Indels:	47
DB:	1	Gaps:	14

US-09-970-076-1 (1-1414) x US-08-482-293A-46 (1-1155)

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QY 28 GCGCGCTCCCTGAGGCTCGTGCGAGGCTGCGAGGCGGAGAGGAGCGGACCTGCTCT 87
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 93 GlyLeuSerLeuValAlaAspThrAsnAsnSerGlnLeuAlaGlySerProThrAla 112
QY 88 CCCCAGGCTGCGGCGC-----CATGCCACGCGCGAGCGGAGAGCCCTCGGCATCGG 138
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 113 GlnArgAlaCysAlaIleAlaSerMetTyrAlaIleGlySerCys-LeuLeuLeuGlySerSe 132
QY 139 CTTCCAGTGGCTCTCTTTGGCCACTCTGGTCTCATCTGGCGCGCGGCGGAGGAGCGAGC 198
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 132 rLeuGlnPheIleGlnAlaIleProAlaThrMet----- 143
QY 199 GGAGATGAGGAGGCTGCTACCGC--GGATTGACCTGTACTGATTTTGGACAA 255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 144 -----ProGluCysProGluGlnGluMetAspIleAlaPheLeuIleAspG 159
QY 256 ATCAGAGAGTG--CTGCACCACTGGAATGAATCTTACTTTGTGGACAGCTTGGC 312
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 159 ySerGlySerIleAspGlnSerAspPheThrGlnMetCysAspPheValIleAlaLeu 179
QY 313 TCACAATTCATGAGCCACAGTGAAGATGCTTTATTTGTTTCCACCGGAGAAC 372
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 179 tGlyGlnLeuAlaSerThrSerThrSerPheSerLeuMetGlnTyrSerAsnIleLeu 199
QY 373 AACCTTAATGAACTGACAGAGACAGAG-----GAACAAATCCGTCAGAG 417
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 199 eThrIlePheThrPheThrGlnPheLeuYserIleSerLeuSerProGlnSerLeuValAsp 219
QY 418 CCTAGAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGCATGAGAGATTGA 477
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 219 aIleValGlnLeuGln-----GlyLeuThrIleThrAlaSerGlyIleG 234
QY 478 AAGGCGCAGTGAAGCATTTATTATGAAAACAGACAGGTACAGACAGCC--AGCG 534
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 234 nlybValIleValGlnLeuPheIleSerIleYAsnGlyAlaArgIleSerIleAlaYls 254
QY 535 CATCATTTGTTTACTGATGAGAACTCCATGAAGATCTTTTTCATTCAGAG----- 589
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 254 eIleuIleValIleThrAspGlyGlnIlybSerArgAspProLeuGlnIlyrArgIleVal 274
QY 590 -AGGAGGCTAATAGTCTCGAGATCTTGTCGAATGTTTACTGTGTGGTGTGAAGA 648
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 274 eProGlnAlaGlnIlybAla-----GlyIleIleArgTyrAlaIleGlyValGlys 291
QY 649 T---TTCAATGAG---ACACAGCTGGCCCGGATT-----CGGACAGCTAA 687
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 291 palApeArgIlybProThrAlaLeuGlnGluLeuAsnThrIleGlySerAlaProSerG 311

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QY 688 GGATCATGTGTTCCCGTGATGACGCGCTTGACGCTTGCAAGGCATCATCACTCAAT 747
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 311 nAspIleValPheIlybValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnI 330
QY 748 TTTGAAGAAGTCTGTCATGCAAAATCTAGCAGCTGACATGCATGCATGTCAGAGAG 807
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 330 eGlnGlnIlyb-----IlePheAlaIleGlnGlnIlybThrGlnSerArgSerSe 346
QY 808 GTCAATTCAGTGTGTCAGAGAGAAACGCTTCCGACATGCCCCGACAGTGGAC 862
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 346 rSerPheGlnIleGlnMetSerGlnGlnIlybThrGlnSerArgSerMetAsp 364

```

RESULT 7

US-08-943-363-46
 ; Sequence 46, Application US/08943363
 ; Patent No. 5837478

GENERAL INFORMATION:
 APPLICANT: Gallatin, W. Michael
 APPLICANT: Van der Vieren, Monica
 TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
 NUMBER OF SEQUENCES: 114
 CORRESPONDENCE ADDRESS:
 ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 233 South Wacker Drive, 6300 Sear Tower
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States
 ZIP: 60606-6402

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/943,363
 FILING DATE: 530

CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994
 APPLICATION NUMBER: US 08/362,652
 ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.
 REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/32684
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448
 TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1155 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: protein
 US-08-943-363-46

Alignment Scores:

Pred. No.:	2,086-08	Length:	1155
Score:	167.00	Matches:	77
Percent Similarity:	42.47%	Conservative:	50
Best Local Similarity:	25.75%	Mismatches:	125
Query Match:	6.57%	Indels:	47
DB:	1	Gaps:	14

US-09-970-076-1 (1-1414) x US-08-943-363-46 (1-1155)

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QY 28 GCGCGCTCCCTGAGGCTCGTGCGAGGCTGCGAGGCGGAGAGGAGCGGACCTGCTCT 87

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Db      93  G|YLeuSerIeuValAlaAepThrAenSerGlnLeuLeuAlaCySgIyProthra1a 112
QY      88  CCCCggGCTGCGGGC-----CATGGCCAGCGCGAGAGAGAGCCCTCGGCATCGG 138
Db      113  GlnArgAlaCyAlaIyAenMetYrAlaIySgIySerCyS-LeuLeuLeuGlySerase 132
QY      139  CTTCCAGTGGCTCTTTGGCCACTCTGGTCTCATCTGGCGCGGCGAGAGGGAGCGCAG 198
Db      132  rLeuGlnPheIleGlnAlaIleProAlaThrMet----- 143
QY      199  GGAGAGTGGGGGTCCAGCTGCTACGGC---GGATTGACCTGTAATTCTATTGGACAA 255
Db      144  -----ProGluCySProGlyGlnGluMetAspIleAlaPheLeuIleAspG1 159
QY      256  ATCAGAAAGTGTG---CTGCACCACTGGAATGAATCTATTACTTTGGAAACAGTTGGC 312
Db      159  ySerGlySerIleAspGlnSerAepPheThrGlnMetIyAAspPheValIySAlaLeuMe 179
QY      313  TCACAAATTATCATGCCACCACTTGAGAAATGCTCTTATTGTTTCTCCACCGGAGAAC 372
Db      179  rGlyGlnLeuAlaSerThrSerThrSerPheSerLeuMeGlnIySerAenIleLeuIy 199
QY      373  AACCTTAATGAACCTGACAGAAAGACAG-----GAACAAATCCGTCAGAG 417
Db      199  sThrHisPheThrPheThrGluPheIySerserLeuSerProGlnSerIeuValAspAl 219
QY      418  CCTAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGCAATGAGAGATTGA 477
Db      219  aIleValGlnLeuGln-----GlyLeuThrTyThrAlaSerGlyIleG1 234
QY      478  AAGGGCCAGTGAGACAGATTATTATGAAAACAGAACAGGTCACAGACAGCC--AGCGT 534
Db      234  nIyValIyAllySgIyIyLeuPheHisSerIySAsnGlyAlaArgIySerAlaIySyl 254
QY      535  CATCATGCTTTTGCATGAGAAACCTCAATGAAGACTCTTTTTCATTTCAGAG----- 589
Db      254  eIeuIleValIleThrAspGlnIySAsnGlyIySAsnGlyIySAsnGlyIySAsnGlyI 274
QY      590  -AGGAGGCTAATAGTCTCGAAGATCTTGGTGCATTTGTTTACTGTGTGGTGAAGA 648
Db      274  eProGluAlaGluIySAla-----GlyIleIleArgTyAlaIleGlyAlaGlyAs 291
QY      649  T---TTCAATGAG--ACACAGCTGGCCCGGATT-----GGGACAGTAA 687
Db      291  pAlaPheArgGluProThrAlaLeuGlnGluIyLeuAenThrIleGlySerAlaProSerG1 311
QY      688  GGATCATGTTTCCCGTGAAATGACGGCTTCAGGCTCTGCAAGGCAATCCATCCATCAAT 747
Db      311  nAepHisValPheIyValGlyAen--PheValAlaLeuArgSerIleGlnArgGlnI1 330
QY      748  TTGGAAGAAGTCTCGATCGAAATTTCTAGACAGTGAACCATCCATATGTGACAGAGA 807
Db      330  eGlnGluIyS-----IlePheAlaIleGluGlyThrGluSerArgSerserse 346
QY      808  GTCATTTCAAAGTTCTCGTGAAGAGAAACGCTTCGACATGCCCGCAACGTGCAGC 862
Db      346  rSerPheGlnHisIleGluMetSerGlnGlyIyPheSerSerAlaLeuSerMetAep 364

RESULT 8
US-09-193-043-46
; Sequence 46, Application US/09193043
; Patent No. 6251395
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 6251395el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/193. 043
; CURRENT FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173, 497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286, 889

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; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362, 652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943, 363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-193-043-46

Alignment Scores:
Pred. No.: 2.08e-08 Length: 1155
Score: 167.00 Matches: 77
Percent Similarity: 42.47% Conservative: 50
Best Local Similarity: 25.75% Mismatches: 125
Query Match: 6.57% Indels: 47
DB: 2 Gaps: 14

US-09-970-076-1 (1-1414) x US-09-193-043-46 (1-1155)
QY      28  GGCGCGTCCCTGAGGCTGTCGCGAGTTCGCGAGCGTGGAAAGACCGACCTGCTCT 87
Db      93  G|YLeuSerIeuValAlaAepThrAenSerGlnLeuLeuAlaCySgIyProthra1a 112
QY      88  CCCCggGCTGCGGGC-----CATGGCCAGCGCGAGAGAGCCCTCGGCATCGG 138
Db      113  GlnArgAlaCyAlaIyAenMetYrAlaIySgIySerCyS-LeuLeuLeuGlySerase 132
QY      139  CTTCCAGTGGCTCTTTGGCCACTCTGGTCTCATCTGGCGCGGCGAGAGGGAGCGCAG 198
Db      132  rLeuGlnPheIleGlnAlaIleProAlaThrMet----- 143
QY      199  GGAGAGTGGGGGTCCAGCTGCTACGGC---GGATTGACCTGTAATTCTATTGGACAA 255
Db      144  -----ProGluCySProGlyGlnGluMetAspIleAlaPheLeuIleAspG1 159
QY      256  ATCAGAAAGTGTG---CTGCACCACTGGAATGAATCTATTACTTTGGAAACAGTTGGC 312
Db      159  ySerGlySerIleAspGlnSerAepPheThrGlnMetIyAAspPheValIySAlaLeuMe 179
QY      313  TCACAAATTATCATGCCACCACTTGAGAAATGCTCTTATTGTTTCTCCACCGGAGAAC 372
Db      179  rGlyGlnLeuAlaSerThrSerThrSerPheSerLeuMeGlnIySerAenIleLeuIy 199
QY      373  AACCTTAATGAACCTGACAGAAAGACAG-----GAACAAATCCGTCAGAG 417
Db      199  sThrHisPheThrPheThrGluPheIySerserLeuSerProGlnSerIeuValAspAl 219
QY      418  CCTAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGCAATGAGAGATTGA 477
Db      219  aIleValGlnLeuGln-----GlyLeuThrTyThrAlaSerGlyIleG1 234
QY      478  AAGGGCCAGTGAGACAGATTATTATGAAAACAGAACAGGTCACAGACAGCC--AGCGT 534
Db      234  nIyValIyAllySgIyIyLeuPheHisSerIySAsnGlyAlaArgIySerAlaIySyl 254
QY      535  CATCATGCTTTTGCATGAGAAACCTCAATGAAGACTCTTTTTCATTTCAGAG----- 589
Db      254  eIeuIleValIleThrAspGlnIySAsnGlyIySAsnGlyIySAsnGlyIySAsnGlyI 274
QY      590  -AGGAGGCTAATAGTCTCGAAGATCTTGGTGCATTTGTTTACTGTGTGGTGAAGA 648
Db      274  eProGluAlaGluIySAla-----GlyIleIleArgTyAlaIleGlyAlaGlyAs 291
QY      649  T---TTCAATGAG--ACACAGCTGGCCCGGATT-----GGGACAGTAA 687
Db      291  pAlaPheArgGluProThrAlaLeuGlnGluIyLeuAenThrIleGlySerAlaProSerG1 311
QY      688  GGATCATGTTTCCCGTGAAATGACGGCTTCAGGCTCTGCAAGGCAATCCATCCATCAAT 747

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Db      311 nAphSVaIphelyVaIGlyAsn---PheVaIaIaLeuArSeriIeGIaRgInI1 330
Qy      748 TTTGAAGAAGTCTGCATGCAATTTAGACAGTCGACCATCCACATATGTGACAGAGA 807
Db      330 eGIInGIuLyS-----IlePheIaIaIeGIuLyThRgInGIuSerArSeriSe 346
Qy      808 GTCAATTCAAGTTGTGTGAGAGAAACGGCTTCCGACATGCCCGACAGTGCAG 862
Db      346 rSerPheGIInIaGIuMeSerGIInGIuLyPheSerSerAlaLeuSerMetCap 364

RESULT 9
US-09-688-307A-46
/ Sequence 46, Application US/09688307A
/ Patent No. 6432404
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 6432404el Human Beta-2
/ FILE REFERENCE: 27866/36646
/ CURRENT FILING DATE: 2000-10-13
/ PRIOR APPLICATION NUMBER: 09/193,043
/ PRIOR FILING DATE: 1998-11-16
/ PRIOR APPLICATION NUMBER: 08/605,672
/ PRIOR FILING DATE: 1996-02-22
/ PRIOR APPLICATION NUMBER: 08/173,497
/ PRIOR FILING DATE: 1993-12-23
/ PRIOR APPLICATION NUMBER: 08/286,889
/ PRIOR FILING DATE: 1994-08-05
/ PRIOR APPLICATION NUMBER: 08/362,652
/ PRIOR FILING DATE: 1994-12-21
/ PRIOR APPLICATION NUMBER: 08/943,363
/ PRIOR FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 46
/ LENGTH: 1155
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-688-307A-46

Alignment Scores:
Pred. No.: 2,08e-08 Length: 1155
Score: 167.00 Matches: 77
Percent Similarity: 42.47% Conservative: 50
Best Local Similarity: 25.75% Mismatches: 125
Query Match: 6.57% Indels: 47
DB: 2 Gaps: 14

US-09-970-076-1 (1-1414) x US-09-688-307A-46 (1-1155)
Qy      28 GGGCGCTCCCTGAGGGTCGTGCGGAGTGGCGAAGCGAGCCCTGCTCT 87
Db      93 GILyLeuSerLeuVaIaIaAepThraSmaSerGIInleuVaIaCySgIyProtrAla 112
Qy      88 CCCCGGCTGCGCGG-----CATGGCCAGCGCGAGCGGAGACCCCTCGGCATCG 138
Db      113 GIaArGIaIaCyAlaIaYsaInMeTyRAlaIaYgIySeCyS-LeuLeuIeInIySe 132
Qy      139 CTTCACGTGGCTCTCTTTGGCCACTCTGCTGCTCACTGCGCGGCGAAGGGGAGCG 198
Db      132 rLeuGIInPheIleGIaIaIleProAlaThrMet----- 143
Qy      199 GGAGATGGGGGTCCAGCGCTGTAAGGC---GGATTGACCTGACTTCATTTTGGACA 255
Db      144 -----ProGIuCyErProGIuGIInGIuMeIaSpIIaIaPheIuIleA 159
Qy      256 ATCAGAGAGTGTG---CTGCACCACTGGAATGAATCTATTCTTGTGGAACAGTTGC 312
Db      159 ySeThrGISeThrIeArSgInSeArSphEThrGIInMeIaYsaPheVaIaIaLeu 179
Qy      313 TCACAAATTCATAGGCCCAAGTGTGAGATGTCCTTATTGTTTCTCCACCGAGAGAC 372
Db      313 TCACAAATTCATAGGCCCAAGTGTGAGATGTCCTTATTGTTTCTCCACCGAGAGAC 372
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Db      179 rGIyInIeUaIaSeThrSeThrSePheSeRleuMeGIInTySeSaInIleuLy 199
Qy      373 AACCTTAATGAACATGACAGAGACAGA-----GAACAAATCCGTCAAG 417
Db      199 eThrInISePheThrPheThrGIInPheIySeSerIeUSeRProGIInSeRleuVaIa 219
Qy      418 CCTAAGAAATCTCCAGAAAGTTCTCGACAGAGACACTTACATGACATGAAGATTGA 477
Db      219 aIleVaIaGIInleuGIIn-----GIyLeuThrTyRAlaIaSeGIyIleGI 234
Qy      478 AAGGCCCATGACAGATTATATGAACACAGACAGAGGTACAGACAGCC---AGCGT 534
Db      234 nIySeVaIaIyLySGIuLeuPheISeRlySaInGIyAlaArGySeSerAlaIyLyS 254
Qy      535 CATCATTTGCTTGCATGATGAGAACTCCATGAAGATCTTTTCTTATTCAGAG----- 589
Db      254 eIeUleVaIaIeThrArSgInIyGIInIyPheArSphProIeUGIuTyRArGIhIaI 274
Qy      590 -AGGAGGCTAATAGGCTCGAGATCTTGTCGAATGTTTACTGTGTGTGTGAAGA 648
Db      274 eProGIuIaGIuLySaIa-----GIyIleIeArGIyRAlaIleGIyVaIaGIy 291
Qy      649 T---TTCAATGAG---ACAACAGTGGCCCGGATT-----GCCGACAGTAA 687
Db      291 PaIaPheArGIuProThrAlaIeGIInGIuIeUaInThrIleGIySeRAlaProSeRGI 311
Qy      688 GGAATCATGTGTTCCCGTGAATGAGGCTTTCAGGCTGCAAGGACATCATCTCAAT 747
Db      311 nAphSVaIphelyVaIGlyAsn---PheVaIaIaLeuArSeriIeGIaRgInI1 330
Qy      748 TTTGAAGAAGTCTGCATGCAATTTAGACAGTCGACCATCCACATATGTGACAGAGA 807
Db      330 eGIInGIuLyS-----IlePheIaIaIeGIuLyThRgInGIuSerArSeriSe 346
Qy      808 GTCAATTCAAGTTGTGTGAGAGAAACGGCTTCCGACATGCCCGACAGTGCAG 862
Db      346 rSerPheGIInIaGIuMeSerGIInGIuLyPheSerSerAlaLeuSerMetCap 364

RESULT 10
US-09-350-259-46
/ Sequence 46, Application US/09350259
/ Patent No. 6620915
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 6620915el Human 2
/ FILE REFERENCE: 27866/35004
/ CURRENT APPLICATION NUMBER: US/09/350,259
/ CURRENT FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: 09/193,043
/ PRIOR FILING DATE: 1998-11-16
/ PRIOR APPLICATION NUMBER: 08/173,497
/ PRIOR FILING DATE: 1993-12-23
/ PRIOR APPLICATION NUMBER: 08/286,889
/ PRIOR FILING DATE: 1994-08-05
/ PRIOR APPLICATION NUMBER: 08/362,652
/ PRIOR FILING DATE: 1994-12-21
/ PRIOR APPLICATION NUMBER: 08/943,363
/ EARLIER FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 46
/ LENGTH: 1155
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-350-259-46

Alignment Scores:
Pred. No.: 2,08e-08 Length: 1155
Score: 167.00 Matches: 77
Percent Similarity: 42.47% Conservative: 50
Best Local Similarity: 25.75% Mismatches: 125
Query Match: 6.57% Indels: 47
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Db 179 tGlyInLeuAlaSerThrSerThrSerPheSerLeuMetGlnTyrSerAsnIleLeu 199
Qy 373 AACCTTAATGAACATGACAGAACAGCA-----GAACAAAATCCGTCAAGG 417
Db 199 eThrHisPheThrPheThrGluPheLeuSerSerLeuSerProGlnSerLeuValAspAl 219
Qy 418 CCTAGAAAGACTCCAGAAAGTTCTGCGACGAGAGACACTTACATGATGAAGAATTGA 477
Db 219 aIleValGlnLeuGln-----GlyLeuThrTyrThrAlaSerGlyIleG 234
Qy 478 AAGGCCCATGACGACAGATTATTATGAAAACAGACAGAGGTACAGACAGCC---AGCCT 534
Db 234 nlyeValValLysGluLeuPheHisSerLysAsnGlyAlaArgLysSerAlaLysAl 254
Qy 535 CATCATGCTTGTGACTGATGAGAACTCCATGAAGATCTTTTCTTATTCAGAG----- 589
Db 254 eleuIleValIleThrAspGlyGlnLysPheArgAspProLeuGluTyrArgHisValI 274
Qy 590 -AGGAGGCTAATAGGCTCTCGAGATCTTGTCATTTGTTTACTGTGTGTGAAGA 648
Db 274 eProGluAlaGluLysAla-----GlyIleIleArgTyrAlaIleGlyValGlyAs 291
Qy 649 T---TTCAATGAG---ACACAGCTGCGCCGGAT-----GCGGACAGTAA 687
Db 291 pAlaPheArgGluProThrAlaLeuGlnGlnLeuAsnThrIleGlySerAlaProSerG 311
Qy 688 GATCATGATGTTCCCGTGAATGACGCGCTTTCAGGCTTCGAAAGCATCATCACTCAT 747
Db 311 nAspHisValIlePheLysValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnI 330
Qy 748 TTTGAAGAAGTCCGTGATGAAATTTAGACAGCTGAACCATCAATATGTGCAGAGA 807
Db 330 eGlnGlnLys-----IlePheAlaIleGlnGlnGluThrGlnLysArgSerSerSe 346
Qy 808 GTCATTTCAGTTGTCGTGAGAGAAACGCTTCCGACATGCCCGCAAGTGCAC 862
Db 346 rSerPheGlnHisGlnMetSerGlnGlnLysPheSerSerAlaLeuSerMetCasp 364

RESULT 12
US-08-362-652-53
Sequence 53, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-53

Alignment Scores:
Pred. No.: 2,08e-08 Length: 1161
Score: 167.00 Matches: 77
Percent Similarity: 42.47% Conservative: 50
Best Local Similarity: 25.75% Mismatches: 125
Query Match: 6.57% Indels: 47
DB: 1 Gaps: 14

US-09-970-076-1 (1-1414) x US-08-362-652-53 (1-1161)

Qy 28 GCGCGGCTCCGAGGCTGTCGCGAGTTCGCGAGCCGTGGAGAAGCGGACCTGCTCT 87
Db 93 GlyLeuSerLeuValAlaAspThrAsnAsnSerGlnLeuAlaCysGlyProThrAla 112
Qy 88 CCCCAGGCTGCGGCG-----CATGGCCACGCGCGGAGCGGAGAGCCCTCGCATCGG 138
Db 113 GlnArgAlaCysAlaLysAsnMetCysAlaLysGlySerCys-LeuLeuLeuGlySerSe 132
Qy 139 CTTCAAGTGGCTCTCTTGGGCCACTGTGCTCATCTGCGCGGCAAGGGGAGCGAG 198
Db 132 rLeuGlnPheIleGlnAlaIleProAlaThrMet----- 143
Qy 139 GGAGATAGGGGCTCCAGCGCTGTAAGGC---GATTGACCGTACTTCATTTTGGACAA 255
Db 144 -----ProGluCysProGlyGlnGlnMetAspIleAlaPheLeuIleAspG 159
Qy 256 ATCAGAAAGTGTG---CTGCACCACTGGAATGAATCTATTCTTGTGGAACAGTTGCG 312
Db 159 ySerGlySerIleAspGlnSerAspPheThrGlnMetLysAspPheValLysAlaLeu 179
Qy 313 TCACAAATTCATCAGCCCACTGGAAGAAATGCTTTATTTGTTCTCCACCCGAGAAC 372
Db 179 tGlyInLeuAlaSerThrSerThrSerPheSerLeuMetGlnTyrSerAsnIleLeu 199
Qy 373 AACCTTAATGAACATGACAGAACAGCA-----GAACAAAATCCGTCAAGG 417
Db 199 eThrHisPheThrPheThrGluPheLeuSerSerLeuSerProGlnSerLeuValAspAl 219
Qy 418 CCTAGAAAGACTCCAGAAAGTTCTGCGACGAGACACTTACATGATGAAGAATTGA 477
Db 219 aIleValGlnLeuGln-----GlyLeuThrTyrThrAlaSerGlyIleG 234
Qy 478 AAGGCCCATGACGACAGATTATTATGAAAACAGACAGAGGTACAGACAGCC---AGCCT 534
Db 234 nlyeValValLysGluLeuPheHisSerLysAsnGlyAlaArgLysSerAlaLysAl 254
Qy 535 CATCATGCTTGTGACTGATGAGAACTCCATGAAGATCTTTTCTTATTCAGAG----- 589
Db 254 eleuIleValIleThrAspGlyGlnLysPheArgAspProLeuGluTyrArgHisValI 274
Qy 590 -AGGAGGCTAATAGGCTCTCGAGATCTTGTCATTTGTTTACTGTGTGTGAAGA 648
Db 274 eProGluAlaGluLysAla-----GlyIleIleArgTyrAlaIleGlyValGlyAs 291
Qy 649 T---TTCAATGAG---ACACAGCTGCGCCGGAT-----GCGGACAGTAA 687
Db 291 pAlaPheArgGluProThrAlaLeuGlnGlnLeuAsnThrIleGlySerAlaProSerG 311
Qy 688 GATCATGATGTTCCCGTGAATGACGCGCTTTCAGGCTTCGAAAGCATCATCACTCAT 747
Db 311 nAspHisValIlePheLysValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnI 330


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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentln Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/482,293A
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ INFORMATION FOR SEQ ID NO: 53:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1161 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-482-293A-53

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Alignment Scores:
Pred. No.: 2,086-08 Length: 1161
Score: 167.00 Matches: 77
Percent Similarity: 42.47% Conservative: 50
Best Local Similarity: 25.75% Mismatches: 125
Query Match: 6.57% Indels: 47
DB: 1 Gaps: 14

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US-09-970-076-1 (1-1414) x US-08-482-293A-53 (1-1161)

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QY 28 GGCGGCTCCCTGAGGGCTGCGAGCTTCGCGAGCGGAGGACCGACCTGCTCT 87
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 93 GlyLeuSerLeuValAlaIleAspThrAsnAsnSerGlnLeuLeuAlaCysGlyProThrAla 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 88 CCCCAGGCTGCGGCGC-----CATGGCCACGGCGGAGCGGAGGCGCTGGCATCGG 138
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 113 GlnArgAlaCysAlaLeuAsnMetCysAlaCysGlySerCys-LeuLeuLeuGlySerSe 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 139 CTTCCAGTGGCTCTCTTGGCCACTGTGGTGCATCTGCGCGGCGGAGGAGGAGCGAG 198
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 132 rleuGlnPheIleGlnAlaIleProAlaIleMet----- 143
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 199 GGAGGATGGGGGTCCAGCCTGCTACCGC---GGATTGACCTGTACTTCATTGTCAGCAA 255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 144 -----ProGluCysProGlnGlnMetAspIleAlaPheLeuIleAspI 159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 256 ATCAGGAAGTGTG---CTGCACCACTGGAATGAAATCTTACTTGTGGAAACAGTTGGC 312
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 159 ySerGlySerIleAspGlnSerAspPheThrGlnMetCysAspPheValIlyAlaLeuMe 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 313 TCACAAATTCATCAGCCCAACAGTGAAGATGTCCTTATGTTTCTCCACCGGAGAAC 372
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 179 rclYglnLeuAlaSerThrSerThrSerPheSerLeuMetGlnIlySerAsnIleLeuIly 199
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 373 AACCTTAATGAACCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 199 rthrthsrPheThrPheThrGlnPheLeuSerSerLeuSerProGlnSerLeuValAspI 219
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 418 CCTAGAGAACTTCAGAGAAAGTTCTGCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 477
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

DB 219 alIeValGlnLeuGln-----GlyLeuThrYrThrAlaSerGlyIleG 234
QY 478 AAGGCCAGTACGACGATTTATTATGAAAACAGACAGGGTACAGACAGCC---AGCGT 534
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 234 nlySerValIlyGlnLeuPheIleSerIlySerIlySerIlySerIlySerIlySerIly 254
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 535 CATCATTCCTTGGCTGATGAGAAATCCAGTAAGATCTCTTTTCTATTACAGAG----- 589
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 254 eleuIleValIleThrAspGlyGlnLysPheArgAspProLeuGlnIlyrArgIleValI 274
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 590 -AGGAGGCTAATAGCTCCGAGATCTTGTCATGTTTTCATGTTGTTGTTGTTGTTGTT 648
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 274 eProGlnIleGlnIlyVala-----GlyIleIleArgIlyrAlaIleGlyValaGly 291
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 649 T---TTCAATGAG---ACACAGCTGCGCCGAGTT-----GCCGACAGTAA 687
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 291 palAheArgGlnUpProThrAlaLeuGlnGlnLeuAsnThrIleGlySerAlaProSerI 311
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 688 GGATCATGTGTTCCCGTGAATGACGCGCTTTCAGGCTTCGACAGCATCATCACTCAAT 747
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 311 nAspIleValPheIlySerValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnI 330
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 748 TTTGAAAGAACTCTGCATCGAAATCTTAGACGCTGAACCATCCACCATTTGCGAGAA 807
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 330 eGlnGlnIlyS-----IlePheAlaIleGlnGlnIlyrGlnIlySerArgSerSe 346
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 808 GTCATTTCAGTGTGTCGTAGAGAGAAAGCGCTTCGACATGCCCGCAACGTGAC 862
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 346 rSerPheGlnIleGlnIlyMetSerGlnGlnIlyPheSerSerAlaLeuSerMetAsp 364
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RESULT 15
US-08-943-363-53
/ Sequence 53, Application US/08943363
/ Patent No. 5837478
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 114
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentln Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943,363
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ INFORMATION FOR SEQ ID NO: 53:

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SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-53

Alignment Scores:
Pred. No.: 2.08e-08 Length: 1161
Score: 167.00 Matches: 77
Percent Similarity: 42.47% Conservative: 50
Best Local Similarity: 25.75% Mismatches: 125
Query Match: 6.57% Indels: 47
DB: 1 Gaps: 14

US-09-970-076-1 (1-1414) x US-08-943-363-53 (1-1161)

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QY 28 GGGCGCTCCTGAGGGCTGTGCGAGTTCCGGAGCGTGGAAAGAGCGGACCTGTCT 87
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DB 93 GlyLeuSerLeuValAlaAspThrAsnAsnSerGlnLeuLeuAlaCysGlyProThrAla 112
   ||| ||| |||
QY 88 CCCCAGGCTGCGGGC-----CATGCCACGCGGAGCGGAGAGCCCTCGGCATCGG 138
   ||| ||| |||
DB 113 GlnArgAlaCysAlaLysAsnMetTyrAlaLysGlySerCys-LeuLeuLeuGlySerSe 132
   ||| ||| |||
QY 139 CTTCCAGTGGCTCTCTTTGGCCACTGTGTCATCTGCGCGGCGAAGGGGACGCGAG 198
   ||| ||| |||
DB 132 rLeuGlnPheIleGlnAlaIleProAlaThrMet----- 143
   ||| ||| |||
QY 199 GAGAGATGGGGTCCAGCTGTACGGC--GGATTGACCTGTACTTTCATTGTGACAA 255
   ||| ||| |||
DB 144 -----ProGlyCysProGlyGlnGluMetAspIleAlaPheLeuIleAspGln 159
   ||| ||| |||
QY 256 ATCAGAGAAGTGTG--CTGCACCACTGGAATGAATCTATTACTTTGTGACAGTTGGC 312
   ||| ||| |||
DB 159 ySerGlySerIleAspGlnSerAspPheThrGlnMetLysAspPheValLysAlaLeuMe 179
   ||| ||| |||
QY 313 TCACAAATTATCATGCCACCAAGTTGAGAATGCTTATTGTTTCTCCACCGAGAGAC 372
   ||| ||| |||
DB 179 rGlyGlnLeuAlaSerThrSerPheSerLeuMetGlnTyrSerAsnIleLeuLy 199
   ||| ||| |||
QY 373 AACCTTAATGAATCTGACAGAAAGACAG-----GACCAATCCGTCMAAG 417
   ||| ||| |||
DB 199 eThrIlePheThrPheThrGlnPheLysSerSerLeuSerProGlnSerLeuValAspAl 219
   ||| ||| |||
QY 418 CTTAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGACATTACATGCATGAAGGATTGA 477
   ||| ||| |||
DB 219 aIleValGlnLeuGln-----GlyLeuThrTyrThrAlaSerGlyIleGln 234
   ||| ||| |||
QY 478 AAGGGCCAGTGAAGCATTTATTATGAAAAACACAAAGGTACAGACAGC--AGCGT 534
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DB 234 nLysValLysIleLeuPheIleSerLysSerLysValAlaArgLysSerAlaLysLysI 254
   ||| ||| |||
QY 535 CATCATTCCTTTCATGTGAGAGAACTCCATGAAGATCTCTTTTCATTACAGAG----- 589
   ||| ||| |||
DB 254 eLeuIleValIleThrAspGlyGlnLysPheArgAspProLeuGlnTyrArgHisValI 274
   ||| ||| |||
QY 590 -AGGAGGCTTAATAGTCTCGAGATCTTGTCATTTGTTACTGTGTGTGTAAGA 648
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DB 274 eProGlnAlaGlnLysAla-----GlyIleIleArgTyrAlaIleGlyValGlyAs 291
   ||| ||| |||
QY 649 T---TTCAATGAG--ACACAGCTGGCCCGGATT-----GGGACAGTAA 687
   ||| ||| |||
DB 291 pAlaPheArgGlnProThrAlaLeuGlnGlnLeuAsnThrIleGlySerAlaProSerG 311
   ||| ||| |||
QY 688 GGATCATGTGTTTCCGGAATGACGGGTTTCAAGCTCTGCAAGCATCATCCATCAAT 747
   ||| ||| |||
DB 311 nAspHisValAlaPheLysValGlyAsn--PheValAlaLeuArgSerIleGlnArgGlnI 330
   ||| ||| |||
QY 748 TTGGAAGAAGTCTGCATCGAAATTTCTAGAGCTGAACCATCCACATATGTGACAGAGA 807
   ||| ||| |||
DB 330 eGlnGlnLys-----IlePheAlaIleGlnGlyThrGlnSerArgSerSerSe 346
```

```
QY 808 GTGATTTCAGTTGTCTGTAGAGAAACGAGCTTCCGACATGCCCGCAAGTGGAC 862
   ||| ||| |||
DB 346 rSerPheGlnHisGlnMetSerGlnGlyPheSerSerAlaLeuSerMetAsp 364
   ||| ||| |||
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Job time : 63.1092 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: December 14, 2005, 11:59:14 ; Search time 212.268 Seconds
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5566.636 Million cell updates/sec

Title: US-09-970-076-1

Perfect score: 2540
Sequence: 1 agggaccgcggaggagggcc.....aaaaaaaaaaaaaaaaaaaa 1414

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications_AA_Main -OPMT=faetan -SUFFIX=rapbm -MINMATCH=0.1
-LOORCL=0 -LOOEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DLOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFM=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076@CGN_1_1_604@runat_14122005_110511_26579
-NCPU=6 -ICPU=3 -NO_MMAP -LARGECQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications_AA_Main:
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3: /cgcn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1914	75.4	368	6 US-11-047-278-2	Sequence 2, Appli
2	1894	74.6	564	3 US-09-918-715-187	Sequence 187, App
3	1894	74.6	564	3 US-09-918-715-232	Sequence 232, App
4	1894	74.6	564	4 US-10-301-822-199	Sequence 199, App
5	1894	74.6	564	4 US-10-408-765A-1823	Sequence 1823, App
6	1894	74.6	564	4 US-10-474-794-187	Sequence 187, App
7	1894	74.6	564	4 US-10-474-794-232	Sequence 232, App
8	1894	74.6	564	5 US-10-979-159-187	Sequence 187, App
9	1894	74.6	564	5 US-10-979-159-232	Sequence 232, App
10	1894	74.6	564	6 US-11-047-278-6	Sequence 6, Appli
11	1889	74.4	403	3 US-09-833-245-621	Sequence 621, App
12	1870	73.6	403	3 US-09-833-245-620	Sequence 620, App

13	1793	70.6	562	3 US-09-918-715-194	Sequence 194, App
14	1793	70.6	562	3 US-09-918-715-301	Sequence 301, App
15	1793	70.6	562	4 US-10-474-794-194	Sequence 194, App
16	1793	70.6	562	4 US-10-474-794-301	Sequence 301, App
17	1793	70.6	562	5 US-10-979-159-194	Sequence 194, App
18	1793	70.6	562	5 US-10-979-159-301	Sequence 301, App
19	1670	65.7	551	4 US-10-038-307-18	Sequence 18, Appli
20	1670	65.7	551	4 US-10-038-307-18	Sequence 18, Appli
21	1654.5	65.1	564	4 US-10-038-307-20	Sequence 20, Appli
22	1654.5	65.1	564	4 US-10-201-292-20	Sequence 20, Appli
23	1649	64.9	333	3 US-09-796-753-12	Sequence 12, Appli
24	1649	64.9	333	4 US-10-038-307-2	Sequence 2, Appli
25	1649	64.9	333	4 US-10-201-292-2	Sequence 2, Appli
26	1649	64.9	333	6 US-11-047-278-8	Sequence 8, Appli
27	1649	64.9	345	4 US-10-038-307-24	Sequence 24, Appli
28	1649	64.9	345	4 US-10-201-292-24	Sequence 24, Appli
29	1636	64.4	328	4 US-10-038-307-26	Sequence 26, Appli
30	1636	64.4	328	4 US-10-201-292-26	Sequence 26, Appli
31	1636	64.4	543	4 US-10-038-307-14	Sequence 14, Appli
32	1636	64.4	543	4 US-10-201-292-14	Sequence 14, Appli
33	1634.5	64.4	342	4 US-10-038-307-22	Sequence 22, Appli
34	1634.5	64.4	342	4 US-10-201-292-22	Sequence 22, Appli
35	1633	64.3	543	4 US-10-038-307-16	Sequence 16, Appli
36	1633	64.3	543	4 US-10-201-292-16	Sequence 16, Appli
37	1626	64.0	543	4 US-10-038-307-10	Sequence 10, Appli
38	1626	64.0	543	4 US-10-201-292-10	Sequence 10, Appli
39	1555	61.2	534	4 US-10-038-307-12	Sequence 12, Appli
40	1495	58.9	534	4 US-10-201-292-12	Sequence 12, Appli
41	1495	58.9	534	4 US-10-201-292-34	Sequence 34, Appli
42	1434.5	51.5	479	4 US-10-201-292-32	Sequence 32, Appli
43	1307	47.0	460	4 US-10-201-292-28	Sequence 28, Appli
44	1193	46.6	460	4 US-10-201-292-30	Sequence 30, Appli
45	1183	46.6	460	4 US-10-201-292-30	Sequence 30, Appli

ALIGNMENTS

RESULT 1
US-11-047-278-2
; Sequence 2, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296, 97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-047-278-2

Alignment Scores:

Pred. No.: 1,46e-170 Length: 368
Score: 1914.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 75.35% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-1 (1-1414) x US-11-047-278-2 (1-368)
QY 104 ATGGCAGCGGAGGAGCGAGCCCTCGCATCGGCTTCAGTGGCTCTCTTTGGCCACT 163

Db 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaTrp 20
QY 164 CTGGTGCCTCATCTGCCCGGCGAAGGGGAGACGAGGAGAGATGGGGGTCTCACCTGCTAC 223
Db 21 LeuValLeuIleCysValaGlyngInglyArgArgGlyAspGlyGlyProAlaCysTrp 40
QY 224 GCGGATTTGACCTGACTTCAATTTTGGACAATTCAGAAAGTGTGTGACCACTGGAAAT 283
Db 41 GlyGlyPheAspLeuTrpPheIleLeuAspLysSerGlySerValLeuIleHisTrpAsn 60
QY 284 GAAATCTATTACTTTGTGGAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAATG 343
Db 61 GluIleTrpLeuValaGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
QY 344 TCCCTTATTGTTTTCTCCACCGGAGAAACACTTAAATGAATGTGACAGAGACACTTACATG 403
Db 81 SerPheIleValaPheSerThrArgGlyThrTrpLeuMetLysLeuThrGluAspArgGlu 100
QY 404 CAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 463
Db 101 GlnIleArgGlnGlnLeuGlnLeuGlnLysValLeuProGlyGlyAspThrTrpMet 120
QY 464 CATGAAGATTTGAAAAGGCGCAGTGAAGATTTATTATGAATAACAGACAAAGGTAACAG 523
Db 121 HisGluGlyPheGluArgAlaSerGlnGlnIleTrpTrpGluAsnArgGlnGlyArg 140
QY 524 ACAGCCAGGCTCATCTTGTGACTGATGAGAACTCCAGAAATCTCTTTTCTAT 583
Db 141 ThrAlaSerValIleIleIleAlaLeuThrAspGlyGlnLeuHisGlnAspLeuPhePheTrp 160
QY 584 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTGCAATTTGTTACTGTGTGTGTG 643
Db 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTrpCysValaGlyVal 180
QY 644 AAAGATTTCAATGAGACACAGCTGGCCCGGATTTGCGAGACAGTAAGATCATGTGTTCC 703
Db 181 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
QY 704 GTGAATGAGGCTTTTACAGGCTCTGCAAGGAGCATCATCTCAATTTTGAAGAAGTCTTCC 763
Db 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
QY 764 ATCGAAATTTAGACAGCTGAACCATCCACATATGTGACAGAGATCATTTCAAGTTTTC 823
Db 221 IleGlnIleLeuAlaIleGluProSerThrIleCysAlaGlyGlnSerPheGlnValIle 240
QY 824 GTGAGAGAAACGGCTTCCGACATGCGCCGCAACGTGACAGAGGCTCTGACAGTTTCAAG 883
Db 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
QY 884 ATCAATGATCGGCTGACACTCAATGAGAAAGCCCTTTTGTGGAACAACATTTATTAACG 943
Db 261 IleAsnAspSerValThrLeuAsnGlnLysProPheSerValGlnAspThrTrpTrpLeu 280
QY 944 TGTCCAGGCTATCTTAAAGAAAGTTGGATGAAGAGTGAAGTCACTCCAGGTCAGATGAAC 1003
Db 281 CysProAlaProIleLeuLysGlnValaGlyMetLysAlaIleLeuGlnIleAspMetAsn 300
QY 1004 GATGGCTCTTTTATTTCTCAAGTTGTGATCATGACCAACACACACTGTTTGAAGGT 1063
Db 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThrHisCysSerAspGly 320
QY 1064 TCCATCTCTGGCCATGGCCCTGCTGATCCCTGTTCTCTCTAGCCCTGGCTCTCTCTGG 1123
Db 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340
QY 1124 TGGTTCTGGCCCTCTGCTGACATGTGATATCAAGAGAGTCCCTCACCCCTGCGAG 1183
Db 341 TrpPheTrpProLeuCysCysThrValIleIleLysGlnValaProProProAlaGln 360
QY 1184 GAGAGTGAAGAAATTAATAA 1207

Db 361 GluSerGluGluAsnLysIleLys 368
RESULT 2
US-09-918-715-187
; Sequence 187, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-918-715-187
Alignment Scores:
Pred. No.: 1,3e-168 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.57% Indels: 0
Gaps: 0
DB: 3
US-09-970-076-1 (1-1414) x US-09-918-715-187 (1-564)
QY 104 ATGGCAGAGGAGGAGGAGGAGGAGCCCTCGGATCGGCTTCAGTGGCTCTTTGGCCACT 163
Db 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaTrp 20
QY 164 CTGGTGCCTCATCTGCCCGGCGAAGGGGAGACGAGGAGAGATGGGGGTCTCACCTGCTAC 223
Db 21 LeuValLeuIleCysValaGlyngInglyArgArgGlyAspGlyGlyProAlaCysTrp 40
QY 224 GCGGATTTGACCTGACTTCAATTTTGGACAATTCAGAAAGTGTGTGACCACTGGAAAT 283
Db 41 GlyGlyPheAspLeuTrpPheIleLeuAspLysSerGlySerValLeuIleHisTrpAsn 60
QY 284 GAAATCTATTACTTTGTGGAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAATG 343
Db 61 GluIleTrpLeuValaGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
QY 344 TCCCTTATTGTTTTCTCCACCGGAGAAACACTTAAATGAATGTGACAGAGACACTTACATG 403
Db 81 SerPheIleValaPheSerThrArgGlyThrTrpLeuMetLysLeuThrGluAspArgGlu 100
QY 404 CAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 463
Db 101 GlnIleArgGlnGlnLeuGlnLeuGlnLysValLeuProGlyGlyAspThrTrpMet 120
QY 464 CATGAAGATTTGAAAAGGCGCAGTGAAGATTTATTATGAATAACAGACAAAGGTAACAG 523
Db 121 HisGluGlyPheGluArgAlaSerGlnGlnIleTrpTrpGluAsnArgGlnGlyArg 140
QY 524 ACAGCCAGGCTCATCTTGTGACTGATGAGAACTCCAGAAATCTCTTTTCTAT 583
Db 141 ThrAlaSerValIleIleIleAlaLeuThrAspGlyGlnLeuHisGlnAspLeuPhePheTrp 160
QY 584 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTGCAATTTGTTACTGTGTGTGTG 643
Db 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTrpCysValaGlyVal 180

QY 644 AAAGATTTCATGATGACACAGCTGGCCCGGATTGCCGACATGAAGTCAATGTTTCCC 703
DB 181 LysAspPheAsnGluThrGlnLeuAlaArg1LeuAlaSerIleuAspHisValPhePro 200
QY 704 GTGAATGACGGCTTTGAGGCTCTGCAAGGATCATCCACTCAATTTGAAGAAGTCTGCG 763
DB 201 ValAsnAspGlyPheGlnAlaLeuGlnGly1IleIleHisSerIleuGlySerCys 220
QY 764 ATCGAAATTCATGACAGCTGAACCATCCACATATGTGCAGAGAGTCAATTCAGTTGTC 823
DB 221 IleGlnIleuAlaIleuAlaGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
QY 824 GTGAGAGGAAACGGCTTCCGACATGCCCCGCAAGCTGACAGAGGCTCTGCAAGTTCAAG 883
DB 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
QY 884 ATCAATGACTCGGTCACACTCAATGAGAGGCCCTTTCTGTGAAAGACATTTATTACTG 943
DB 261 IleAsnAspSerValThrLeuAsnGluLysPheProPheSerValGluAspThrTyrlleu 280
QY 944 TGTCACAGCGCTATCTTAAAGAGTTGGCATGAAAGCTGCACCTCCAGTCAAGCATGAAC 1003
DB 281 CysProAlaProIleuLeuLysGluValGlyMetLysAlaIleuGlnValSerMetAsn 300
QY 1004 GATGGCCTCTTTTATCTCCAGTTCGTGATCATCATCACACACACACTGTTCTGACGGT 1063
DB 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
QY 1064 TCCATCCTGGCCATCGCCCTGCTGATCTGTTCTGCTCTGAGCCCTGAGCTCTCTCTGG 1123
DB 321 SerIleuAlaIleuAlaLeuLeuIleuPheLeuLeuAlaLeuAlaLeuLeuTrp 340
QY 1124 TGGTTCTGGCCCTCTGCTGCTGCATGTGATTATCAAGAGAGTCCCTCCAGCCCTGCGAG 1183
DB 341 TrpPheTrpProLeuLysCysThrValIleIleLysGluValPropProProAlaGlu 360
QY 1184 GAGAGTGAAGAA 1195
DB 361 GluSerGluGlu 364

RESULT 3

US-09-918-715-232
Sequence 232, Application US/09918715
Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918.715
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: PatSeq for Windows Version 3.0
SEQ ID NO 232
LENGTH: 564
TYPE: PR
ORGANISM: Homo sapiens
US-09-918-715-232

Alignment Scores:
Pred. No.: 1,36-168
Score: 1894.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 74.57%

Length: 564
Matches: 364
Conservative: 0
Mismatch: 0
Indels: 0

DB: 3 Gaps: 0
US-09-970-076-1 (1-1414) x US-09-918-715-232 (1-564)
QY 104 ATGGCCACGGCGGAGGAGGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTGGCCACT 163
DB 1 MetAlaThrAlaGluArgAlaLeuGly1IleGlyPheGlnTrpLeuSerLeuAlaThr 20
QY 164 CTGTGCTCATCTGCGCCGGGGCAAGGGGAGCGAGGAGGAGTGGGGGTCAGCTGTAC 223
DB 21 LeuValLeuIleCysAlaGlyGlnGlyArgArgGluAspGlyGlyProAlaCysTrp 40
QY 224 GCGGATTTGACCTGACTCATTTTGGACAAATTCAGGAAGTGTGTCACCACTGGAAT 283
DB 41 GlyGlyPheAspLeuTyrlleuAspLysSerGlySerValLeuHisSerTrpAsn 60
QY 284 GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCACTTGAGATG 343
DB 61 GluIleTyrlleuPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80
QY 344 TCCCTTATTTGTTTCTCCACCCGAGAAACAACCTTAATGAACATGACAGAAAGACAGAA 403
DB 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
QY 404 CAATCCGTCAGGCGCTAGAAAGAACTCCAGAAAGTTCTGCAGAGAGGAGACATTACATG 463
DB 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrlleu 120
QY 464 CATGAAGATTGAAAGGCGCAGTGAGACAGATTATTAATAACAGACAGAGGTACAG 523
DB 121 HisGlnGlyPheGluArgAlaSerGlnGlnIleTyrlleuGlnLysArgGlnGlyArg 140
QY 524 ACAGCCGCTCATCATGCTTTGACTGATGAGGAACATCCATGAAGTCTCTTTGAT 583
DB 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluLysLeuPhePheTyrlleu 160
QY 584 TCAGAGAGGAGGCTAATGATGATCTGCAGATCTTGATGTCATGTTGTTACTGTGTGTG 643
DB 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrlleuCysValGlyVal 180
QY 644 AAAGATTTCATGATGACACAGCTGGCCCGGATTGCCGACATGAAGTCAATGTTTCCC 703
DB 181 LysAspPheAsnGluThrGlnLeuAlaArg1LeuAlaSerIleuAspHisValPhePro 200
QY 704 GTGAATGACGGCTTTGAGGCTCTGCAAGGATCATCCACTCAATTTGAAGAAGTCTGCG 763
DB 201 ValAsnAspGlyPheGlnAlaLeuGlnGly1IleIleHisSerIleuGlySerCys 220
QY 764 ATCGAAATTCATGACAGCTGAACCATCCACATATGTGCAGAGAGTCAATTCAGTTGTC 823
DB 221 IleGlnIleuAlaIleuAlaGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
QY 824 GTGAGAGGAAACGGCTTCCGACATGCCCCGCAAGCTGACAGAGGCTCTGCAAGTTCAAG 883
DB 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
QY 884 ATCAATGACTCGGTCACACTCAATGAGAGGCCCTTTCTGTGAAAGACATTTATTACTG 943
DB 261 IleAsnAspSerValThrLeuAsnGluLysPheProPheSerValGluAspThrTyrlleu 280
QY 944 TGTCACAGCGCTATCTTAAAGAGTTGGCATGAAAGCTGCACCTCCAGTCAAGCATGAAC 1003
DB 281 CysProAlaProIleuLeuLysGluValGlyMetLysAlaIleuGlnValSerMetAsn 300
QY 1004 GATGGCCTCTTTTATCTCCAGTTCGTGATCATCATCACACACACTGTTCTGACGGT 1063
DB 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
QY 1064 TCCATCCTGGCCATCGCCCTGCTGATCTGTTCTGCTCTGAGCCCTGAGCTCTCTCTGG 1123
DB 321 SerIleuAlaIleuAlaLeuLeuIleuPheLeuLeuAlaLeuAlaLeuLeuTrp 340
QY 1124 TGGTTCTGGCCCTCTGCTGCTGCATGTGATTATCAAGAGAGTCCCTCCAGCCCTGCGAG 1183

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Db 341 TnpPheTPrProLeucYcSthrVallelleleYgLuValProProProProAlaGlu 360
QY 1184 GAGAGTGAGGAA 1195
Db 361 GluSerGluGlu 364

RESULT 4
US-10-301-822-199
; Sequence 199, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamelkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MP001-029P2RM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-199

Alignment Scores:
Pred. No.: 1,3e-168 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.57% Indels: 0
DB: 4 Gaps: 0

US-09-970-076-1 (1-1414) x US-10-301-822-199 (1-564)
QY 104 ATGGCCAGCGGCGGAGGAGAGCCCTCGGCGCTTCAGAGGCTCTTTGGCCACT 163
Db 1 MetAlaThrAlaGluIuArgAlaGluValGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
QY 164 CTGGTGCTCATCTGCGCCGGGCAAGGGGACCGCAGGAGGATGGGGCTCGACGCTCTAC 223
Db 21 LeuValLeuIleCysAlaGluGlnGlyIuArgAlaGluIuSerGlyGluProAlaCysTrp 40
QY 224 GCGGAGTTTGACCTGTACTTTCATTTTGGACAAATTCAGAAAGTGTCTGCACCACTGGAAT 283
Db 41 GlyGlyPheAspLeuTrpPheIleuAspLysSerGlySerValLeuHisIleTrpAsn 60
QY 284 GAAATCTATTACTTTGGGAAAGTGGCTCAAAATTCAGCCCAAGTTGAGAGATG 343
Db 61 GluIleTrpTyrrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
QY 344 TCCCTTATGTTTCTCCACCAGAAACACCTTAATGAACTGACAGAAAGACAGAA 403
Db 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
QY 404 CAAATCCGTCAGGCGCTAGAAAGATTCAGAAAGTTTGCAGAGAGAGACACTTACG 463
Db 101 GlnIleArgGlnGlnIleuGluGluLeuGlnLysValLeuProGlyLysPThrTrpMet 120
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QY 464 CATGAGGATTTGAAAGGCCAGTGACAGATTTATTTAGAAACAGACAGGTTACAG 523
Db 121 HisGluGlyPheGluIuArgAlaSerGluGlnIleTrpTyrrGluAsnArgGlnGlyArg 140
QY 524 ACAGCCAGCGGTATCATTTGCTTGTGACTGTAGAGAACTTCAGAAAGATCTTTTCTAT 583
Db 141 ThrAlaSerValIleIleIleLeuThrAspGlyGluLeuHisGluAspLeuPhePheTrp 160
QY 584 TCAGAGAGGAGGCTAATAGTCTGAGATCTTGGGCAATTTGTTACTGTGTGTG 643
Db 161 SerGluIuArgGlnAlaAsnArgSerTrpAspLeuGlyAlaIleValTrpCysValGlyVal 180
QY 644 AAAGATTTCAATAGACACACAGCTGCCCGGATGGCGACAGTAAGATCATGTGTTCC 703
Db 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspIleValPhePro 200
QY 704 GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAGTCTGC 763
Db 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
QY 764 ATCGAAATTTGACGCTGAACCATCCACATATGTCAGAGAGATTTCAAGTTGTC 823
Db 221 IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
QY 824 GTGAGAGGAAACGGCTTCGACATGCCGCAACGTGACAGGAGTCTCTGACGTTCAAG 883
Db 241 ValArgGlyAsnGlyPheArgHisAlaIArgAsnValAspArgValLeuCysSerPheLys 260
QY 884 ATCAATGACTCGGCTCACTCAATGAAAGCCCTTTCTGTGGAAGACATTATTACG 943
Db 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTrpLeuLeu 280
QY 944 TGTCCAGCGCTATCTTAAAGAAGTGGCATGAAGCTGCACTCCAGGTCAGCATGAAC 1003
Db 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
QY 1004 GATGGCTCTCTTTATCTCCAGTTCTGTGATCATTCACCAACACACAGCTGTTCGACGT 1063
Db 301 AspGlyLeuSerPheIleSerSerValIleIleThrThrThrIleCysSerAspGly 320
QY 1064 TCCATCTCTGCGCATGCCCTGCTGATCCGTGTTCTCTGCTCTGACCTGCTCTCTG 1123
Db 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340
QY 1124 TGGTTCGCGCCCTGCTGCACTGTGATTATCAAGAGAGTCCCTCCACCCCTGCCGAG 1183
Db 341 TnpPheTPrProLeucYcSthrVallelleleYgLuValProProProProAlaGlu 360

QY 1184 GAGAGTGAGGAA 1195
Db 361 GluSerGluGlu 364

RESULT 5
US-10-408-765A-1823
; Sequence 1823, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fany, Bojin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1823
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; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1823

Alignment Scores:
Pred. No.: 1,3e-168 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.57% Indels: 0
DB: 4 Gaps: 0

US-09-970-076-1 (1-1414) x US-10-408-765A-1823 (1-564)

QY 104 ATGGCCAGCGGAGCGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTTTGGCCACT 163
   |||||
Db 1 MetAlaThrAlaGluArgAlaGluAlaGluYIleGlyPheGlnIleThrLeuSerLeuAlaThr 20

QY 164 CTGGTGTCTATCTGGCCGCGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGTCTAC 223
   |||||
Db 21 LeuValLeuIleCysAlaGluGlnGlyAlaArgGluAlaSerGlyProAlaCysTyr 40

QY 224 GGGGAGTTTGACCTGTACTTCATTTTGAGCAAAATCAGAAATGCTGTCAGCACTGGAAAT 283
   |||||
Db 41 GlyGlyPheAspLeuTyrPheIleLeuAspLeuSerGlySerValIleuHisIleTyrAsn 60

QY 284 GAAATCTATTACTTTGTGAAACAGTTGGCTCACAATTCATCAGCCCACTTGAGATG 343
   |||||
Db 61 GluIleTyrTyrPheValGluGlnLeuAlaHisIleValIleSerProGlnLeuAlaGlnMet 80

QY 344 TCTCTTATTTGTTTCTCCACCCGAGAACAACTTAAATGAATCTGACAGAAAGCAGAA 403
   |||||
Db 81 SerPheIleValPheSerThrArgGlyThrThreuMetLeuValLeuThrGluAspArgGlu 100

QY 404 CAATCCGTCAGGCGCTAGAAAGAACTCCAGAAAGTTCTGCGAGGAGGACACTTACATG 463
   |||||
Db 101 GlnIleArgGlnGlyLeuGlnGluGlnLeuGlnValLeuProGlnGlyAspThrTyrMet 120

QY 464 CATGAAGATTGTGAAGAGCGCAGTGAAGCAATTTATTAAGAAACAGACAAAGGTACAGG 523
   |||||
Db 121 HisGlnIlePheGluArgAlaSerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140

QY 524 ACAGCCAGCGTCATCATTTGCTTTGATGAGGAGAACTCCATGAAGATCTTTTCTAT 583
   |||||
Db 141 ThrIleSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyr 160

QY 584 TCGAGAGGAGGAGCTATAGGCTCGAGATCTTGGTGCATTTGTTTCTGCTGGTGGAGTG 643
   |||||
Db 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180

QY 644 AAGATTTCATATGACAGACAGCTGGCCGAGATTGCGGACAGTAAGATCATGTGTTCCC 703
   |||||
Db 181 LysAspPheAsnGlnIleThrGlnLeuAlaArgIleAlaAspSerGlyValAspHisValPhePro 200

QY 704 GTGAATACGCGCTTTCAGGCTCTGCAAGGACATCATCACTCAATTTTGAAGAGTCTTCC 763
   |||||
Db 201 ValAsnAspArgGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuValGlySerCys 220

QY 764 ATGCAATTTCTAGAGAGTGAACCATTCACCAATATGTCAGAGAGATGATTTCAAGTTGTC 823
   |||||
Db 221 IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240

QY 824 GTGAGAGAAACGCGCTTCGACATGCCCGCAACGTGACAGAGGTCTCTGAGCTTCAAG 883
   |||||
Db 241 ValArgGlyAsnGlnPheArgHisAlaArgAsnAlaAspArgValIleuCysSerPheLys 260

QY 884 ATCAATGACTGGTCACTCAATGAGAAAGCCCTTTTCTGTGGAAGACCTTATTACTG 943
   |||||
Db 261 IleAsnAspSerValThrLeuAsnGlnIleuArgProPheSerValGluAspThrTyrLeuLeu 280

QY 944 TGTCAGGCTTAATCTTAAAGAAAGTTGGCATGAAGTGCATCCAGGTCAAGATGAAC 1003
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Db 281 CysProAlaProIleLeuValGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300

QY 1004 GATGGCCTCTTTTATCTCCAGTTCTGTGCATCATACCAACACACACTGTTTGACGGT 1063
   |||||
Db 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrIleCysSerAspGly 320

QY 1064 TCCATCTGGCCATCGCCCTGTGATCTCTGTTCTCTGCTAGCCCTGGCTCTCTGG 1123
   |||||
Db 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTyr 340

QY 1124 TGGTTCGACCCCTCTGCTGTCACCTGATTAATCAAGAGGCTCTCAACCCCTGCCAG 1183
   |||||
Db 341 TrpPheTyrProLeuCysCysThrValIleIleIleGlyValProProProProAlaGlu 360

QY 1184 GAGAGTGAGAA 1195
   |||||
Db 361 GluSerGluGlu 364

RESULT 6
US-10-474-794-187
; Sequence 187, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-187

Alignment Scores:
Pred. No.: 1,3e-168 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.57% Indels: 0
DB: 4 Gaps: 0

US-09-970-076-1 (1-1414) x US-10-474-794-187 (1-564)

QY 104 ATGGCCAGCGGAGCGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTTTGGCCACT 163
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Db 1 MetAlaThrAlaGluArgAlaGluAlaGluYIleGlyPheGlnIleThrLeuSerLeuAlaThr 20

QY 164 CTGGTGTCTATCTGGCCGCGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGTCTAC 223
   |||||
Db 21 LeuValLeuIleCysAlaGluGlnGlyAlaArgGluAlaSerGlyProAlaCysTyr 40

QY 224 GGGGAGTTTGACCTGTACTTCATTTTGAGCAAAATCAGAAATGCTGTCAGCACTGGAAAT 283
   |||||
Db 41 GlyGlyPheAspLeuTyrPheIleLeuAspLeuSerGlySerValIleuHisIleTyrAsn 60

QY 284 GAAATCTATTACTTTGTGAAACAGTTGGCTCACAATTCATCAGCCCACTTGAGATG 343
   |||||
Db 61 GluIleTyrTyrPheValGluGlnLeuAlaHisIleValIleSerProGlnLeuAlaGlnMet 80

QY 344 TCTCTTATTTGTTTCTCCACCCGAGAACAACTTAAATGAATCTGACAGAAAGCAGAA 403
   |||||
Db 81 SerPheIleValPheSerThrArgGlyThrThreuMetLeuValLeuThrGluAspArgGlu 100
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QY 404 CAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGACATTACATG 463
DB 101 GlnlleArgInglyleuGlnIuleGlnIyValIleuProGlyGlyAspThrTyrmet 120
QY 464 CATGAAGATTGAAAAGGCGCAGTGCAGATTATTATGAAAACAGACAGAGGTACAG 523
DB 121 HlsgIuglyPhgIuArgIAspSerGlnIleTyrTylGluAsnArgInglyTyrAsp 140
QY 524 ACAGCAGGCTCATCTTGCTTGACTGATGAGAACTCCATGAAGATCTCTTTCTAT 583
DB 141 ThrAlaSerValIleIleAlaIeuThrAspGlyGlnIleuHlsgIuAspIeuPhePheTyr 160
QY 584 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTCAGATTGTTACTGTGTGTGTG 643
DB 161 SerGluArgGluAlaAsnArgSerArgAspIeuGlyAlaIleValIleTyrCysValIleGlyVal 180
QY 644 AAAAGATTTCATGAGACACAGCTGGCCCGATTTGGCGACAGTAAAGATCATGTGTTCCC 703
DB 181 LysAspPheAsnGlyuThrGlnIleuAlaArgIleAlaAspSerLysAspHlsgValIlePhePro 200
QY 704 GTGAATGAGCGGCTTTCAGGCTCGCAAGGCATCATCAATTTGAAAGAGTCTGCG 763
DB 201 ValAsnAspGlyPheGlnAlaIeuGlnIyIleIleHlserIleuIySlySerCys 220
QY 764 ATCGAAATTCAGACAGTGAACCATCCACATATGTGCAAGAGATCATTTCAAGTTGTC 823
DB 221 HlgluIleuAlaIleAlaIleuProSerThrIleCysAlaIleGlyIuSerPheGlnValVal 240
QY 824 GTGAGAGAAACGGCTTCCGACATGCCCCGACAGTGCAGAGGCTCTGCGAGTTCAAG 883
DB 241 ValArgGlyAsnGlyPheArgHlsgAlaArgAsnValAspArgValIleuCysSerPheLys 260
QY 884 ATCAATGACTCGGTGCACACTCAATGAGAAAGCCCTTTCTGTGAGAGACATTATTACG 943
DB 261 HlAsnAspSerValThrIeuAsnGlyLysProPheSerValGluAspThrTyrIleuLeu 280
QY 944 TGTCACGCGCTATCTTAAAGAGTGGCATGAAGCTGCAGTCCAGTCCAGTCAAGTGAAC 1003
DB 281 CysProAlaProIleuLysGlnValIleGlyMetIyAlaAlaIeuGlnValIleSerMetAsn 300
QY 1004 GATGCGCTCTCTTTATCTTCAGATTCTGTCAATATCAACCCACACAGTCTTGCAGGT 1063
DB 301 AspGlyLysSerPheHlserSerSerValIleIleThrThrHlsgCysSerAspGly 320
QY 1064 TCCATCTGGCCATCGCCGCTGATCTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1123
DB 321 SerIleIeuAlaIleAlaIeuIleuIleuPheIleuIleuAlaIeuAlaIeuIleuTyr 340
QY 1124 TGGTCTGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1183
DB 341 TrpPheTyrProIeuCysCysThrValIleIleIleGlyValIleProProProAlaGln 360
QY 1184 GAGAGTGAGGAA 1195
DB 361 GluSerGluGln 364
RESULT 7
US-10-474-794-232
Sequence 232, Application US/10474794
Publication No. US20040213793A1
GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107,00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01

NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 232
LENGTH: 564
TYPE: PRF
ORGANISM: Homo sapiens
US-10-474-794-232
Alignment Scores:
Pred. No.: 1,3e-168 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.57% Indels: 0
DB: 4 Gaps: 0
US-09-970-076-1 (1-1414) x US-10-474-794-232 (1-564)
QY 104 ATGGCCACGCGGAGCGAGAGCCCTCGGATCGGCTTCAGTGGCTCTTTGGCCACT 163
DB 1 MetAlaThrAlaGluArgArgAlaIeuGlyIleGlyPheGlnThrIleuSerIleuAlaThr 20
QY 164 CTGTCCTCATCTGGCGCGCGGCGAGGCGGAGCCGAGGAGAGATGGGGGTCCAGCTCTAC 223
DB 21 LeuValIleuIleCysAlaIleGlnIyGlyArgArgGluAspGlyGlyProAlaCysTyr 40
QY 224 GCGGATTTGACCTGATCTTCAATTTTGACAATTCAGAAAGTGTGTCGACCACTGGAAT 283
DB 41 GlyGlyPheAspIeuTyrPheIleIeuAspIySerGlySerValIleuHlserIleuPhe 60
QY 284 GAAATCTATTAATTTGTGGAAAGTGGCTCAAAATTCATATCAAGCCACAGTTGAGAAATG 343
DB 61 GluIleTyrTyrPheValGluIleuAlaHlsgLysPheIleSerProGlnIleuArgMet 80
QY 344 TCCCTTATTTGTTTCTCCACCGGAGAAACAACCTTAATGAATCTGACAGAGACAGAGA 403
DB 81 SerPheIleValPheSerThrArgGlyThrIleuMetLysIeuThrGluAspArgGlu 100
QY 404 CAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGACATTACATG 463
DB 101 GlnlleArgInglyleuGlnIuleGlnIyValIleuProGlyGlyAspThrTyrmet 120
QY 464 CATGAAGATTGAAAAGGCGCAGTGCAGATTATTATGAAAACAGACAGAGGTACAG 523
DB 121 HlsgIuglyPhgIuArgIAspSerGlnIleTyrTylGluAsnArgInglyTyrAsp 140
QY 524 ACAGCAGGCTCATCTTGCTTGACTGATGAGAACTCCATGAAGATCTCTTTCTAT 583
DB 141 ThrAlaSerValIleIleAlaIeuThrAspGlyGlnIleuHlsgIuAspIeuPhePheTyr 160
QY 584 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTCAGATTGTTACTGTGTGTGTG 643
DB 161 SerGluArgGluAlaAsnArgSerArgAspIeuGlyAlaIleValIleTyrCysValIleGlyVal 180
QY 644 AAAAGATTTCATGAGACACAGCTGGCCCGATTTGGCGACAGTAAAGATCATGTGTTCCC 703
DB 181 LysAspPheAsnGlyuThrGlnIleuAlaArgIleAlaAspSerLysAspHlsgValIlePhePro 200
QY 704 GTGAATGAGCGGCTTTCAGGCTCGCAAGGCATCATCAATTTGAAAGAGTCTGCG 763
DB 201 ValAsnAspGlyPheGlnAlaIeuGlnIyIleIleHlserIleuIySlySerCys 220
QY 764 ATCGAAATTCAGACAGTGAACCATCCACATATGTGCAAGAGATCATTTCAAGTTGTC 823
DB 221 HlgluIleuAlaIleAlaIleuProSerThrIleCysAlaIleGlyIuSerPheGlnValVal 240
QY 824 GTGAGAGAAACGGCTTCCGACATGCCCCGACAGTGCAGAGGCTCTGCGAGTTCAAG 883
DB 241 ValArgGlyAsnGlyPheArgHlsgAlaArgAsnValAspArgValIleuCysSerPheLys 260
QY 884 ATCAATGACTCGGTGCACACTCAATGAGAAAGCCCTTTCTGTGAGAGACATTATTACG 943
DB 261 HlAsnAspSerValThrIeuAsnGlyLysProPheSerValGluAspThrTyrIleuLeu 280


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/ CURRENT FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US/09/918,715
/ PRIOR FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: 60/222,599
/ PRIOR FILING DATE: 2000-08-02
/ PRIOR APPLICATION NUMBER: 60/224,360
/ PRIOR FILING DATE: 2000-08-11
/ PRIOR APPLICATION NUMBER: 60/282,850
/ PRIOR FILING DATE: 2000-04-11
/ NUMBER OF SEQ ID NOS: 358
/ SOFTWARE: FASTSEQ for windows Version 3.0
/ SEQ ID NO 232
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-979-159-232

Alignment Scores:
Pred. No.: 1,3e-168 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.57% Indels: 0
DB: 5 Gaps: 0

US-09-970-076-1 (1-1414) x US-10-979-159-232 (1-564)
QY 104 ATGGCCAGGCGGAGGCGGAGAGCCCTCGGCATCGCTTCAGAGGCTCTTTGGCCACT 163
Db 1 MetAlaThrAlaGluArgAlaGluAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaTrp 20
QY 164 CTGTGCTCATCTGCGCCGCGGAGGCGGAGGCGGAGGAGATGCGGCTCGAGCTGCTAC 223
Db 21 LeuValLeuIleIleCysValaIleGlyGlnGlyArgArgGluAspGlyIleProAlaCysTrp 40
QY 224 GGGCGATTGACCTGACTTCACTTCACTTTTGGACAAATTCAGAAAGTGCTGTCACCACTGGAA 283
Db 41 GlyGlyPheAspLeuTrpPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60
QY 284 GAAATCTATTACTTTGTGGAACAGTGGGCTCCCAATTCATATGAGCCACAGTGGAGAA 343
Db 61 GlnIleTrpTrpPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
QY 344 TCCCTTATGTTTCTCCACCCGAGGAGAACCTTATGAACTGACAGAAAGACAGAA 403
Db 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
QY 404 CAAATCCGTCAGAGGCTTAGAAGAACTCCAGAAAGTTCTGCGAGGAGGAGACACTTACATG 463
Db 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTrpMet 120
QY 464 CATGAGAGTTTGAAGGGCGAGTGAAGCATTTATGAAAGACAGACAGGCTCAG 523
Db 121 HisGlnGlyPheGlnIleArgLysSerGlnGlnIleTrpTrpGluAsnArgGlnGlyTrpArg 140
QY 524 ACAGCAGAGGTCATCATTTGCTTGACTGATGAGAACTCCATGAGATCTTTTCTAT 583
Db 141 ThrAlaSerValIleIleAlaLeuThrArgGlyGlnLeuHisGlnLysPhePheTrp 160
QY 584 TCAGAGAGGAGGCTTAATAGGCTTCGAGATCTTGGTCAATTTGTTACTGTGGTGGTGG 643
Db 161 SerGlnArgGlnAlaAsnArgSerArgAspLeuGlyAlaIleValTrpCysValGlyVal 180
QY 644 AAAAGATTTCAATGAGCACAGCTGGCCCGGATGGCGGACAGTAAAGATCATGTGTTCC 703
Db 181 LysAspPheAsnGlnIleThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
QY 704 GTGAATGACGGCTTTCAGGCTTCGACAGGATCATCATCAATTTTGAAGAAGTCTGCG 763
Db 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
QY 764 ATCGAAATTTCTACAGCTGAACCATCCACCAATATGTGCGAGAGAGTCAATTCAGTTGTC 823
Db 764 ATCGAAATTTCTACAGCTGAACCATCCACCAATATGTGCGAGAGAGTCAATTCAGTTGTC 823
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Db 221 IleGlnIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
QY 824 GTGAGAGAAAACGGCTTCCGACATGCGCCGAACTGAGACAGGGTCTCTGACGTTCAAG 883
Db 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerThrLys 260
QY 884 ATCAATGACCTCGGCACACTCAATGAGAGCCCTTTCTGTGGAAAGACATTATTTACTG 943
Db 261 IleAsnAspSerValThrLeuAsnGlnLysProPheSerValGluAspThrTrpLeuLeu 280
QY 944 TGTCCAGGCGCTTCTTAAAGAACTGAGTGAAGTGCATCAGCTCAGCTCAGTCAAGTAA 1003
Db 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnAlaSerMetCys 300
QY 1004 GATGCGCTCTCTTTATCTCCAGTTCTGTATCATCATCACCCACACACTGTTCTGACG 1063
Db 301 AspGlyLeuSerPheIleSerSerValIleIleThrThrThrHisCysSerAspGly 320
QY 1064 TCCATCTGGCCCATGCGCCCTGCTGATCTCTTCTGCTTCCTAGCCCTGCTCTCTGG 1123
Db 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340
QY 1124 TGGTCTGAGCCCTCTGCTGTCATCTGATTAACAAGAGGTCCCTCCACCCCTGCCAG 1183
Db 341 TrpPheTrpProLeuCysCysThrValIleIleLysGluValProProProAlaGlu 360
QY 1184 GAGAGTGAAGAA 1195
Db 361 GluSerGlnGlu 364
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RESULT 10

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US-11-047-278-6
/ Sequence 6, Application US/11047278
/ Publication No. US20050196407A1
/ GENERAL INFORMATION:
/ APPLICANT: Young, John A.T.
/ APPLICANT: Bradley, Kenneth A.
/ APPLICANT: Collier, Robert J.
/ APPLICANT: Mogridge, Jeremy S.
/ TITLE OF INVENTION: Anthrax Toxin Receptor
/ FILE REFERENCE: 960296, 97745
/ CURRENT APPLICATION NUMBER: US/11/047,278
/ PRIOR FILING DATE: 2005-01-31
/ PRIOR APPLICATION NUMBER: US/09/970,076
/ PRIOR FILING DATE: 2001-10-03
/ PRIOR APPLICATION NUMBER: 60/251,481
/ PRIOR FILING DATE: 2000-12-05
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-047-278-6
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Alignment Scores:
Pred. No.: 1,3e-168 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.57% Indels: 0
DB: 6 Gaps: 0
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US-09-970-076-1 (1-1414) x US-11-047-278-6 (1-564)

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QY 104 ATGGCCAGGCGGAGGCGGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTTTGGCCACT 163
Db 1 MetAlaThrAlaGluArgAlaGluAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaTrp 20
QY 164 CTGTGCTCATCTGCGCCGCGGAGGCGGAGGCGGAGGAGATGCGGCTCGAGCTGCTAC 223
Db 21 LeuValLeuIleCysValaIleGlyGlnGlyArgArgGluAspGlyIleProAlaCysTrp 40
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QY 764 ATCGAATTCCTAGCAGCTGAACCATTCACCATATGTGCAGAGAGTGCATTTCAGATTGTC 823
| | | | |
Db 221 IIEGLUIIELEUALIAIAGIUPROSETRHILECYALAGLYGUSERPHEGINVALI 240
| | | | |
QY 824 GTGAGAGAAACGGCTTCCGACATGCGCCGCAAGTGGACAGGGTCTCTGCGAGCTTCAAG 883
| | | | |
Db 241 VALARGIYAASNDIYPHEARGHISALARGAENVALAPARGVALLEUCYSSERPHELYS 260
| | | | |
QY 884 ATCAATGACTCGGTCACTCAATGAGAAGCCCTTTTGTGGAGACATTATTAACG 943
| | | | |
Db 261 IIEAENAPSERVALTHREUAENGLIUPROPHSERVALGIUNSPHRYRILEUEN 280
| | | | |
QY 944 TGTCCAGGCCCTATCTTAAAGAAGTTGGCATGAAGCTGCACTCCAGTCCAGTCAAGTGAAC 1003
| | | | |
Db 281 CYSPTOLAPROIIIELEULYSGIUALGIYMETLYALALALEUENIVALSERMETAN 300
| | | | |
QY 1004 GATGCGCTCTCTTTATCTTCACAGTTCTGCATATACCAACCAACACTGTTCTGACGGT 1063
| | | | |
Db 301 AEPGLYLEUSERPHEILIESEISERVALIIEIETHTHTRHISCYSSERAPGLY 320
| | | | |
QY 1064 TCCATCTGAGCCATCGCCCTGCTGATCTGTTCTGCTCTGAGCCCTGGCTCTCTG 1123
| | | | |
Db 321 SERIIELEUALIAIIEALALEUENIIELEUPHEULEUHALALEUALEUENTRP 340
| | | | |
QY 1124 TGGTTCTGACCCCTCTGCTGCACTGTGATTATCAAGAGAGTCCCTCCACCCCTGCCGAG 1183
| | | | |
Db 341 TRPHEIETRPHEUCYSCYSTRVALIIEIIEIYGLIUALPPOBPROBPROIAGIU 360
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QY 1184 GAGAGTGAG 1192
| | | | |
Db 361 GLUSERGLU 363
| | | | |

RESULT 12

US-09-833-245-620
; Sequence 620, Application US/09833245
; Publication No. US2004010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCR
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 620
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (320)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (331)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (368)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-620

Alignment Scores:

Pred. No.: 2,07e-166 Length: 403
Score: 1870.00 Matches: 360
Percent Similarity: 99.17% Conservative: 0

Beet Local Similarity: 99.17% Mismatches: 3
Query Match: 73.62% Indels: 0
DB: 3 Gaps: 0
US-09-970-076-1 (1-1414) x US-09-833-245-620 (1-403)

QY 104 ATGGCCAGCGCGAGAGAGAGCCCTCGCATCGGCTTCAGTGCCTCTTTGGCCACT 163
| | | | |
Db 1 METALATNPALAGIUAARGIALALEUGLIIEGLYPHEGINTRPHEUSERLEUALATHR 20
| | | | |
QY 164 CTGGTCTCATGTGGCCCGGCGCAAGGGGAGCCAGGAGAGATGGGGGTCCACCTGCTAC 223
| | | | |
Db 21 LEUVALILEULIECYALAGIYGLIYATGAGIUALAPGLYGLYPTOLACYSTRY 40
| | | | |
QY 224 GSCGATTTGACCTTACTTCTTATTTGGACAATCAGAAAGTGTCTGCACTGAGTGAAT 283
| | | | |
Db 41 GIYGLYPHEAPHEULIYRPHLEULEUAPLYSSERGLYSERVALLEUHSISTRPMAN 60
| | | | |
QY 284 GAAATCTATTACTTTGTGGAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATG 343
| | | | |
Db 61 GIUIETRYRYPHEVALIGIUGIINLEUALHISLYSPHEILIESETRPGLINLEUARPMET 80
| | | | |
QY 344 TCCCTTATTTGTTTTCACCCGAGAGAACCTTATGAACATGACAGAACAGAGAA 403
| | | | |
Db 81 SERPHEILEVALPHESETRHTARGIYTHRTHEUMELYSPHEUTHGLIUSPARIGIU 100
| | | | |
QY 404 CAATCCGTCAAGGCTTGAAGAAGTCCAGAAAGTTCTGCGAGAGACACTTAACATG 463
| | | | |
Db 101 GINIEAARGINGIYLEUGIUGIUEUGIINYSVALLEUPROGLIYASPHRYRTHET 120
| | | | |
QY 464 CATGAAGATTGAAAGGCCAGTGAGAGATTTATGAAACAGCAAGGTTACAG 523
| | | | |
Db 121 HSGIUGIYPHEGLIUAARGIALASERGIUGIINLETYRTRYGLIUSANARGIINGIYTRARG 140
| | | | |
QY 524 ACAGCCAGCTCATATGCTTTGACSTGATGAGAACTCCATGAAGATCTCTTTTCAT 583
| | | | |
Db 141 THRILASERVALIIEIIEALALEUTHRASPGLIYGLIUEUHSIIGIUSPHEUHEPHEIYR 160
| | | | |
QY 584 TCAGAGAGAGAGGCTTAATAGCTCTGAGATCTTGTGCAATGTTTACTGTGTGGTGG 643
| | | | |
Db 161 SERGIUAARGIUALIASHRISERTRGPSPHEUGIYALIAIE**TYRCYSVALIGIYVAL 180
| | | | |
QY 644 AAAGATTTCAATGAGACACAGCTGGCCCGATGGGACAGTGAAGATCATGTGTTCCC 703
| | | | |
Db 181 LYSAPRPHAEANGIUTHRGILEUHALARGIIEALASPSERLYASPHISVALPHEPRO 200
| | | | |
QY 704 GTGAATGACGGCTTCAAGCTCTGCAAGGCATCATCCACTCAATTTTGAAGAAGTCTGCG 763
| | | | |
Db 201 VALAENAPGLYPHEGLIALALEUGIINGIYIIEIHSERILEULEULYSYSERCY 220
| | | | |
QY 764 ATCGAATTCCTAGCAGCTGAACCATTCACCATATGTGCAGAGAGTGCATTTCAGATTGTC 823
| | | | |
Db 221 IIEGLUIIELEUALIAIAGIUPROSETRHILECYALAGLYGUSERPHEGINVALI 240
| | | | |
QY 824 GTGAGAGAAACGGCTTCCGACATGCGCCGCAAGTGGACAGGGTCTCTGCGAGCTTCAAG 883
| | | | |
Db 241 VALARGIYAASNDIYPHEARGHISALARGAENVALAPARGVALLEUCYSSERPHELYS 260
| | | | |
QY 884 ATCAATGACTCGGTCACTCAATGAGAAGCCCTTTTGTGGAGACATTATTAACG 943
| | | | |
Db 261 IIEAENAPSERVALTHREUAENGLIUPROPHSERVALGIUNSPHRYRILEUEN 280
| | | | |
QY 944 TGTCCAGGCCCTATCTTAAAGAAGTTGGCATGAAGCTGCACTCCAGTCCAGTCAAGTGAAC 1003
| | | | |
Db 281 CYSPTOLAPROIIIELEULYSGIUALGIYMETLYALALALEUENIVALSERMETAN 300
| | | | |
QY 1004 GATGCGCTCTCTTTATCTTCACAGTTCTGCATATACCAACCAACACTGTTCTGACGGT 1063
| | | | |
Db 301 AEPGLYLEUSERPHEILIESEISERVALIIEIETHTHTRHISCYSSERAPGLY 320
| | | | |
QY 1064 TCCATCTGAGCCATCGCCCTGCTGATCTGTTCTGCTCTGAGCCCTGGCTCTCTG 1123
| | | | |
Db 321 SERIIELEUALIAIIEALALEUENIIELEUPHEULEUHALALEUALEUENTRP 340
| | | | |

Percent Similarity: 97.75% Conservative: 6
Best Local Similarity: 96.07% Mismatches: 8
Query Match: 70.59% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-1 (1-1414) x US-09-918-715-301 (1-562)

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128 CTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACTGTGGTCACTTCGCCGGGCGAA 187
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Db LeuGlyAlaGlyLeuAlaArgGlyLeuCyValAlaAlaLeuValLeuValCyAlaGlyHis 26

188 GGGGGACGACGAGGATGGGGGCTCCAGCCCTGACGGCGGATTTGACTGTACCTTCA 247
27 GlyGlyArgArgGlyLeuArgGlyGlyProAlaCyValGlyGlyPheAspLeuTyrPheIle 46

248 TTGGAAATTCAGGAGTGTGCGACCACTGGAAATGAAATGAAATTCCTTTGGACAG 307
47 LeuAspLysSerGlySerValLeuHisStrPaSngLilLetyTyrPheValGluGln 66

308 TTGGCTCACAATTCATCAGCCACAGTTGAGAATGCTCTTATGTTTTCACCCGA 367
67 LeuAlaHisArgPheIleSerProGlnLeuAlaArgMetSerPheIleValPheSerThrArg 86

368 GGAACAACCTTAATGAACCTGACAGACAGAGAAACAATCCGTCAAGGCTTAGAGAA 427
87 GlyThrThrLeuMetLysLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGluGln 106

428 CTCGCAAAAGTTTCTGACAGAGAGACACTTACATCAGAGATTTGAAAGGCGCAGT 487
107 LeuGlnLysValLeuProGlyGlyAspThrTyrMetHisGlnLysPheGlnArgAlaSer 126

488 GAGCAGATTATATGAAAAACAGACAAAGGATCAGGACAGCCAGCTCATCTTGCTTG 547
127 GluGlnIleLetyTyrGluAsnSerGlnGlyTyrArgThrAlaSerValIleIleAlaLeu 146

548 ACTGATGAGAACTCCATGAAGATCTCTTTTCTATTCAGAGGAGGCTAATAGTCT 607
147 ThrAspGlyGluLeuHisGlnAspLeuPhePheTyrSerGluArgLysAlaAsnArgSer 166

608 CGAGATCTTGGTGCATTTGTTTACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 667
167 ArgAspLeuGlyAlaIleValTyrCyValGlyValLysAspPheAsnGlnThrGlnLeu 186

668 GCCCGGATTCGCGACAGTAAGATCATGTGTTCCCGTGAATGACGGCTTCAGGCTGT 727
187 AlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAlaLeu 206

728 CAAGCATCATCTCAATTTGAAAGAGCTCTGCAATCGAAATTTAGACGCTGAACA 787
207 GlnGlyIleIleHisSerIleLeuLysLysSerCyAlaGlnIleLeuAlaIleGlnPro 226

788 TCACACATATGTCAGAGAGTCAATTTCAGTTGTGTGAGAGAAACGGCTCCGACAT 847
227 SerThrIleCyValAlaGlyLysSerPheGlnValValAlaArgLysAsnGlyPheAlaGlyHis 246

848 GCCCGCAACGTGACAGAGGCTCTCTGACGCTCAAGATCATGATCCTGCTCACACTCAAT 907
247 AlaArgAsnValAspArgValLeuCySerPheLysIleAsnAspSerValThrLeuAsn 266

908 GAGAACCCCTTTCTGTGAAAGACATTATTTACTGTGTCCAGCGCTATCTTAAAGAA 967
267 GluLysProPheAlaValGluAspThrTyrLeuLeuCySerProAlaProIleLeuLysGln 286

968 GTTGGCATGAACCTCCACCTCCAGGTGACAGATGAAGATGAGGCTCTTTTATCTCAAT 1027
287 ValGlyMetLysAlaAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIleSerSer 306

1028 TCTGTATCATCAACACACACTGTTTGAAGGTTTCACTCTGGCCATCGGCTGTG 1087
307 SerValIleIleThrThrThrHisCySerAspGlySerIleLeuAlaIleAlaLeuLeu 326

1088 ATCTGTCTCTGCTCTAGCCCTGAGCTCTCTGTGTGTTGTGGCCCTCTGCTGCACT 1147
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Db 327 ValLeuPheLeuLeuAlaLeuAlaLeuLeuTyrTrpPheTyrProLeuCySerThr 346
Qy 1148 GTGATTATCAAGAGATCCCTCCACCCCTGCGGACGAGAGTAGAGAA 1195
Db 347 ValIleIleLysGlnValProProProProValGlnLysSerGlnGln 362

RESULT 15

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US-10-474-794-194
; Sequence 194, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOMETRIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; PRIOR APPLICATION NUMBER: 2003-10-14
; PRIOR FILING DATE: 60/282,850
; PRIOR APPLICATION NUMBER: 2001-04-11
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 562
; SEQ ID NO 194
; TYPE: PRF
; ORGANISM: Mus musculus
US-10-474-794-194
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Alignment Scores:

Pred. No.: 4,05e-159 Length: 562
Score: 1793.00 Matches: 342
Percent Similarity: 97.75% Conservative: 6
Best Local Similarity: 96.07% Mismatches: 8
Query Match: 70.59% Indels: 0
DB: 4 Gaps: 0

US-09-970-076-1 (1-1414) x US-10-474-794-194 (1-562)

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128 CTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACTGTGGTCACTTCGCCGGGCGAA 187
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Db LeuGlyAlaGlyLeuAlaArgGlyLeuCyValAlaAlaLeuValLeuValCyAlaGlyHis 26

188 GGGGGACGACGAGGATGGGGGCTCCAGCCCTGACGGCGGATTTGACTGTACCTTCA 247
27 GlyGlyArgArgGlyLeuArgGlyGlyProAlaCyValGlyGlyPheAspLeuTyrPheIle 46

248 TTGGAAATTCAGGAGTGTGCGACCACTGGAAATGAAATGAAATTCCTTTGGACAG 307
47 LeuAspLysSerGlySerValLeuHisStrPaSngLilLetyTyrPheValGluGln 66

308 TTGGCTCACAATTCATCAGCCACAGTTGAGAATGCTCTTATGTTTTCCTCACCCGA 367
67 LeuAlaHisArgPheIleSerProGlnLeuAlaArgMetSerPheIleValPheSerThrArg 86

368 GGAACAACCTTAATGAACCTGACAGACAGAGAAACAATCCGTCAAGGCTTAGAGAA 427
87 GlyThrThrLeuMetLysLeuThrGluAspArgGluGlnIleArgGlnLysPheGlnArgAlaSer 126

428 CTCGCAAAAGTTTCTGACAGAGAGACACTTACATGATGAGATTTGAAAGGCGCAGT 487
107 LeuGlnLysValLeuProGlyGlyAspThrTyrMetHisGlnLysPheGlnArgAlaSer 126

488 GAGCAGATTATATGAAAAACAGACAAAGGATCAGGACAGCCAGCTCATCTTGCTTG 547
127 GluGlnIleLetyTyrGluAsnSerGlnGlyTyrArgThrAlaSerValIleIleAlaLeu 146

548 ACTGATGAGAACTCCATGAAGATCTCTTTTCTATTCAGAGGAGGCTAATAGTCT 607
147 ThrAspGlyGluLeuHisGlnAspLeuPhePheTyrSerGlnArgLysAlaAsnArgSer 166

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QY 608 CGAGATCTGTGCAATTTGTTTACTGTTGTTGTGAAAAGATTTCATGAGACACAGCTG 667
Db 167 ArgAspLeuGlyAlaIleValIyrCyValGlyValysAspPheAsnGluThrGlnLeu 186
QY 668 GCCCGGATTCGGGACAGTAAGATCATGTGTTTCCCGTAATGACGGCTTTCAAGCTCTG 727
Db 187 AlaArgIleAlaAspSerLysAspHisLeuAlaPheProValAsnAspGlyPheGlnAlaLeu 206
QY 728 CAAGGCATCATCCACTCAATTTTGAAGAAGTCTGCATCGAATTCGAATTCAGCAGTGAACCA 787
Db 207 GlnGlyIleIleHisSerIleLeuLysSerCyAlleGluIleLeuAlaIleGluPro 226
QY 788 TCACACCATATGTGAGAGAGAGTCAATTCAAGTTGTCGTGAGAGAAAGGCTTCGACAT 847
Db 227 SerThrIleCyAlaGlyGlnSerPheGlnValValArgGlyAsnGlyPheArgHis 246
QY 848 GCCCGCAACGTGACAGGGTCTCTGCAGCTTCAGATCAATGACTCGATCAGCTCAAT 907
Db 247 AlaArgAsnValAspArgValIleuCySerPheLysIleAsnAspSerValThrLeuAsn 266
QY 908 GAGAAAGCTTTTCTGTGAAAGACATTATTACTGTGTCCAGCGCTTATTTAAAGAA 967
Db 267 GluLysProPheAlaValGluAspThrTyrLeuLeuCyAspAlaProIleLeuLysGlu 286
QY 968 GTTGGCATGAAGCTGCACTCCAGGTGAGATGAAGATGAGGCTCTTTTATCTCAGT 1027
Db 287 ValGlyMetLysAlaAlaLeuGlnValSerMechAsnAspGlyLeuSerPheIleSerSer 306
QY 1028 TCTGTCAATCAACACACACACTGTTCTGACGGTTCATCTCGGCATCGCCCTGCTG 1087
Db 307 SerValIleIleThrThrThrHisCySerAspGlySerIleLeuAlaIleAlaLeuLeu 326
QY 1088 ATCCTGTTCTGCTCTAGCCCTGCTGCTCTCTGTGGTTCTGGCCCTCTGCTGCACT 1147
Db 327 ValLeuPheLeuLeuAlaLeuAlaLeuAlaLeuLeuTrpPheTrpProLeuCyCySerThr 346
QY 1148 GTGATTATCAAGAGAGTCCCTCCACCCCTGCGAGAGAGAGTGAAGAA 1195
Db 347 ValIleIleLysGluValProProProValGlnGlnSerGlnGlu 362
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Search completed: December 14, 2005, 12:54:52
Job time : 230.268 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: December 14, 2005, 11:59:39 ; Search time 7.30024 Seconds

(without alignments)
2608.649 Million cell updates/sec

Title: US-09-970-076-1

Perfect score: 2540
Sequence: 1 aggagccgcggaggaagggcc.....aaaaaaaaaaaaaaaa 1414

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Egapop 6.0 , Egapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 51441 seqs, 6734002 residues

Total number of hits satisfying chosen parameters: 102882

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xip
-Q=/cgn2_1/USPTO.spool.p/US09970076/runat.14122005.110512.26598/app.query.fasta_1.2894
-DB=Published Applications AA New -QFMT=fastean -SUFFIX=rapbn -MINMATCH=0.1
-LOOPEC=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdt -LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076 @CGN 1 1 1 @runat.14122005.110512.26598
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_AA_New:*

1: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1894	74.6	564	US-11-186-284-199	Sequence 199, App
2	145.5	5.7	1152	US-11-080-026-4	Sequence 4, Appl
3	134.5	5.3	3063	US-11-186-284-26	Sequence 26, Appl
4	126.5	5.0	739	US-11-057-047-2	Sequence 2, Appl
5	126.5	5.0	764	US-11-057-047-1	Sequence 1, Appl
6	126.5	5.0	798	US-10-821-234-1034	Sequence 1034, Ap
7	119.5	4.7	761	US-11-057-047-6	Sequence 6, Appl
8	113.5	4.5	915	US-10-131-826A-294	Sequence 294, Appl
9	113.5	4.5	956	US-11-113-424-39	Sequence 39, Appl
10	111	4.4	1141	US-10-601-368-24	Sequence 24, Appl

11	111	4.4	1166	US-10-601-368-22	Sequence 22, Appl
12	111	4.4	1188	US-10-601-368-21	Sequence 21, Appl
13	107	4.2	1141	US-10-601-368-6	Sequence 6, Appl
14	107	4.2	1166	US-10-601-368-4	Sequence 4, Appl
15	107	4.2	1188	US-10-601-368-3	Sequence 3, Appl
16	107	4.2	1188	US-11-000-463-338	Sequence 338, App
17	107	4.2	1188	US-11-000-463-810	Sequence 810, App
18	104.5	4.1	828	US-10-995-561-983	Sequence 983, App
19	104.5	4.1	918	US-10-995-561-982	Sequence 981, App
20	104.5	4.1	1019	US-10-995-561-982	Sequence 982, App
21	103.5	4.1	182	US-10-601-368-25	Sequence 25, Appl
22	100	3.9	678	US-11-102-240-34	Sequence 34, Appl
23	99.5	3.9	182	US-10-601-368-7	Sequence 7, Appl
24	97	3.8	384	US-10-510-385-158	Sequence 158, App
25	95.5	3.8	1179	US-11-097-125-1	Sequence 1, Appl
26	95.5	3.8	1196	US-10-995-561-921	Sequence 921, App
27	95	3.7	1167	US-11-097-125-2	Sequence 2, Appl
28	94.5	3.7	627	US-10-467-657-5432	Sequence 5432, Ap
29	94	3.7	353	US-11-137-465-44	Sequence 44, Appl
30	94	3.7	448	US-11-137-465-45	Sequence 45, Appl
31	93.5	3.7	619	US-10-999-886-3	Sequence 3, Appl
32	93.5	3.7	640	US-10-999-886-4	Sequence 4, Appl
33	91	3.6	184	US-10-467-657-5670	Sequence 5670, Ap
34	91	3.6	1167	US-10-601-368-18	Sequence 18, Appl
35	90.5	3.6	436	US-11-116-939-9	Sequence 9, Appl
36	88	3.5	1062	US-11-137-465-43	Sequence 43, Appl
37	87	3.4	1467	US-10-821-234-1688	Sequence 1688, Ap
38	85.5	3.4	1798	US-10-995-561-1033	Sequence 1033, Ap
39	85.5	3.4	1798	US-10-995-561-1034	Sequence 1034, Ap
40	85	3.3	494	US-10-467-657-592	Sequence 592, App
41	84.5	3.3	948	US-10-523-477-14	Sequence 14, Appl
42	83.5	3.3	495	US-10-770-726-81	Sequence 81, Appl
43	83.5	3.3	513	US-11-000-463-458	Sequence 458, App
44	83.5	3.3	730	US-11-082-389-358	Sequence 358, App
45	83	3.3	432	US-11-084-624-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-11-186-284-199
Sequence 199, Application US/11186284
Publication No. US2005026493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kametkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MP001-02922RM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 199
LENGTH: 564
TYPE: PRT
ORGANISM: Homo Sapiens
US-11-186-284-199

Alignment Scores:

Pred. No.: 1,24e-162 Length: 564
 Score: 1894.00 Matches: 364
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 74.57% Indels: 0
 DB: 7 Gaps: 0

US-09-970-076-1 (1-1414) x US-11-186-284-199 (1-564)

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QY 104 ATGGCCAGCGGCGAGAGCCCTCGGCATGCGCTTCCTGCTTGGCCACT 163
DB 1 MetAlaThrAlaGluArgAlaLeuGlyLeuGlyPheGlnTrpLeuSerLeuAlaThr 20
QY 164 CTGGGTCTATCTGGCGCGGCGAAAGGGGGCGAGGAGAGATGGGGGCTCAGCTTCAC 223
DB 21 LeuValLeuIleCysValaGlyGlnGlyArgGlnuSpGlyGlyProAlaCysTyr 40
QY 224 GCGGATTTGACCTGTACTTTCATTTTGGACAATTCAGAAATGCTGCGACCACTGGAAT 283
DB 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisTyrPhe 60
QY 284 GAAATCTATTACTTTGTGGAACGTTGGCTCACAAATTCATCAGCCCAAGTTGAGATG 343
DB 61 GluIleTyrTyrPheValaGluGlnLeuAlaHisLeuPheIleSerProGlnLeuArgMet 80
QY 344 TCGTTATTGTTTTCCTCCACCGGAGAACACCTTAATGAAATCTGACAGAACAGAGAA 403
DB 81 SerPheIleValaPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
QY 404 CAATCCGTCAAGGCTAGAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 463
DB 101 GlnIleArgGlnGlyLeuGlnGlyLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
QY 464 CATGAAGATTGAAAAGGCGCAGTGAAGCATTTATTATGAAAACAGACAGGGGTACAG 523
DB 121 HisGlnGlyPheGlnuArgAlaSerGlnGlnIleTyrTyrGluuAsnArgGlnGlyArg 140
QY 524 AACGCGAGGTCATCATTTGCTTGAAGTGAAGTCAATGAAATCTCTTTTCTAT 583
DB 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGluAspLeuPhePheTyr 160
QY 584 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTGCAATTGTTACTGTGTGTGTGTG 643
DB 161 SerGluArgGluuAlaAsnArgSerArgAspLeuGlyAlaIleValIleTyrCysValaGlyVal 180
QY 644 AAAGATTTCAATGAGACACAGCTGCGCCCGAGTTGCGAGACATGATGTTTCCC 703
DB 181 LysAspPheAsnGlnuThrGlnLeuAlaArgIleAlaAspSerLysAspHisValaPhePro 200
QY 704 GTGAATGAGGCTTGAAGCTCGAGGATCATCAATTTTGAAGAGCTCTCG 763
DB 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
QY 764 ATCGAATTTCTAGCAGCTGAACCATCCACATATGTGCAAGAGATCATTTCAAGTTGTC 823
DB 221 IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnValaI 240
QY 824 GTGAGAGAAAAGCGCTTCCGACATGCCCGCAAGTGAAGAGGCTCTGCGAGCTTCAAG 883
DB 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValaAspArgValaLeuCysSerPheLys 260
QY 884 ATCAATGATCGGCTCACTCATGAGAGAGCCCTTTTGTGGAAGACCTTATTATACG 943
DB 261 IleAsnAspSerValThrLeuAsnGlnLysProPheSerValGluuAspThrTyrLeuLeu 280
QY 944 TGTCCAGCGCTATCTTAAAGAGTGGCATGAAAGTGCATCCAGGTCAGCATGAAC 1003
DB 281 CysPheAlaProIleLeuLysGluValaGlyMetLysAlaAlaLeuGlnValaSerMetAsn 300
QY 1004 GATGGCTCTCTTTTATCTTCAAGTTGTGTCATATCAACACACACTGTTTGAAGGT 1063
  
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DB 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThrHisCysSerAspGly 320
QY 1064 TCCATCTGGGACCATGACCCCTGTGATCTGTTCTGCTGACCCCTGCTCTCTG 1123
DB 321 SerIleLeuAlaIleAlaLeuLeuIleuPheLeuLeuAlaLeuAlaLeuLeuTyr 340
QY 1124 TGGTTCTGGCCCTCTGTGTCATCTGATATCAAGAGAGTCCCTGCACCCCTGCGAG 1183
DB 341 TrpPheTrpProLeuCysCysThrValIleIleLysGluValaProProProAlaGlu 360
QY 1184 GAGAGTGAGGAA 1195
DB 361 GluSerGlnGlu 364
  
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RESULT 2

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US-11-080-026-4
/ Sequence 4, Application US/11080026
/ Publication No. US20050260192A1
/ GENERAL INFORMATION:
/ APPLICANT: Springer, Timothy A.
/ APPLICANT: Shimooka, Motomu
/ APPLICANT: Lu, Chafen
/ TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
/ FILE REFERENCE: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME
/ CURRENT FILING DATE: 2005-03-15
/ PRIOR FILING DATE: 2005-03-15
/ PRIOR APPLICATION NUMBER: 09/945,265
/ PRIOR FILING DATE: 2001-08-31
/ PRIOR APPLICATION NUMBER: US 60/229,700
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 1152
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-080-026-4
  
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Alignment Scores:

Pred. No.: 1.3e-05 Length: 1152
 Score: 145.50 Matches: 60
 Percent Similarity: 45.85% Conservative: 45
 Best Local Similarity: 26.20% Mismatches: 81
 Query Match: 5.73% Indels: 43
 DB: 7 Gaps: 12

US-09-970-076-1 (1-1414) x US-11-080-026-4 (1-1152)

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QY 233 GACCTGTACTTCTATTTGGACAATCAGAGAGTGTGCTG---CACCACTGAATGAATC 289
DB 150 AspIleAlaPheLeuIleAspGlySerGlySerIleIleProHisAspPheArgMet 169
QY 290 TATTACTTTGTGGAACAGTTGGCTCACAATTCATCAGCCACAGTTGGAATGTCTTT 349
DB 170 LysGluPheValaSerThr-----ValMetGluGlnLeuLysLysSerLys 184
QY 350 ATTTGTTTCTCACCCGAGAGAACCACTTATGAATACGACAGAGAC----- 397
DB 185 ThrLeuPheSer-----LeuMetGlnTyrSerGluGluPheArgIleHis 199
QY 398 -----AGAGAAACAATCCGTCAAGGCGCTAGAGAACTCCAG 433
DB 200 PheThrPheLysGluPheGlnAsnAsnProAsnProArgSerLeuValLysProIleThr 219
QY 434 AAAGTTCTGCCAGAGAGACACTTATGATGAAGATTGGAAGGCGCCAGTGACGAG 493
DB 220 GlnLeuLeu-----GlyArgThrHisTyrAlaThrGlnGlyIleArgLysValaValaArgGln 237
QY 494 ATTATTATGAAGAACAGACAGAGTACAGGAGC---AGGATCATCTGCTTGACT 550
DB 238 LeuPheAsnIleThrAsnGlyAlaArgLysAsnAlaPheLysIleLeuValaValIleThr 257
  
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QY 551 GATGAGAACTCCATGAGATCTTTTCTATTACAG-----AGGAGGCTAATAGG 604
DB 258 AaPGLyGLuPheGLyAaPProLeuGLyTfGLuAaPValLeProGLuAaPAG 277
QY 605 TCTCGAGATCTTGTCATTTGTTTCTGTGTGTGTGTAAGATTTCAATGAGACAG 664
DB 278 GLU-----GLyAlLeaGLyTfValLeGLyValGLyAaPLeaPAGsSerGLu 294
QY 665 CTGGCCCGG-----ATTGGGACAGT-----AAGATCATGTGTTTCCC 703
DB 295 LysSerArgGLuGLuLeuAaPnThrLeaLaserLysProPArgAaPnHsValPheGLn 314
QY 704 GTGAATGACGGCTTTCAGGCTCGACAGCATCATCCATCTTTTGAAGAGTCTCTGC 763
DB 315 ValAaPnAaPn---PheGLuAaLeuLysThrLeGLnAaPnGLuAaPnGLuLys----- 331
QY 764 ATCGAATTTCTACAGCTGTAACCATCCATATGTGTCAGAGAGTCAATTTCAAGTTGTC 823
DB 332 -----LlePheAlLeGLuGLuThnGLnThnGLySerSerSerPheGLuHsGLu 349
QY 824 GTGAGAGAAACGGCTTCCGACATGCC 850
DB 350 MetSerGLnGLuGLyPheSerAlaAla 358

RESULT 3
US-11-186-284-26
; Sequence 26, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamakkar, Shubhangl
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186, 284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301, 822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339, 971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361, 978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381, 988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 3063
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-26

Alignment Scores:
Pred. No.: 0.000164 Length: 3063
Score: 134.50 Matches: 81
Percent Similarity: 43.10% Conservative: 44
Best Local Similarity: 27.93% Mismatches: 123
Query Match: 5.30% Indels: 42
DB: 7 Gaps: 17

US-09-970-076-1 (1-1114) x US-11-186-284-26 (1-3063)
QY 233 GACCTGTAATTCATTTTGAACAAATGAGAGTGTG---CTGACCACTGGAATGAATC 289
DB 440 AaPLeaValPheLeuValAaPGLySerLysSerLysLeGLyLeaAaPnHsValLysVal 459

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QY 290 TATTACTTTGTGAACAGTTGGCTCCAAATTC---ATCAGGCCA---CAGTTGAGATG 343
DB 460 ArgAlaPheLeuGLuValLeuValLysSerPheGLuLeSerProAaPnArgValGLnLe 479
QY 344 TCTTTATTTGTTTCTCCACC-----CGAGAACAACTTAAATGAATGACAGAA 394
DB 480 SerLeuValGLnLysSerArgAaPProHsThnGLuPheThrLeuLysPheThrLys 499
QY 395 GACAGAGAAACAAATCCGTCAAGCCCTAGAAAGTCCAGAAAGTTCTGCA-----GGA 448
DB 500 ValGLuAaPnLeLe-----GluAlLeaAaPnThrPheProLysArgGLy 514
QY 449 GGAGACACTTACATGCATGAGAGATTTGAAGGGCCAGACAGATTTATTATTAAGAAAC 508
DB 515 GLySerThraAaPnThrGLyAaPnLamethrLysValArgGLuLysLlePheValProSer 534
QY 509 AGACAAAGGTACAGACA-----GCCAGCTCATCATTTGCTTGAAGTGAAGAACTC 562
DB 535 Lys---GLySerArgSerAaPnValProLysValMetLeuLeuLysPheArgGLyLys--- 552
QY 563 CATGAAGATCTCTTTTCTATTACAGAGAGGAGGCTAATAGGCTCGAGATCTTGCA 622
DB 553 SerSerAaPnAlaPhe-----ArgAaPProAlaLleLysLeuArgAaPnSerAaPnVal 569
QY 623 ATTGTTACTGTGTGTGTAAGATTTCAATGAGACACAGCTGCCCGATGCGGAC 682
DB 570 GLuLlePheAlaValGLyValLysAaPnAlaValArgSerGLuLeuGLnAlaLeaLaser 589
QY 683 -----AGTAAGATCATGTGTTTCCGTAATGACGGCTTTCAGGCTTGCAGAGCATC 736
DB 590 ProProAlaGLuThrHsValPheThrValGLuAaP---PheAaPnAlaPheGLnArgLys 608
QY 737 ATCCATCAATTTTGAAGAGTCTGCATCGAAATTCGACGCTAACCATCCACATCA 796
DB 609 SerPheGLuLeuThrxInserLleCysLeuArgLys-----GLuGLnGLuLeuAla 625
QY 797 TGTGACAGAGATCATTTCAAGTTGTCGTGAGAGAAACGGCTTCCGACATGCCCCCAAC 856
DB 626 AlaLleLysLysValaLysValPProProLysAaPLeuSerPheSerGLuValThrSer 645
QY 857 GTGACAGAGGTCCTGTCAGCTTCAAGATCAATGACTCGTCACTCAATGAGAAAGCC 916
DB 646 Tyr-----GLyPheLysThraAaPnLysSer---ProAlaGLyGLuAaPnVal 659
QY 917 TTTTCTGTGGAAGACATTTACTGTGTCCAGCCCATATCTTAAAGAGTTGCGAG 976
DB 660 PheSerLysHsLleThrLys-----LysGLuAlaAlaGLy 671
QY 977 AAGCTGACCTCCAGGTGACATGAGATGAGTGGCTCTTTTATCTCAAGTTCTGTATC 1036
DB 672 AaPnAaPnValaThrVal---ValGLuPro-AlaAaPnThrSerThrSerValaLysLeuSer 690
QY 1037 ATCCACCAACACACATGTTCTGACGGTT 1064
DB 690 LysLysProGLuThrLeuLysLeuVal 699

RESULT 4
US-11-057-047-2
; Sequence 2, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilleson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057, 047
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543, 594
; PRIOR FILING DATE: 2004-02-10

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; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; PRIOR FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 739
; TYPE: PR
; ORGANISM: Homo sapiens
US-11-057-047-2

Alignment Scores:
Pred. No.: 0.000586 Length: 739
Score: 126.50 Matches: 74
Percent Similarity: 37.99% Conservative: 70
Best Local Similarity: 19.53% Mismatches: 128
Query Match: 4.98% Indels: 107
DB: 7 Gaps: 19

US-09-970-076-1 (1-1414) x US-11-057-047-2 (1-739)
QY 59 GGAGCGTGGGAAGAGCGGACCGCTCTCCCGGCGTCCGCGCCATGGCCACGCGCGAG 118
DB 184 GlyserrtrpserglythrcluproserCysglnasrserPheMetTyrAspThrProgin 203
QY 119 CGAGAGCCCTCGCGCTCCAGTGCCTCTTTGGCCCTCTGGTGCATCTGC 178
DB 204 Glu-----ValalaglualapheleuserSerleuthrcluthrile----- 217
QY 179 GCCGGCAAGGGGAGCGACGAGAGATGGG--GGTCCAGCC----- 217
DB 218 -----GluGlyValalapralaglualaprglyhaglYProGlyGluInglInlysarGly 235
QY 218 -----TGCTACGGCGGATTTGACCTGTACTTATTGTCACAAATCAGAACT 265
DB 236 lvalleuaprpserglyserMetasnilletYrleuValleuaprglyserAspSer 255
QY 266 GTG-----CTGCACCACTGGAATGAATCATATTGTTGNGAACAGTTG 310
DB 256 lleglylaserasrphenethrclYalalyblyCyaleuValasleuileglulysval 275
QY 311 GGTCAAAATTCATCAGCCCACTGAGAAATGCTTTATGTTTCTCCACCCGAGGA 370
DB 276 AlaserTyrGlyVallyserPro-----ArgTyrGlyleuValThrYrnlathrTyrPro 293
QY 371 ACAACCTTATGAAATCTGACAGAA-----GACAGAGAACAAATCCGTCAAGCC 418
DB 294 lylsetrpVallyserglualasrserSerAsnAlasprValThrlysgln 313
QY 419 CTAGAAAGAACTC-----CAGAAAGTTCTGCGCAGAGGAGACACTTACATGCAT 466
DB 314 leuasnGluilleentYrclupserhlyblyleuYrserGlyThrAsnThr----- 330
QY 467 GAAGATTGAAAGGCGCAGTGCAGAGATTATTATGAAACAGA----- 511
DB 331 -----lyelYalaleuGlnalValYrSerMetMetesertrProaspaVal 347
QY 512 -----CAAGGGTAC--AGGAGCCGACGCTCATCTTGTGCTGATGGA----- 556
DB 348 ProProGluGlyThrpanhrgthrArgHlsvalilleleuMetthrAspGlyLeuHls 367
QY 557 -----GAACTCATGAGATCTCTTTTCTAT 583
DB 368 AsnMetGlyGlyAspProlethrValilleasprGluilleargAspleuleuTyrillegly 387
QY 584 TCAGAGAGGAGGCTTAATAGTCTTCAGATCTTGTGCAATGTTTACTGTGTGCT--- 640
DB 388 lYsAspArglyAsnProArgrglualasrYrleuAspValYrValbheglyValglYPro 407
QY 641 ---GTGAAAGATTTCATGAGACACAGCTGGCCCGGATGGCGACAGTAAAGTCAATG 697
DB 408 leuValasnGlnValasnilleasnAlaleuAlaserlyblyAspAsnGluInhlsVal 427
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QY 698 TTTCCTGGAATGACGGCTTTCAGCGCTGTGCAAGCATCATCTCAATTTTGAAGAAG 757
DB 428 PheIysValYAsp---MetGluasleuGluuAspValPheTyrGlnMetIleAspGlu 446
QY 758 TCTTCATCGAATTTCTAGACGCTGACACCATCCATATGTGTGACAGAGATTCATCA 817
DB 447 Ser-----GlnserLeuSerLeuCyS----- 453
QY 818 GTTTCGTGAGAGAAACGGCTTCGACATGCGCCGCAACGTGACAGAGGCTCTTCAGC 877
DB 454 -----GlyMetValYrpluhlsarGlybGlyThrAsp----- 464
QY 878 TTCAGATCATATGATCTCGTTCACACTCATGAGAACCCCTTTTGTGGAACAATTAT 937
DB 465 -----TyrhlsyGlnProtrpGlnAlalysIleSerVal 476
QY 938 TTACTGTGCCAGCCCTATCTTAAAGAAAGTTGACATGAAGAGTGCACCTCGACGTCAC 997
DB 477 -----lleargProserlybGlyhIagIuserCysewctgly----- 488
QY 998 ATGAACGATGGCTCTTTTATCTCCAGTTCTGTCATCATGACACACACAGCTGT 1054
DB 489 -----AlaValaserGlyYrPheValleuthrAlalahlscys 502

RESULT 5
US-11-057-047-1
; Sequence 1, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilkeson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057,047
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; PRIOR FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 764
; TYPE: PR
; ORGANISM: Homo sapiens
US-11-057-047-1

Alignment Scores:
Pred. No.: 0.000591 Length: 764
Score: 126.50 Matches: 74
Percent Similarity: 37.99% Conservative: 70
Best Local Similarity: 19.53% Mismatches: 128
Query Match: 4.98% Indels: 107
DB: 7 Gaps: 19

US-09-970-076-1 (1-1414) x US-11-057-047-1 (1-764)
QY 59 GGAGCGTGGGAAGAGCGGACCGCTCTCCCGGCGTCCGCGCCATGGCCACGCGCGAG 118
DB 209 GlyserrtrpserglythrcluproserCysglnasrserPheMetTyrAspThrProgin 228
QY 119 CGAGAGCCCTCGGATCGGCTTCCAGTGCCTCTTTGGCCACTGTGCTGCATCTGC 178
DB 229 Glu-----ValalaglualapheleuserSerleuthrcluthrile----- 242
QY 179 GCCGGCAAGGGGAGCGACGAGAGATGGG--GGTCCAGCC----- 217
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Db 447 LyAspArgLyAsnProArgLysLeuAspTyrLeuAspValTyrValPheGlyValGlyPro 466
QY 641 ---GTGAAGATTTCATGAGACACAGCTGGCCGGATTGGACATGAAGATCATGTG 697
Db 467 LeuValAsnGlnValAsnIleAsnIleAsnIleSerLeuValAspAsnGlnIleVal 486
QY 698 TTTCCCGTGAATGACGGCTTTTCAGGCTTCGACAGGATCATCAATTTTGAAGAAG 757
Db 487 PheLysValLysAsp---MetGlnAsnLeuGlnAspValPheTyrGlnMetIleAspGln 505
QY 758 TCTCGATCGAAATTTACAGCTGAACCATCCACATATGTGACAGAAAGTCATTCA 817
Db 506 Ser-----GlnSerLeuSerLeuGln----- 512
QY 818 GTTGTGAGAGAAACGGCTTCGACATGCCCGGACGATGACAGGATCTTCGACG 877
Db 513 -----GlyMetValTyrGlnIleArgLysGlyThrAsp----- 523
QY 878 TTCAGATCATGACTCGGTCACTCACTAGAACCCCTTTCTGTGAGACACTTAT 937
Db 524 -----TyrHisLysGlnProTyrGlnIleValIleSerVal 535
QY 938 TTAAGTGTCCAGCCCTTCTTAAAGAACTTGACATAAGCTGCACTCCAGCTCAGC 997
Db 536 -----IleArgProSerLysGlyHisGlnSerCysMetGly----- 547
QY 998 ATGAACGATGCGCTCTTTTATCTCCAGTTCTGTGATCATCAACACACACTGT 1054
Db 548 -----AlaValValSerGlyTyrPheValLeuThrAlaHisCys 561

RESULT 7
US-11-057-047-6
Sequence 6, Application US/11057047
Publication No. US20050260198A1
GENERAL INFORMATION:
APPLICANT: Hoiers, Vernon
APPLICANT: Thurman, Joshua
APPLICANT: Taube, Christian
APPLICANT: Gelfand, Erwin
APPLICANT: Gilkeson, Gary
TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
TITLE OF INVENTION: Methods Related Thereto
FILE REFERENCE: 2848-66
CURRENT APPLICATION NUMBER: US/11/057,047
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,594
PRIOR FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: 60/636,239
PRIOR FILING DATE: 2004-12-14
PRIOR APPLICATION NUMBER: US04/015040
PRIOR FILING DATE: 2004-05-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6
LENGTH: 761
TYPE: PRT
ORGANISM: Mus musculus
US-11-057-047-6

Alignment Scores:
Pred. No.: 0.00251 Length: 761
Score: 119.50 Matches: 78
Percent Similarity: 37.37% Conservative: 67
Best Local Similarity: 20.10% Mismatches: 118
Query Match: 4.70% Indels: 125
DB: 7 Gaps: 22

US-09-970-076-1 (1-1414) x US-11-057-047-6 (1-761)

QY 59 GGAGCTGGGAGAGAGACGACCTGCTCCCGGGGCTGGGGCCATGACAGGGGAG 118
Db 206 GlySerTyrSerGlyThrGlnProSerCysGlnAspSerPheMetTyrAspSerProGln 225

QY 119 CGAGAGCCCTCGGACCTGCTCCAGTGGCTCTCTTTGGCCACTCTGGTCTCATCTGC 178
Db 226 Gln-----ValAlaGlnAlaPheLeuSerSerLeuThrGlnThrIle----- 239
QY 179 GCCGGGCAAGGGGACGACGAGAGATGGG----- 208
Db 240 -----GlnGlyAlaAspAlaGlnAspGlyHisSerProGlyGlnGlnIleLysArgLys 257
QY 209 -----GGTCCAGCTGCTACCGGAGATTGACCTGTACTTCAATTTTGAACAATCA 259
Db 258 IleValIleAspProSer-----GlySerMetAsnIleTyrLeuValLeuAspGlySer 275
QY 260 GGAAGCTG-----CTGCACCACTGGAATGAA 286
Db 276 AspSerIleGlySerSerAsnPheThrGlyAlaLysArgCysLeuThrAsn----- 292
QY 287 ATCTTACTTGTGTGGAACAGTTGGCTCACAATTCATCAGCCCACTGAGAAATGTC 346
Db 293 -----LeuIleGlnValValAlaSerTyrGlyValArgPro-----ArgTyrGly 307
QY 347 TTTATGTTTCTCCACCGAGAACCAACTTAATGAACATGACAGAAAGACAGA----- 400
Db 308 LeuLeuThrTyrAlaThrValProLysValLeuValArgValSerAspGlnArgSerSer 327
QY 401 -----GAACAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTG 442
Db 328 AspAlaAspTyrValThrGlnLysLeuAsnGlnIleSerTyrGlnAspHisLysLeuLys 347
QY 443 CGAGAGGAGACACTTACATGATGAGATTGAAAGGCCAGTGACAGATTTATTTAT 502
Db 348 SerGlyThrAsnThr-----LysArgAlaLeuGlnAlaValTyrSer 361
QY 503 -----GAAACAGACAGAGGTAC---AGCACCCAGCGCTATC 538
Db 362 MetMetSerTyrAlaGlyAspAlaProProGlnGlyTyrPheAsnArgThrArgHisValIle 381
QY 539 ATGTCTTGACTGATGAGAACTCCAT-----GAA 568
Db 382 IleIleMetThrAspGly---LeuHisAsnMetGlyGlyAsnProValThrValIleGln 400
QY 569 GATCTCTTTTCTATTTCAGAG-----AGGAGGCTAATAGCTTCGAAAT-----CTT 616
Db 401 AspIleArgAlaLeuLeuAspIleGlyArgAspProLysAsnProArgGlnAspTyrLeu 420
QY 617 GGTGCAATGTTTACTGTGTGTG-----GTGAAGATTTCATGAGACAGCTGGCC 670
Db 421 AspValTyrValPheGlyValGlyProLeuValAspSerValAsnIleAsnIleAla 440
QY 671 CGAATTCGAGACGATGAGATCATGTGTTCCGTGAATGACGCGCTTCAGGCTTGCA 730
Db 441 SerLysLysAspAsnGlnHisHisValPheLysValLysAsp---MetGlnAspLeuGln 459
QY 731 GGCATCATCACTCAATTTTGAAGAGTCTGCATCGAAATTTACAGCTGAACCATCC 790
Db 460 AsnValPheTyrGlnMetIleAspGlnThr-----LysSerLeu 472
QY 791 ACCAATGTGACAGAGATCATTTCAAGTTGCTGAGAGAAACGGCTTCGACATGCC 850
Db 473 SerLeuGln-----GlyMetValTyrGlnHisLys 482
QY 851 CGCAACGTGAGACAGGCTCTGACGCTTCAGATCATGATGATCGGTCACTCAATGAG 910
Db 483 LysGlyAsnAspTyrHisLysGlnProTyrGlnAlaLysIleSerValIle----- 499
QY 911 AAGCCCTTTTCTGTGGAACACTTATTTACTGTGTCCAGCCGCTTCTTAAAGAAAGTT 970
Db 500 ArgProLeuLysGlyHisGlnThr-----CysMetGlyAlaVal----- 512
QY 971 GGCAGAAAGCTGCACTCAGGTCAAGATGAAGATGAGCTCTTTTATCTCCAGTTCT 1030
Db 513 -----ValSerGlyTyr 516
QY 1031 GTCATCATCAACACACACACTGT 1054

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Db          517 PheValLeuThrAlaAlaHisCys 524
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RESULT 8
US-10-131-826A-294
Sequence 294, Application US/10131826A
Publication No. US20050245730A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroli, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Aneelin J.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Macanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zhenli
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131, 826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 294
LENGTH: 915
TYPE: PRT
ORGANISM: Homo Sapien
US-10-131-826A-294
Alignment Scores:
Pred. No.: 0.00911 Length: 915
Score: 113.50 Matches: 55
Percent Similarity: 43.90% Conservative: 53
Best Local Similarity: 22.36% Mismatches: 103
Query Match: 4.47% Indels: 35
DB: Gaps: 13
US-09-970-076-1 (1-1414) x US-10-131-826A-294 (1-915)
Oy          233 GACCTGTACTTCTTTTGGACAAATCAGAAAGTGTG--CTGCACACCTGAAATGAAATC 289
Db          57 AepLeuValPheIleIleAepSerArgSerValanhthrHisAepTyrAlaIyVal 76
Oy          290 TATTACTTT--CTGAAACAGTTGGCTCACAAATTCATCAGCCACAGTTG--AGATG 343

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Db 77 LysGluPheIleValAspIleLeuGlnPheLeuAspIleGlyProAspValThrArgVal 96
Qy 344 TCCTTATGTTTTCCTCCACCCGAGAACACTTA-----ATGAACTG 388
Db 97 GlyLeuLeuGlnThr-----GlySerThrValLysAsnGluPheSerLeuLysThr 113
Qy 389 ACAGAAGACAGAGAACAAATCCGTCAGAGCCTAGAGAACCTCCAGAAAGTTCTGCCAGGA 448
Db 114 PheLysArgLysSerGluValGlnLysArgLysValLysArgMetArgHisLeuSerThrGly 133
Qy 449 GGAACACATTACATGCATGAAGATTGTGAAGGGCCAGTCGACGATTATTAATGAAAC 508
Db 134 ThrMetThrGlyLeuValIleGlnThr-----AlaLeuAsnIleAlaPheSerGlu 150
Qy 509 AGACAGAGGTACACG-----ACAGCCAGACCTCATCATGCTTTGACTCAT 553
Db 151 AlasGlnGlyAlaArgProLeuArgLysGlnAsnValProArgValIleMetIleValThrAsp 170
Qy 554 GGAACATCCATGACAGATCTCTTTTCTATTCCAGAGAGGAGCTTAATAGCTCTCGAT 613
Db 171 GlyArgProGlnAspSerVal-----AlaGluValAlaAlaLysAlaArgAsp 186
Qy 614 CTGGTGCATATGTTTACTGTCTGTGTGTG-----AAAGATTCAATGAGACACACTG 666
Db 187 ThrGlyIleLeuLeuPheAlaIleGlyValGlyGlnValAspPheAsnThrLeuLysSer 206
Qy 668 GCCCGAGTTGCCGACAGTAGATCATGTGTTTCCCGTAATGACGCGCTTTCAGGCTCTG 727
Db 207 IleGlySerGluProHisGluAspHisValPheLeuValAlaAsn---PheSerGlnIle 225
Qy 728 CAAGGATCATCCACTCAATTTTGAAGAAGTCCTGCATCGAATTTAGACGCTGAACCA 787
Db 226 GluThrIleThrSerValPheGlnLysLysLeuCyThrAlaHisMetCysSerThrLeu 245
Qy 788 TCACCATATGTGCAGAGAGTCATTTCACGTGTCGAGAGAGAAACGCTTCCGACAT 847
Db 246 GluHisAsnCysAla-----HisPheCysIleAsnIleProGlySerTyrValCysArg 263
Qy 848 GCCCGC-----AACGTGACAGAGGTCCTCTGACGCTTCACATCAATCAATGAC 892
Db 264 CysIleAsnGlnLysTyrIleLeuAsnSerAspGlnThrThrCys-----ArgIleGlnAsp 287
Qy 893 TCGGTCACTCAATGAG 910
Db 282 LeuCysAlaMetCgluAsp 287

RESULT 9
US-11-113-424-39
/ Sequence 39, Application US/11113424
/ Publication No. US20050260713A1
GENERAL INFORMATION:
APPLICANT: Gangoli et al.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-225
CURRENT APPLICATION NUMBER: US/11/113,424
CURRENT FILING DATE: 2005-04-21
PRIOR APPLICATION NUMBER: 60/256,704
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/311,590
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/257,314
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/311,613
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/315,617
PRIOR FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: 60/307,506
PRIOR FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: 60/322,358
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/294,075
PRIOR FILING DATE: 2001-05-29

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/ PRIOR APPLICATION NUMBER: 60/288,153
/ PRIOR FILING DATE: 2001-05-02
/ NUMBER OF SEQ ID NOS: 190
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 39
/ LENGTH: 956
/ TYPE: PR
/ ORGANISM: Homo sapiens
US-11-113-424-39

Alignment Scores:
Pred. No.: 0.00922 Length: 956
Score: 113.50 Matches: 55
Percent Similarity: 43.90% Conservative: 53
Best Local Similarity: 22.36% Mismatches: 103
Query Match: 4.47% Indels: 35
DB: Gaps: 13

US-09-970-076-1 (1-1414) x US-11-113-424-39 (1-956)
QY 233 GACCTGACTTCAATTTGGCAAAATCGGAAAGTGTG---CTGCAACGCTGAATGAATC 289
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 57 AepLervaiPheIleIeasPserAgservAlasnthriIsapTyralalysval 76
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 290 TATTACTTT---GTGGAACAGTTGGCTCAAAATTCATCAGCCCAAGTTG--AGAAAG 343
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 77 LysGIuPheIleValapIleleuGIInPheIeupApIleGIyProapvalThraGval 96
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 344 TCCTTATTGTTTCTCCACCCGGAACAACCTTA-----ATGAAACTG 388
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 97 GIuLeuGIInTy-----GIyserThvalIyIsangIuPheIeulysrThr 113
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 389 ACGAAGACGAGACAAATCCGTCAAGGCTGAAGAACTCCAGAAAGTTCGCCAGGA 448
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 114 PheIyArGIyserGIuValGIuArGIalavalIyArGweArGIshIeuserThrGIy 133
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 449 GGAGACACTTACATGATGATGAGATTTGAAAGGCCAGTACAGATTTATTAAGAAAC 508
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 134 ThmetThreGIyLeuAlaIleGIInTy-----AlaIeuanIleAlaPheIserGIu 150
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 509 AGACAAAGGTAACG-----ACAGCCAGCTCATCTATGCTTTGACTGAT 553
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 151 AlaGIuGIyAlaArProIeuaArGIuAsnvalProArGIvalIleuGIeIvalThraP 170
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 554 GGAGAACTCCATGAAGATCTTTTCTATTACAGAGGAGGCTAATAGGTCTCGAGAT 613
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 171 GIuArProGIInAsPserval-----AlaGIuValAlaIalylvalAlaArGAp 186
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 614 CTGAGTGAATTTGTTACTGTGTGTGTG-----AAAGATTTCAATGACACAGCTG 667
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 187 ThreGIyIleuIlePheAlaIleGIyValGIyGIInvalAsPheAsnthriIeulysser 206
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 668 GCCCGAATTCGGACAGTAAGATCATGTGTTCCTGCAATGACGGCTTTCAGGCTCTG 727
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 207 IleGIyserGIuProIIsGIuAsPheIAsnvalPheIeulvalAlaAsn--PheIserGIInIle 225
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 728 CAAGGATGATCACTCAATTTTGAAGAACTCGATCGAATGCAATTCGACAGTGAACA 787
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 226 GIInThIeulThIservalPheGIInIyIyIeulCyserThralaniIshetCysserThIeul 245
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 788 TCCACCATATGTCAGAGAGAGATTTCAAGTTGTCTGAGAGAAACGGCTTCCGACAT 847
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 246 GIInIAsnIAsnval-----HisPheCyIleAsnIleProGIyserTyIvalCyAsnG 263
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 848 GCCCGC-----AACGTGACAGAGGCTCTGCAAGCTTCAAGATCAATGAC 892
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 264 CyuIyGIInGIyTyIleIeulAsnserAsPGIInThrIeulCyAsn--ArgIleGIInAsP 281
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 893 TCGGTCACTCAATGAG 910
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 282 LeuCyAlaIeulGIuAsP 287
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT 10
```

```
US-10-601-368-24
/ Sequence 24, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 24
/ LENGTH: 1141
/ TYPE: PR
/ ORGANISM: Mus musculus
US-10-601-368-24

Alignment Scores:
Pred. No.: 0.0162 Length: 1141
Score: 111.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 4.37% Indels: 38
DB: Gaps: 9

US-09-970-076-1 (1-1414) x US-10-601-368-24 (1-1141)
QY 218 TCGTACGGGGATTGACCTGTACTTTCATTTGCAAAATCAGAAAGTGTGTCACAC 277
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 159 CysGIInThrTyMeAsPleIvalIleValIeulAsPGIyserAsnserIle---IyrPro 177
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 278 TCGAATGAATATTACTTTGTGGAACAGTTGGCTCACAATTC--ATCAGCCCA--- 331
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 178 TrpvalGIuValGIInIlePheIeulIeAsnIleIeulYelYerPheTyIleGIyProGIy 197
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 332 CAGTTGAGAAATGCTTTATTTGTTTCTCCACCCGAGAAACAACCTTAATGAACAGACA 391
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 198 GIInIleGIInvalGIyIlevalGIInTyGIyGIuAsPvalAlaIshetIleGIInArGIy 216
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 392 GAAGACAGACAAATCCGTCAAGGCTGAAGAACTCCAGAAAGTTCGCCAGGAGGA 451
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 217 AsnArTyArGIservalIyAsPvalvalGIuAlaIAserIleIleGIInArGIy 236
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 452 GACACTTACATGATGAAAGATTTGAA-----AGGCGCAGTGAAGATTTATAT 502
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 237 GIyThrGIInThArGIThralPheGIyIleGIInPheAlaArGserGIuIalPheGIInIys 256
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 503 GAAACAGACAAAGGTAACAGACAGACAGCGCTCATGTTGCTTGAATGAGAAATC 562
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 257 GIyGIuArGIyGIyGIyAlaIys-----IyvalIeulIeAlaIleThraPGIyGIuser 274
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 563 CATGAAGAT----- 571
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 275 HisAsPserProAsPleuGIuIyvalIleArGIInserGIuIyAsPvalIThraG 294
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 572 -----CTTTTCTTATTCAGAGAGGAGGCTAATGAGTCTCGAATCTT 616
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 295 TyralavalAlavalIeulGIyTyIleAsnArGArGIyIleAsnProGIuThrPheIu 314
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 617 GGTGCAATTTTACTGTGTGTGTGTAAGAT-----TTCAATGACACAG 664
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 315 AsnGIuIleIyTyIleAlaIserArProArAsPvalIyHisPheIeAsnvalIThraP 334
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 665 CTTGCCCGGATTCGGACAGTAAGATCATGTGTTCCTGCAATGACGGCTTTCAGGCT 724
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 335 GIuAlaIaleu-----IyAsPleIlevalIeArIaleuGIyAsPArGIlePheIser 351
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 725 CTGCAAGGC 733
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Db 352 LeuGluGly 354

RESULT 11
US-10-601-368-22
Sequence 22, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:

APPLICANT: Pan, Yang
APPLICANT: Lore, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
CURRENT APPLICATION NUMBER: US/10/601,368
CURRENT FILING DATE: 2003-06-23
PRIORITY FILING DATE: 2000-04-27
PRIORITY FILING DATE: 1999-05-28
PRIORITY FILING DATE: 1999-05-28
NUMBER OF SEQ. ID NOS: 40
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 22
LENGTH: 1166
TYPE: PRT
ORGANISM: Mus musculus
US-10-601-368-22

Alignment Scores:
Pred. No.: 0.0163 Length: 1166
Score: 111.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 4.37% Indels: 38
DB: 6 Gaps: 9

US-09-970-076-1 (1-1414) x US-10-601-368-22 (1-1166)

QY 218 TGCTACGGCGGATTTGACCTGCTACTTTCATTTTGACAAATCAGAGAGTGTGTCACACC 277
DB 137 CygelnThrTyrcetAspIleValIleValIleuAspGlySerAsnSerIle---TyrPro 155
QY 278 TGGAAATGAATCTATTACTTTGTGGAACAGTTGGCTCACAATTC---ATCAGCCCA--- 331
DB 156 TrpValGluValGlnHisPheLeuIleAsnIleLeuLysPheTyrIleGlyProGly 175
QY 332 CAGTTGAGAAATGTCCTTATTGTTTCTCCACCCGAGAAACAACCTTAATGAATGACA 391
DB 176 GlnIleGlnValGlyIleValGlnTyrGlyGluAspAlaValHisGluPheHisLeu--- 194
QY 392 GAAGACAGAGAACAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTCTGCCAGAGA 451
DB 195 AsnAspTyrArgSerValLysAspValValGluAlaAlaSerHisIleGluGlnArgGly 214
QY 452 GACACTTACATGCATGAGAGATTGAA-----AGGCGCAGTGACAGATTATTAT 502
DB 215 GlyThrGluThrArgHisAlaPheGlyIleGluPheAlaArgSerGluAlaPheGlnLys 234
QY 503 GAAAAACAGACAGAGGTACAGACAGCCGTCATCATCTGTTGACTGATGAGAACTC 562
DB 235 GlyGlyArgGlyGlyAlaLys-----LysValMetIleValIleThrAspGlyGluSer 252
QY 563 CATGAAGAT----- 571
DB 253 HisAspSerProAspLeuGluLysValIleArgGlnSerGluLysAspAsnValThrArg 272
QY 572 -----CTCTTTTCTATTACAGAGGAGGCTAATAGTCTCGAGATCTT 616
DB 273 TyrAlaValAlaValIleuGlyTyrTyrAsnArgArgGlyIleAsnProGluThrPheLeu 292
QY 617 GGTGCAATTGTTTACTGTGTGTGTGTAAGAT-----TTCATGACACACAG 664
DB 293 AsnGluIleuTyrIleAlaSerAspProAspAspLysHisPheAsnValThrAsp 312
QY 665 CTGCGCCGGATTTGGGACAGTAAGATCATGTGTTCCCGTAATGACGCGTTTCAAGCT 724

Db 313 GluAlaAlaLeu-----LysAspIleValAlaAspAlaLeuGlyAspArgIlePheSer 329

QY 725 CTGCAAGGC 733
DB 330 LeuGluGly 332

RESULT 12
US-10-601-368-21
Sequence 21, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:

APPLICANT: Pan, Yang
APPLICANT: Lore, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
CURRENT APPLICATION NUMBER: US/10/601,368
CURRENT FILING DATE: 2003-06-23
PRIORITY FILING DATE: 2000-04-27
PRIORITY FILING DATE: 1999-05-28
PRIORITY FILING DATE: 1999-05-28
NUMBER OF SEQ. ID NOS: 40
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 1188
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(22)
US-10-601-368-21

Alignment Scores:
Pred. No.: 0.0164 Length: 1188
Score: 111.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 4.37% Indels: 38
DB: 6 Gaps: 9

US-09-970-076-1 (1-1414) x US-10-601-368-21 (1-1188)

QY 218 TGCTACGGCGGATTTGACCTGCTACTTTCATTTTGACAAATCAGAGAGTGTGTCACACC 277
DB 159 CygelnThrTyrcetAspIleValIleValIleuAspGlySerAsnSerIle---TyrPro 177
QY 278 TGGAAATGAATCTATTACTTTGTGGAACAGTTGGCTCACAATTC---ATCAGCCCA--- 331
DB 178 TrpValGluValGlnHisPheLeuIleAsnIleLeuLysPheTyrIleGlyProGly 197
QY 332 CAGTTGAGAAATGTCCTTATTGTTTCTCCACCCGAGAAACAACCTTAATGAATGACA 391
DB 198 GlnIleGlnValGlyIleValGlnTyrGlyGluAspAlaValHisGluPheHisLeu--- 216
QY 392 GAAGACAGAGAACAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTCTGCCAGAGA 451
DB 217 AsnAspTyrArgSerValLysAspValValGluAlaAlaSerHisIleGluGlnArgGly 236
QY 452 GACACTTACATGCATGAGAGATTGAA-----AGGCGCAGTGACAGATTATTAT 502
DB 237 GlyThrGluThrArgHisAlaPheGlyIleGluPheAlaArgSerGluAlaPheGlnLys 256
QY 503 GAAAAACAGACAGAGGTACAGACAGCCGTCATCATCTGTTGACTGATGAGAACTC 562
DB 257 GlyGlyArgGlyGlyAlaLys-----LysValMetIleValIleThrAspGlyGluSer 274
QY 563 CATGAAGAT----- 571
DB 275 HisAspSerProAspLeuGluLysValIleArgGlnSerGluLysAspAsnValThrArg 294
QY 572 -----CTCTTTTCTATTACAGAGGAGGCTAATAGTCTCGAGATCTT 616

Db 295 TyrAlaValAlaValLeuGlyTyrTyrAsnArgArgGlyIleAsnProGluThrPheLeu 314
Qy 617 GGTCATTTGTTTACTGTGTGGTGGTGAAGAT-----TTCAATGAGACACAG 664
Db 315 AengluilelyTyrIleAlaSerProAspAspIleHisPheAsnValThrAsp 334
Qy 665 CTGGCCCGGATTCGGACAGTAAGATCATGTGTTCCCGTGAATGACGGCTTCAGGCT 724
Db 335 GluAlaIleLeu-----LysAspIleValAspAlaLeuGlyAspArgIlePheSer 351
Qy 725 CTGCAGGC 733
Db 352 LeuGluGly 354

RESULT 13
US-10-601-368-6
Sequence 6, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lora, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
CURRENT APPLICATION NUMBER: US/10/601,368
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 1141
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(22)
US-10-601-368-6

Alignment Scores:
Pred. No.: 0.037 Length: 1141
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 4.21% Indels: 38
Gaps: 9
DB: 6

US-09-970-076-1 (1-1414) x US-10-601-368-6 (1-1141)

Qy 218 TGCTACGGCGGATTTGACCTGTACTTTCATTTTGGACAATTCAGGAAGTGGTCGACAC 277
Db 159 CysGlnThrTyrMetAspIleValIleValLeuAspGlySerAsnSerIle---TyrPro 177
Qy 278 TGGAAATGAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTC---ATCAGCCCA--- 331
Db 178 TrpValGluValGlnHisPheLeuIleAsnIleLeuIleYelPheTyrIleGlyProGly 197
Qy 332 CAGTTAGAAATGCTCTTATTTGTTTCTCCACCCGAGGAACAACCTTAATGAATCTGACA 391
Db 198 GlnIleGlnValGluValGlnTyrGlyGluAspValValHisGluPheHisLeu--- 216
Qy 392 GAAGACAGAGAACAAATCCGTCAAGGCTGAGAGAACTCCAGAAAGTTGTCGACAGAGA 451
Db 217 AsnAspTyrArgSerValLysAspValValGluAlaIleAsnHisIleGluGlnArgGly 236
Qy 452 GACACTTACATGATGAGAGATTGAA-----AGGCCAGTACGACAGATTATTAT 502
Db 237 GlyThrGluThrArgThrAlaPheGlyIleGluPheAlaArgSerGluAlaPheGlnLys 256
Qy 503 GAAACAGACAGAGGTTACGAGACAGCCAGCTCATCTGCTTGACTGATGAGAACTC 562
Db 257 GlyGlyArgIleGlyValLys-----LysValMetIleValIleThrAspGlyGlnSer 274

Qy 563 CATGAAGAT----- 571
Db 275 HisAspSerProAspLeuGluLysValIleGlnGlnSerGluArgAspAsnValThrArg 294
Qy 572 -----CTCTTTTCTTATTCAGAGAGGCTTAATAGCTCTGAGATCTT 616
Db 295 TyrAlaValAlaValLeuGlyTyrTyrAsnArgArgGlyIleAsnProGluThrPheLeu 314
Qy 617 GGTCATTTGTTTACTGTGTGGTGGTGAAGAT-----TTCAATGAGACACAG 664
Db 315 AengluilelyTyrIleAlaSerProAspAspIleHisPheAsnValThrAsp 334
Qy 665 CTGGCCCGGATTCGGACAGTAAGATCATGTGTTCCCGTGAATGACGGCTTCAGGCT 724
Db 335 GluAlaIleLeu-----LysAspIleValAspAlaLeuGlyAspArgIlePheSer 351
Qy 725 CTGCAGGC 733
Db 352 LeuGluGly 354

RESULT 14
US-10-601-368-4
Sequence 4, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lora, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
CURRENT APPLICATION NUMBER: US/10/601,368
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 1166
TYPE: PRT
ORGANISM: Homo sapiens
US-10-601-368-4

Alignment Scores:
Pred. No.: 0.0373 Length: 1166
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 4.21% Indels: 38
Gaps: 9
DB: 6

US-09-970-076-1 (1-1414) x US-10-601-368-4 (1-1166)

Qy 218 TGCTACGGCGGATTTGACCTGTACTTTCATTTTGGACAATTCAGGAAGTGGTCGACAC 277
Db 137 CysGlnThrTyrMetAspIleValIleValLeuAspGlySerAsnSerIle---TyrPro 155
Qy 278 TGGAAATGAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTC---ATCAGCCCA--- 331
Db 156 TrpValGluValGlnHisPheLeuIleAsnIleLeuIleYelPheTyrIleGlyProGly 175
Qy 332 CAGTTAGAAATGCTCTTATTTGTTTCTCCACCCGAGGAACAACCTTAATGAATCTGACA 391
Db 176 GlnIleGlnValGluValGlnTyrGlyGluAspValValHisGluPheHisLeu--- 194
Qy 392 GAAGACAGAGAACAAATCCGTCAAGGCTGAGAGAACTCCAGAAAGTTGTCGACAGAGA 451
Db 195 AsnAspTyrArgSerValLysAspValValGluAlaIleAsnHisIleGluGlnArgGly 214
Qy 452 GACACTTACATGATGAGAGATTGAA-----AGGCCAGTACGACAGATTATTAT 502
Db 215 GlyThrGluThrArgThrAlaPheGlyIleGluPheAlaArgSerGluAlaPheGlnLys 234

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QY 503 GAAACAGACAAAGGCTACAGACAGCCGTCATCTTGACTGAGAGAACTC 562
    |||:::|||||:::|||||:::|||||:::|||||
Db 235 GlyGlyArgGlySerGlyAlaLys-----LysValMetIleValIleThrAspGlyGlnSer 252
QY 563 CATGAAGAT----- 571
    |||:::
Db 253 HisAspSerProAspLeuGlyLysValIleGlnGlnSerGluArgAspAsnValThrArg 272
    572 -----CTCTTTTCTATTACAGAGAGGCTTAATAGCTTCGAGATCTT 616
    |||:::|||||:::|||||
Db 273 TyrAlaValAlaValIleuGlyTyrTyrAsnArgArgGlyIleAsnProGluThrPheLeu 292
QY 617 GGTGCATTTGTTACTGTCTGTGGTGGAAGAT-----TTCAATGAGACACAG 664
    |||:::|||||
Db 293 AsnGluIleuValTyrIleAlaSerAspProAspAspLysHisPhePheAsnValThrAsp 312
QY 665 CTGCCCCGATTCGGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTTCAGGCT 724
    |||:::|||||
Db 313 GluAlaAlaLeu-----LysAspIleValAspAlaLeuGlyAspArgIlePheSer 329
QY 725 CTGCAGAGC 733
    |||:::||||
Db 330 LeuGluGly 332

RESULT 15
US-10-601-368-3
/ Sequence 3, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ PRIOR FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 3
/ LENGTH: 1188
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: (1)...(122)
US-10-601-368-3

Alignment Scores:
Pred. No.: 0.0374 Length: 1188
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 4.21% Indels: 38
DB: 6 Gaps: 9

US-09-970-076-1 (1-1414) x US-10-601-368-3 (1-1188)

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Search completed: December 14, 2005, 12:55:25
Job time : 26.3002 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2005, 07:01:38 ; Search time 5918.11 Seconds
(without alignments)
10603.927 Million cell updates/sec

Title: US-09-970-076-1_COPY_104_1207

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1104	100.0	1414	6	AF421380 Homo sapi
3	1090.8	98.8	5540	6	AX393246 Sequence
4	1090.8	98.8	5540	6	AX393301 Sequence
5	1090.8	98.8	5540	6	AX458370 Sequence
6	1090.8	98.8	5540	6	AF279145 Homo sapi
7	1090.4	98.8	1576	8	AY928975 Homo sapi
8	1090.4	98.8	1658	8	AY928977 Homo sapi
9	1089.4	98.7	1496	8	AY928974 Homo sapi
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16	853.4	77.3	5220	6	AF378762 Mus muscu
17	853.4	77.3	5225	9	BC094544 Mus muscu
18	803.8	72.8	1609	6	AR338517 Sequence

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ALIGNMENTS

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LOCUS AX458366 1414 bp DNA linear PAT 08-JUL-2002
DEFINITION Sequence 1 from Patent WO246228.
ACCESSION AX458366
VERSION AX458366.1 GI:21725038
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 Young,J.A., Bradley,K.A., Collier,R.J. and McGrigge,J.S.
AUTHORS
TITLE Receptor for b. Anthracis toxin
JOURNAL Patent: WO 0246228-A 1 13-JUN-2002;
WISCONSIN ALUMNI RESEARCH FOUNDATION (US)
FEATURES
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location/Qualifiers
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ORIGIN

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Best local similarity 100.0%; Pred. No. 1e-311;
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DB 464 CATGAGAGATTTGAAAAGGCGCACTGAGCAGATTTATATGAAAACAGCAAGGTAACAG 523
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RESULT 3
AX393246 5540 bp DNA linear PAT 23-MAR-2002
LOCUS-
DEFINITION Sequence 176 from Patent WO0210217.
ACCESSION AX393246
VERSION AX393246.1 GI:19701296
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE
1 St Croix B., Kinzler K.W. and Vogelstein B.
TITLE Endothelial cell expression patterns
JOURNAL Patent: WO 0210217-A 176 07-FEB-2002;

FEATURES The Johns Hopkins University (US)
Location/Qualifiers
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ORIGIN

Query Match 98.8%; Score 1090.8; DB 6; Length 5540;
Best Local Similarity 99.8%; Pred. No. 9.3e-308;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCAGCGCGAGGCGAGAGCCCTCGGATCGGCTTCAGTGAGCTCTTTGGCACT 60
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QY 61 CTGGTCTCATCTGCGCCGCGGCAAGGCGGACGCAAGAGATGGGGTCCAGCTGTAC 120
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LOCUS AX393301 5540 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 231 from Patent WO0210217.
ACCESSION AX393301
VERSION AX393301.1 GI:19701322
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 St Croix, B., Kinzler, K.W. and Vogelstein, B.
AUTHORS Endothelial cell expression patterns
TITLE Patent: WO 0210217-A 231 07-FEB-2002;
JOURNAL The Johns Hopkins University (US)
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Best Local Similarity 99.8%; Pred. No. 9.3e-308;
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AX458370
LOCUS AX458370 5540 bp DNA linear PAT 08-JUL-2002
DEFINITION Sequence 5 from Patent WO0246228.
ACCESSION AX458370
VERSION AX458370.1 GI:21725040
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 Young, J.A., Bradley, K.A., Collier, R.J. and Mowridge, J.S.
AUTHORS Receptor for b. Anthracis toxin
TITLE Patent: WO 0246228-A 5 13-JUN-2002;
JOURNAL WISCONSIN ALUMNI RESEARCH FOUNDATION (US)
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Query Match	98.8%	Score 1090.8;	DB 6;	length 5540;
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Matches 1092;	Conservative	0;	Mismatches 2;	Indels 0;
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ACCESSION		AF279145			
VERSION		AF279145.2	GI:14017380		
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ORGANISM		Homo sapiens (human)			
AUTHORS		Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 5540) St. Croix,B., Rago,C., Velculescu,V., Traverso,G., Romans,K.E., Montgomery,E., Lal,A., Riggs,G.J., Lengauer,C., Vogelstein,B. and Kinzler,K.W. Genes expressed in human tumor endothelium Science 289 (5482), 1197-1202 (2000) 10947988 2 (bases 1 to 5540) St. Croix,B., Vogelstein,B. and Kinzler,K.W. Direct Submission Submitted (16-JUN-2000) Johns Hopkins Oncology Center, Johns Hopkins University, 1650 Orleans Street, Baltimore, MD 21231, USA 3 (bases 1 to 5540) St. Croix,B., Vogelstein,B. and Kinzler,K.W. Direct Submission Submitted (09-MAY-2001) Johns Hopkins Oncology Center, Johns Hopkins University, 1650 Orleans Street, Baltimore, MD 21231, USA Sequence update by submitter version replaced gi:9857405. On May 9, 2001 this sequence version replaced gi:9857405. location/Qualifiers 1..5540 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /chromosome="4" 1..5540 /gene="TEM8" 144..1838 /gene="TEM8" /codon_start=1 /product="tumor endothelial marker 8 precursor"			
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ANKEPFSVED

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ACCESSION	AY928975
VERSION	AY928975.1 GI:62870686
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE	1 (bases 1 to 1576) Oberthuer,A., Kehlert,Y., Spitz,R., Skowron,M., Westermann,F., Mehler,K., Berthold,F. and Fischer,M. SAGE-based discovery and characterization of a novel fusion gene in the neuroblastoma cell lines IMR-5, IMR-5/75 and IMR-32 Unpublished
AUTHORS	2 (bases 1 to 1576) Oberthuer,A., Kehlert,Y., Spitz,R., Skowron,M., Westermann,F., Mehler,K., Berthold,F. and Fischer,M. Direct Submission
JOURNAL	Submitted (14-FEB-2005) Pediatric Oncology and Hematology, Cologne Childrens Hospital, University of Cologne, Joseph-Stelzmann-Straasse 9, Cologne, NRW D-50924, Germany
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RESULT 8
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LOCUS Homo sapiens anthrax toxin receptor/neuroblastoma fusion protein
DEFINITION transcribed variant 4 (ANTXR1/NNG1 fusion) mRNA, complete cds.
ACCESSION AY28977
VERSION AY28977.1 GI:62870690
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1658)
AUTHORS Oberthuer,A., Kahler,Y., Splitz,R., Skowron,M., Westermann,F.,
Mehler,K., Berthold,F. and Fischer,M.
TITLE SAGE-based discovery and characterization of a novel fusion gene in
the neuroblastoma cell lines IMR-5, IMR-5/75 and IMR-32
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1658)
AUTHORS Oberthuer,A., Kahler,Y., Splitz,R., Skowron,M., Westermann,F.,
Mehler,K., Berthold,F. and Fischer,M.
TITLE Direct Submission
JOURNAL Submitted (14-FEB-2005) Pediatric Oncology and Hematology, Cologne
Childrens Hospital, University of Cologne, Joseph-Stelzmann-Strasse
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LOCUS AY928974
DEFINITION Homo sapiens anthrax toxin receptor/neuroblastoma fusion protein
transcript variant 1 (ANTXR1/NG1 fusion) mRNA, complete cds.
ACCESSION AY928974
VERSION AY928974.1 GI:62870684
KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
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Oberthuer,A., Kahler,Y., Spitz,R., Skowron,M., Westermann,F.,
Mehler,K., Berthold,F. and Fischer,M.
SAGE-based discovery and characterization of a novel fusion gene in
the neuroblastoma cell lines IMR-5, IMR-5/75 and IMR-32
Unpublished
2 (bases 1 to 1496)
Oberthuer,A., Kahler,Y., Spitz,R., Skowron,M., Westermann,F.,
Mehler,K., Berthold,F. and Fischer,M.
Direct Submission
Submitted (14-FEB-2005) Pediatric Oncology and Hematology, Cologne
Childrens Hospital, University of Cologne, Joseph-Stelzmann-Strasse
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481 TCAGAGAGGAGGTAATAGGTCTCGAGATCTTGCAATTTGTTTACGTGTTGGTGTG 540
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1021 TGGTTCGCGCCCTCTGCTGCACTGATGATTAACAAGAGTCCCTCAACCCCTGCGAG 1080
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LOCUS AY28976
DEFINITION Homo sapiens anthrax toxin receptor/neuroblastoma fusion protein
transcript variant 3 (ANTXR1/NNGI fusion) mRNA, complete cds.
ACCESSION AY28976.1 GI:62870688
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 1578)
Oberthuer A., Kahler Y., Spitz R., Skowron M., Westermann F.,
Mehter K., Berthold F. and Fischer M.
SAGE-based discovery and characterization of a novel fusion gene in
the neuroblastoma cell lines IMR-5, IMR-5/75 and IMR-32
Unpublished
JOURNAL 2 (bases 1 to 1578)
Oberthuer A., Kahler Y., Spitz R., Skowron M., Westermann F.,
Mehter K., Berthold F. and Fischer M.
Direct Submission
Submitted (14-FEB-2005) Pediatric Oncology and Hematology, Cologne
Childrens Hospital, University of Cologne, Joseph-Stelzmann-Strasse
9, Cologne, NRW D-50924, Germany
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624 TCAGAGAGGAGGCTAATAGGCTCGAGATCTTGAGTCAATGTTTAACTGTGTGTGTG 683
541 AAAGATTTCAATGAGACACGCTGGCCCGGATTCGGACAGTAAAGATCATGTGTTTCCC 600
684 AAAGATTTCAATGAGACACGCTGGCCCGGATTCGGACAGTAAAGATCATGTGTTTCCC 743

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QY 661 ATCGAAATTTGACAGCTGAACCATTCACCATATGTGACAGAGAGTCAATTTCAAGTTTC 720
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DB 1044 GATGGCTCTCTTTATCTCCAGTTCTGTCAATCAACACCAACACATCTGTCAGCGGT 1103
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DB 1164 TGGTCTGCGCCCTCTGCTGCACTGTGATTATCAAGAGAGTCCCTCACCCCTGCGAG 1223
QY 1081 GAGAGTGAAGA 1091
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RESULT 11
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DEFINITION Sequence 7 from Patent WO0246228.
ACCESSION AX458372
VERSION AX458372.1 GI:21725042
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 Young, J.A., Bradley, K.A., Collier, R.J. and Mowridge, J.S.
AUTHORS
TITLE Receptor for b. anthracis toxin
JOURNAL Patent: WO 0246228-A 7 13-JUN-2002;
WISCONSIN ALUMNI RESEARCH FOUNDATION (US)
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ORIGIN

Query Match	86.0%	Score 949.4	DB 6	Length 2112
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QY	121	GGGGGATTTGACCGGTACTCTTATTTGAGCAAAATCAGAAAGTGTGTGACCACTGGAAAT	180	
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QY	181	GAATCTATTACTTTTGTGGAACAGTTGGCTCACAAATTCACGCCACAGTTGAGAAATG	240	
DB	293	GAATCTATTACTTTTGTGGAACAGTTGGCTCACAAATTCACGCCACAGTTGAGAAATG	352	
QY	241	TCCTTTATTTGTTTCTCCACCCGAGAAACAACCTTAATGAACCTGACAGAAAGACAGAA	300	
DB	353	TCCTTTATTTGTTTCTCCACCCGAGAAACAACCTTAATGAACCTGACAGAAAGACAGAA	412	
QY	301	CAAAATCGTCAAGCGCTGAGAAAGCTCAGAAAGTTGCGCAGGAGGAGACCTTACATG	360	
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QY	421	ACAAGCCAGCGTCACTGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTCTAT	480	
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QY	481	TCGAGAGGAGGCTTAATAGCTCTCGAGATCTTGTGTCATGTTTCTGTGTGTGTG	540	
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QY	901	GATGGCGCTCTCTTTTATCTCCAGTCTGTCTCATCATCACACCACTGT	951	
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RESULT 12
BC012074
LOCUS
DEFINITION Homo sapiens anchrax toxin receptor 1, transcript variant 3, mRNA

ACCESSION	BC012074	(cDNA clone MGC:19967 IMAGE:4563020), complete cds.
VERSION	BC012074.1	GI:15082332
KEYWORDS	MGC.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	1 (bases 1 to 2112)	
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heisch, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Utsid, T.B., Joshuyuki, S., Carninci, P., Prange, C., Raha, S.S., Loguigliano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.E., Scherch, A., Schen, J.E., Jones, S.J., and Marra, M.A.	
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
PUBMED	12477932	
REFERENCE	2 (bases 1 to 2112)	
AUTHORS	Strausberg, R.	
TITLE	Direct Submission	
JOURNAL	Submitted (02-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov	
COMMENT	Contact: MGC help desk Email: cgabs-remail.nih.gov Tissue Procurement: DCTD/DTF cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@cgsc.bc.ca	
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/HLN at: <http://image.llnl.gov>
Series: IRAL Plate: 29 Row: 9 Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16935552.

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ORIGIN

Query Match 86.0%; Score 949.4; DB 8; Length 2112;
Best Local Similarity 99.9%; Pred. No. 2.3e-266;
Matches 950; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGGCCAGCGCGGAGGAGAGCCCTCGGCATCGCTTCAGTGGCTCTCTTTGGCCACT 60
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901 GATGCGCTCTCTTTTATCTCCAGTTCTGTGATCATCAACCAACACACTGT 951
1013 GATGCGCTCTCTTTTATCTCCAGTTCTGTGATCATCAACCAACACACTGT 1063

RESULT 13

AK223273

LOCUS AK223273 2052 bp mRNA linear PRI 26-APR-2005
DEFINITION Homo sapiens mRNA for tumor endothelial marker 8 isoform 3
precursor variant, clone: STM07451.

ACCESSION

AK223273

VERSION AK223273.1 GI:62898106
KEYWORDS FLI_CDNA; oligo capping.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1

Maruyama, K. and Sugano, S.
Oligo-capping: a simple method to replace the cap structure of
eukaryotic mRNAs with oligoribonucleotides
Gene 138 (1-2), 171-174 (1994)
8125298

JOURNAL

PUBMED

REFERENCE

2

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S.
Construction and characterization of a full length-enriched and a
5'-end-enriched cDNA library
Gene 200 (1-2), 149-156 (1997)
9373149

JOURNAL

PUBMED

REFERENCE

3

(baees 1 to 2052)
Suzuki, Y., Sugano, S., Totoki, Y., Toyoda, A., Takeda, T., Sakaki, Y.,
Tanaka, A. and Yokoyama, S.
Direct Submision
Submitted (22-APR-2005) Akiko Tanaka, RIKEN Yokohama Institute,
Protein Research Group, 1-7-22 Suehito, Tsurumi, Yokohama,
Kanagawa, 230-0045, Japan (E-mail: akitanaka@riken.jp,
URL: http://protein.gsc.riken.jp/, Tel: 81-45-503-9452,
Fax: 81-45-503-9450)

JOURNAL

PUBMED

REFERENCE

4

This work was supported in part by the National Project on Protein
Structural and Functional Analysis, Ministry of Education, Culture,
Sports, Science and Technology of Japan.
Sumio Sugano, Yutaka Suzuki
Laboratory of Functional Genomics Department of Medical Genome
Sciences Graduate School of Frontier Sciences The University of
Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639 Japan email:
sugano@u-tokyo.ac.jp
URL: http://www.k.u-tokyo.ac.jp/index.html.en.
Location/Qualifiers

FEATURES

source

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this clone is also named as hss001003689"
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/note="Start codon is not identified."
/codon_start=1

/evidence=not_experimental
/product="tumor endothelial marker 8 isoform 3 precursor
variant"
/protein_id="BAD96993.1"
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LYFLLKSGSVLHNMBIYVYFESPOLRMSFIYFSRGTTLMTEDRQI
ROGLERLOKLVPGSDPYVMEHGFERSBOIYVENRGTATSVIALITDGLHDLPEY
SERBANSRDLGAIIVCYVKDPNETOLAIADSKHVPVNDGFOALGSIHSILKK
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ORIGIN

Query Match 86.0%; Score 949.2; DB 8; Length 2052;
Best Local Similarity 99.7%; Pred. No. 2,6e-266;
Matches 951; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 ATGGCCACGGCGAGGAGAGCCCTCGCATCGGCTTCCAGTGGCTCTCTTGGCCACT 60
131 ATGGCCACGGCGAGGAGAGCCCTCGCATCGGCTTCCAGTGGCTCTCTTGGCCACT 190
61 CTGGTCTCATCTGCGCGGGGCAAGGGGAGCGAGGAGATGGGGTCCAGCTGTAC 120
191 CTGGTCTCATCTGCGCGGGGCAAGGGGAGCGAGGAGATGGGGTCCAGCTGTAC 250
QY 121 GGGGAGTTTGAAGCTGTAATCTTATTTGACAAATCAGAAAGTGTGTGCACTGGAAT 180
DB 251 GGGGAGTTTGAAGCTGTAATCTTATTTGACAAATCAGAAAGTGTGTGCACTGGAAT 310
QY 181 GAATCTATTACTTGTGGAACAGTTGGCTCACAATTTCAAGCCCAAGTTGAGAAATG 240
DB 311 GAATCTATTACTTGTGGAACAGTTGGCTCACAATTTCAAGCCCAAGTTGAGAAATG 370
QY 241 TCTTTATTTGTTTCTCCACCCGAGAAACAATTATGAATGACAGAGACAGAGAA 300
DB 371 TCTTTATTTGTTTCTCCACCCGAGAAACAATTATGAATGACAGAGACAGAGAA 430
QY 301 CAAATCCGTCAAGGCTTGAAGAACTCCAGAAATTTCTGCCAGAGAGACATTATATG 360
DB 431 CAAATCCGTCAAGGCTTGAAGAACTCCAGAAATTTCTGCCAGAGAGACATTATATG 490
QY 361 CATAAGAGTTTGAAGAGGCGAGTGAAGATTTATTTGAAGACAGAGGTTACAGG 420
DB 491 CATAAGAGTTTGAAGAGGCGAGTGAAGATTTATTTGAAGACAGAGGTTACAGG 550
QY 421 ACAGCCAGCTCATCTTGTGTTGATGATGAGAACTCCATGAAAGTCTTTTCTAT 480
DB 551 ACAGCCAGCTCATCTTGTGTTGATGATGAGAACTCCATGAAAGTCTTTTCTAT 610
QY 481 TCAGAGAGGAGGCTTAATAGTCTGAGATTTTGTGCAATTTTACTGTGTGTGTG 540
DB 611 TCAGAGAGGAGGCTTAATAGTCTGAGATTTTGTGCAATTTTACTGTGTGTGTG 670
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DB 671 AAAGATTTCATGAGACAGCTGGCCGGATTGGCGAGTGAAGATCATGTGTTCCG 730
QY 601 GTGATGAGCGGCTTTCAGGCTCTGCAAGGCTCATCTCAATTTTGAAGAGTCTGCG 660
DB 731 GTGATGAGCGGCTTTCAGGCTCTGCAAGGCTCATCTCAATTTTGAAGAGTCTGCG 790
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QY 721 GTGAGAGAAACGGCTTCCGACATGCCGCAAGTGAAGGATCTGTGAGCTTCAAG 780
DB 851 GTGAGAGAAACGGCTTCCGACATGCCGCAAGTGAAGGATCTGTGAGCTTCAAG 910
QY 781 ATCAATGACTGCTCACAATGAGAAAGCTTTTCTGTGAAAGACATTATTTACTG 840
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QY 841 TGTCCAGCGCTTATTTAAAGAAAGTTGGCATGAAGCTGCACTCCAGTGCAGATGAAC 900
DB 971 TGTCCAGCGCTTATTTAAAGAAAGTTGGCATGAAGCTGCACTCCAGTGCAGATGAAC 1030
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DB 1031 GATGGCCTCTCTTTATCTTCCAGTTTGTTCATCATCAACACACACTGTTCT 1084

RESULT 14

AX393256
LOCUS AX393256 5220 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 186 from Patent WO0210217.
ACCESSION AX393256
VERSION AX393256.1 GI:19701303
KEYWORDS

SOURCE

Mus musculus (house mouse)
Mus musculus
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE

1 St Croix, B., Kinzler, K.W. and Vogelstein, B.
Endothelial cell expression patterns
Patent: WO 0210217-A 186 07-FEB-2002;
The Johns Hopkins University (US)
Location/Qualifiers

FEATURES

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1..5220
/organism="Mus musculus"
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/db_xref="taxon:10090"

ORIGIN

Query Match 77.3%; Score 853.4; DB 6; Length 5220;
Best Local Similarity 87.3%; Pred. No. 3,6e-238;
Matches 935; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 24 CTTCCGATCGGCTTCCAGTGGCTCTTGGCCACTGCTGTCATCTGCGCGGGCA 83
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QY 84 AGGGGAGCGAGGAGATGGGGTCCAGCTCTCAAGCGGATTTGACCTGTAATTCAT 143
DB 351 CCGGGGCGCGGAGAGATGGGGTCCAGCTCTCAAGCGGATTTGACCTGTAATTCAT 410
QY 144 TTTGACAAATTCAGAAAGTGTGTGCACTGGAATGAAATCTATTTCTTTGTGAACA 203
DB 411 CTTGACAAATTCAGAAAGTGTGTGCACTGGAATGAAATCTATTTCTTTGTGAACA 470
QY 204 GTTGGCTCAAAATTCATACAGCCCAAGTGAAGATGCTTTATTTGTTTCTCCACCG 263
DB 471 GTTGGCTCAAAATTCATACAGCCCAAGTGAAGATGCTTTATTTGTTTCTCCACCG 530
QY 264 AGGAACAACCTTATATGAAGTGAAGAGACAGAAACAATCCGTCAAGGCTTGAAGA 323
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QY 324 ACTCCAGAAAGTCTGCGAGAGAGACCTTACATGATGAAGATTTGAAGGCTCAG 383
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QY 864 AGTTGGCATGAAGAGCTGCACTCCAGGTTCAGCATGAAGAGATGGCTCTCTTTATCTCCAG 923
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RESULT 15
AX393370
LOCUS AX393370 5220 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 300 from Patent WO0210217.
ACCESSION AX393370
VERSION AX393370.1 GI:19701356
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 St Croix, B., Kinzler, K.W. and Vogelstein, B.
AUTHORS Endothelial cell expression patterns
TITLE Patent: WO 0210217-A 300 07-FEB-2002;
JOURNAL The Johns Hopkins University (US)
FEATURES
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1. 5220
/organism="Mus musculus"
/mol_type="unassigned DNA"
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ORIGIN
Query Match 77.3%; Score 853.4; DB 6; Length 5220;
Best Local Similarity 87.3%; Pred. No. 3,6e-238;
Matches 935; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 24 CCTGGCATCGGCTTCCAGTGCTCTTTGGCCACTGTGTGCTCATCTGCGCGGACA 83
DB 291 CCGGCTGGCGGCTCGCGGGACTGCGGTGCTGCACTGATGCTGTGCGCGGACA 350
QY 84 AGGAGGACCAAGAGAGATGGGGGTCCAGCTGCTCAAGCGGATTTGACCTGATTCAT 143
DB 351 CCGGGGCGCGCGGAGAGATGGGGACCAAGTGTGCTAAGAGATTCGACCTTCAATTCAT 410

QY 144 TTTGACAAATCAGGAAGTGTGCTGACCACTGGAATGAATCTATCTTTGTGAGACA 203
DB 411 CTTGACAAAGTACAGGAAGTGTGCTGACCACTGGAATGAATCTATCTTTGTGAGACA 470
QY 204 GTTGGCTCAAAATTCATCAAGCCCAAGTTGAGAAATGCTTTATTTGTTTTTCCACCG 263
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QY 384 TGAAGAGATTTATGAAAAAGACAGAGAGATGAGACAGGACGCTATGATGCTTT 443
DB 651 TGAAGAGATTTATGAAAAAGACAGAGAGATGAGACAGGACGCTATGATGCTTT 710
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DB 771 CCGAGACCTTGGTGCATTTGTTTACTGTGTGTGTGTGAAAAGATTTCAATGAAATCAGT 830
QY 564 GGCCTGGATGCGGACAGTAAGGATCATGTTTCCCGTAATGACGGCTTCAAGCTCT 623
DB 831 GGCTGGATGTCAGACAGTAAGGACCAAGTGTCTGTGAACGAGGCTTCAAGCTCT 890
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DB 1251 GGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1310
QY 1044 TGTGATTTATCAAGAGAGTCCCTCCACCCCTGCGGAGAGAGTGAAGAAA 1094
DB 1311 AGTGAATCATCAAGAGAGTCCCTCCACCCCTGTTGAGAGAGTGAAGAAA 1361

Search completed: December 18, 2005, 11:23:36
Job time : 5922.11 secs

PS Claim 7, Page 27-29, 45pp; English.
 CC The present sequence is that of cDNA encoding a human surface-bound
 CC anthrax toxin receptor (ATR). The cDNA is a PCR amplification product
 CC from HeLa cells and human placenta cDNA libraries. Anthrax toxin
 CC protective antigen (PA) binds to the ATR at a von Willebrand factor A
 CC domain located in the extracellular domain of ATR. The invention provides
 CC ATR polypeptides and polynucleotides, vectors, host cells, and transgenic
 CC and knock-out animals. The invention also provides methods for
 CC identifying molecules that bind the ATR and which reduce the toxicity of
 CC anthrax toxin. A claimed method for treating anthrax in a human or animal
 CC involves administering an agent that inhibits binding between PA and ATR
 CC at a level effective to reduce the severity of anthrax. Suitable agents
 CC include ATR or a PA-binding fragment of ATR, a PA-binding polypeptide at
 CC least 80% identical to these, a fusion protein, a monoclonal or
 CC polyclonal antibody, a polysaccharide, a lipid or a nucleic acid. ATR
 CC polypeptides can also be used in the recombinant production of ATR
 CC polypeptides, and as molecular probes

Sequence 1414 BP; 394 A; 344 C; 344 G; 332 T; 0 U; 0 Other;

Query Match 100.0%; Score 1104; DB 6; Length 1414;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 61 CTGTGCTCATCTGCGCCGCGGCAAGGGGAGCGAGGAGAGTGGGGCTTCAGCTGTAC 120
 164 CTGTGCTCATCTGCGCCGCGGCAAGGGGAGCGAGGAGAGTGGGGCTTCAGCTGTAC 223
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 361 CATGAAGATTGTAAGAGGCGCACTGAGAGATTATATGAAGAACTGAGTACAGG 420
 464 CATGAAGATTGTAAGAGGCGCACTGAGAGATTATATGAAGAACTGAGTACAGG 523
 421 ACGACGAGGCTCATCTGCTTGTGACTGATGAGAACTCCATGAGATCTCTTTTCTAT 480
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 601 GTGAATGACGGCTTTCAGGCTCTGCAAGGCAATCATCAATTTTGAAGAACTCTGCG 660
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 QY 781 ATCAATGACCTGGTCACTCAATGAAGCCCTTTCTGTGGAAGACACTTATTTACG 840
 DB 884 ATCAATGACCTGGTCACTCAATGAAGCCCTTTCTGTGGAAGACACTTATTTACG 943
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RESULT 2
 ABL92078 standard; cDNA, 5540 BP.
 ID ABL92078

XX ABL92078;
 XX 30-MAY-2002 (first entry)
 XX DT

DE Human Tumour Endothelial Marker polynucleotide SEQ ID NO 176.

XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis; gene; ss.

XX Homo sapiens.
 OS
 XX
 PN WO200210217-A2.

XX 07-FEB-2002.

XX 01-AUG-2001; 2001WO-US024031.

XX 02-AUG-2000; 2000US-0222599P.

XX 11-AUG-2000; 2000US-0224360P.

XX 11-APR-2001; 2001US-0282850P.

XX (Uydo) UNIV JOHNS HOPKINS.

XX St Croix B, Kinzler KW, Vogelstein B;

XX WPI; 2002-291856/33.

XX An isolated molecule comprising an antibody variable region which
 PT specifically binds to an extracellular domain of a tumor endothelial
 PT marker (TEM) protein, useful for inhibiting tumor growth.

XX Disclosure; Page 121-123; 331pp; English.

XX The invention relates to an isolated molecule comprising an antibody
 CC variable region which specifically binds to an extracellular domain of a
 CC tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM

CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC They are useful for inhibiting tumor growth, neoangiogenesis in subjects
CC bearing a vascularised tumour, polycystic kidney disease, diabetic
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
CC are disclosed, as are marker oligonucleotide sequences: tumour
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
CC (PEM) ABL91903-ABL91995
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XX Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
Query Match 98.8%; Score 1090.8; DB 6; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGCCACGGCGGAGGAGGAGCCCTCGGCATCGGCTTCCAGTGGCTCTTTGGCCACT 60
DB 144 ATGGCCACGGCGGAGGAGGAGCCCTCGGCATCGGCTTCCAGTGGCTCTTTGGCCACT 203
QY 61 CTGGTCTCATCTGCGCCGGGCAAGGGGAGCGAGGAGATGGGGTCCAGCTGTAC 120
DB 204 CTGGTCTCATCTGCGCCGGGCAAGGGGAGCGAGGAGATGGGGTCCAGCTGTAC 263
QY 121 GGGGATTTGACCTGTAATCTCATTTTGGACAATTCAGGAAGTGTGTCGACCACTGGAAAT 180
DB 264 GGGGATTTGACCTGTAATCTCATTTTGGACAATTCAGGAAGTGTGTCGACCACTGGAAAT 323
QY 181 GAATCTAATCTTGTGGAACAGTTGGCTCACAATTCAGCCCAAGTTGAGATG 240
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DB 564 ACAAGCAGGCTCATCTGCTTTGAGCTGATGAGAACTCCATGAAGATCTCTTTTCTAT 623
QY 481 TCAGAGGAGGAGGTAATAGTCTCGAGATCTTGATGCAATGTTTACTGTGTGTG 540
DB 624 TCAGAGGAGGAGGTAATAGTCTCGAGATCTTGATGCAATGTTTACTGTGTGTG 683
QY 541 AAAGATTTCAATGAGACACAGCTGGCCGAGTTGCGAGACAGTAAGATCAATGTTTCCC 600
DB 684 AAAGATTTCAATGAGACACAGCTGGCCGAGTTGCGAGACAGTAAGATCAATGTTTCCC 743
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DB 984 TGTCACAGCGCTATCTTAAAAAGAAAGTTGGCATGAAGCTGCACTCAGGTCAGCATGAAC 1043
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DB 1224 GAGGTGAGGAAA 1237
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ID ABL92104 standard; cDNA; 5540 BP.
XX ABL92104;
AC 30-MAY-2002 (first entry)
XX
DT Human Tumour Endothelial Marker polynucleotide SEQ ID NO 231.
XX
DE Human Tumour Endothelial Marker polynucleotide SEQ ID NO 231.
XX
XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis; gene; ss.
XX
XX Homo sapiens.
OS
PN W0200210217-A2.
XX
PD 07-FEB-2002.
XX
PF 01-AUG-2001; 2001MO-US024031.
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PR 11-AUG-2000; 2000US-0224360P.
PR 11-APR-2001; 2001US-0282850P.
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PA
XX St Croix B, Kinzler KW, Vogelstein B;
PI WPI; 2002-291856/33.
XX P-PSDB; ABB90750.
DR
XX An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
PT marker (TEM) protein, useful for inhibiting tumor growth.
XX
PS Claim 30; Page 207-209; 331pp; English.
XX
CC The invention relates to an isolated molecule comprising an antibody
CC variable region which specifically binds to an extracellular domain of a
CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC They are useful for inhibiting tumor growth, neoangiogenesis in subjects
CC bearing a vascularised tumour, polycystic kidney disease, diabetic
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
CC are disclosed, as are marker oligonucleotide sequences: tumour
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers

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CC (PEM) ABL91903-ABL91995
XX
SQ Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
Query Match 98.8%; Score 1090.8; DB 6; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCAGCGGAGGAGAGAGCCCTCGGCATCGGCTCCAGTGGGCTCTTTGGCCACT 60
DB 144 ATGGCCAGCGGAGGAGAGAGCCCTCGGCATCGGCTCCAGTGGGCTCTTTGGCCACT 203
QY 61 CTGGTCTCATCTGCGCCGGCAAGGGGAGCGCAGGAGAGTGGGGTCCAGCCTCTAC 120
DB 204 CTGGTCTCATCTGCGCCGGCAAGGGGAGCGCAGGAGAGTGGGGTCCAGCCTCTAC 263
QY 121 GGGGAGTTTGAAGCTGATCTTCAATTTTGGACAAATCGAAGAGTGTCTGCACCTGGAA 180
DB 264 GGGGAGTTTGAAGCTGATCTTCAATTTTGGACAAATCGAAGAGTGTCTGCACCTGGAA 323
QY 181 GAAATCTATTACTTTGAGAAAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAATG 240
DB 324 GAAATCTATTACTTTGAGAAAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAATG 383
QY 241 TCCTTTATTGTTTCTCAACCCGAGAAACAACCTTAATGAACTGACAGAAACAGAGAA 300
DB 384 TCCTTTATTGTTTCTCAACCCGAGAAACAACCTTAATGAACTGACAGAAACAGAGAA 443
QY 301 CAAATCCGTCAGGCTTGAAGAACTCCAGAAAGTTCTGCAGAGAGAGACACTTACATG 360
DB 444 CAAATCCGTCAGGCTTGAAGAACTCCAGAAAGTTCTGCAGAGAGAGACACTTACATG 503
QY 361 CATGAAGATTGAAAGGGCCAGTAGAGAGATTTATTAAGAAACAGACAAAGGTTACAG 420
DB 504 CATGAAGATTGAAAGGGCCAGTAGAGAGATTTATTAAGAAACAGACAAAGGTTACAG 563
QY 421 ACAGCCAGGCTCATCTGCTTGAAGTAGAGAACTCCATGAGATCTTTTCTAT 480
DB 564 ACAGCCAGGCTCATCTGCTTGAAGTAGAGAACTCCATGAGATCTTTTCTAT 623
QY 481 TCAGAGAGGAGGCTTAATAGGCTCCAGATCTTGGTGCATTTGTTACTGTGTGGTGG 540
DB 624 TCAGAGAGGAGGCTTAATAGGCTCCAGATCTTGGTGCATTTGTTACTGTGTGGTGG 683
QY 541 AAAAGTTTCAATAGACACAGCTGGCCCGGATGGCGACAGTAAGATCATGTGTTCC 600
DB 684 AAAAGTTTCAATAGACACAGCTGGCCCGGATGGCGACAGTAAGATCATGTGTTCC 743
QY 601 GTGAATGACGGCTTTGAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAGTCTGG 660
DB 744 GTGAATGACGGCTTTGAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAGTCTGG 803
QY 661 ATGGAATTTAGACAGTGAACCATCAATATGTCAGAGAGAGTCAATTTCAAGTTGTC 720
DB 804 ATGGAATTTAGACAGTGAACCATCAATATGTCAGAGAGAGTCAATTTCAAGTTGTC 863
QY 721 GTGAGAGGAAAGGCTTCCGACATGCGCCGACAGTGGAGAGGGTCCCTGACACTCAAG 780
DB 864 GTGAGAGGAAAGGCTTCCGACATGCGCCGACAGTGGAGAGGGTCCCTGACACTCAAG 923
QY 781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAGAGACACTTATTTACTG 840
DB 924 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAGAGTCTTATTTTACTG 983
QY 841 TGTCCAGCGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAC 900
DB 984 TGTCCAGCGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAC 1043
QY 901 GAGGCGCTCTTTTATCTCAATTCGTATATATACCAACCAACACTGTTGACGGT 960
DB 1044 GAGGCGCTCTTTTATCTCAATTCGTATATATACCAACCAACACTGTTGACGGT 1103
QY 961 TCATCTCTGACATCGCCCTGTGATCTGTCTCTGCTCTTACCCCTGCTCTCTCTGG 1020

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DB 1104 TCCATCTCGGCATCGCCCTGCTGATCCGTCTGCTCTAGCCCTGCTCTCTCTGG 1163
QY 1021 TGGTCTGGCCCTCTGCTGCACTGATTAATCAAGAGAGTCCCTCCACCCCTGCGAG 1080
DB 1164 TGGTCTGGCCCTCTGCTGCACTGATTAATCAAGAGAGTCCCTCCACCCCTGCGAG 1223
QY 1081 GAGAGTGAAGAAA 1094
DB 1224 GAGAGTGAAGAAA 1237

RESULT 4
ABV73882
ID ABV73882 standard; cDNA; 5540 BP.
XX
AC ABV73882;
XX
DT 08-JAN-2003 (first entry)
XX
DE Human anthrax toxin receptor cDNA.
XX
KW Anthrax; toxin; receptor; human; TEM8; antibacterial; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 144..1838
FT /tag= a
FT /product= "anthrax toxin receptor"
FT sig_peptide 144..224
FT /tag= b
FT mat_peptide 225..1838
FT /tag= c
XX
PN W0200246228-A2.
XX
PD 13-JUN-2002.
XX
PF 03-OCT-2001; 2001WO-US030941.
XX
PR 05-DEC-2000; 2000US-0251481P.
XX
PA (WISC ) WISCONSIN ALUMNI RES FOUNDD.
XX
PI Young JAT, Bradley KA, COLLIER RJ, Mogridge JS;
XX
DR WPI; 2002-713235/77.
XX
DR P-PSDB; ABP54904.
XX
PT Novel isolated polypeptide useful for identifying agent that prevents or
PT reduces effect of anthrax toxin on host cell, for treating human or non-
PT human animal suffering from anthrax.
XX
PS Disclosure; Page 32-37; 45pp; English.
XX

The present sequence is that of cDNA encoding a human anthrax toxin
receptor (ATR). The cDNA, previously designated TEM8, was originally
isolated by PCR from HeLa cell and human placenta cDNA libraries. It was
identified in a database screening using a newly isolated human cDNA (see
ABV73881) which encodes an ATR (see ABP54903) that is identical to the
TEM8 polypeptide except in the cytoplasmic tail, suggesting differential
splicing of a primary mRNA transcript. TEM8 was not previously identified
as an ATR. The invention provides ATR polypeptides and polynucleotides,
host cells, vectors, and transgenic and knock-out animals. It also
provides methods for identifying molecules that bind the ATR and which
reduce the toxicity of anthrax toxin. A claimed method for treating
anthrax in a human or animal involves administering an agent that
inhibits binding between anthrax toxin protective antigen (PA) and ATR at
a level effective to reduce the severity of anthrax. Suitable agents
include the TEM8 polypeptide or a PA-binding fragment of it, a PA-binding
polypeptide at least 80% identical to these, a fusion protein, a
monoclonal or polyclonal antibody, a polysaccharide, a lipid or a nucleic

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CC acid. ATR polynucleotides can also be used in the recombinant production
 CC of ATR polypeptides, and as molecular probes

XX Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;

Query Match 98.8%; Score 1090.8; DB 6; Length 5540;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ATGGCCAGCGCGGAGCGGAGAGCCCTCGGAGTCGGCTTCAGTGGCTCTCTTGGCCACT 60
DB 144 ATGGCCAGCGCGGAGCGGAGAGCCCTCGGAGTCGGCTTCAGTGGCTCTCTTGGCCACT 203
QY 61 CTGTGTCTCATCTGCGCGCGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGTCTAC 120
DB 204 CTGTGTCTCATCTGCGCGCGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGTCTAC 263
QY 121 GCGGATTTTACCTGTACTTCTTGTGACAAATCAGAAAGTGTGTGACCACTGGAAT 180
DB 264 GCGGATTTTACCTGTACTTCTTGTGACAAATCAGAAAGTGTGTGACCACTGGAAT 323
QY 181 GAAATCTATTACTTGTGAAACAGTTGGCTCACAAATTCATCAGCCCACTGGAGAATG 240
DB 324 GAAATCTATTACTTGTGAAACAGTTGGCTCACAAATTCATCAGCCCACTGGAGAATG 383
QY 241 TCCTTTATTTGTTTCTCCAGCCGAGAAACAACCTTAATGAACTGACAGAAAGACAGAA 300
DB 384 TCCTTTATTTGTTTCTCCAGCCGAGAAACAACCTTAATGAACTGACAGAAAGACAGAA 443
QY 301 CAATCCGTCAGGCGCTAGAAAGCTCAGAAAGTGTGCGAGGAGGAGACACTTACATG 360
DB 444 CAATCCGTCAGGCGCTAGAAAGCTCAGAAAGTGTGCGAGGAGGAGACACTTACATG 503
QY 361 CATGAAGATTGTAAGAGGCGCAGTGAAGATTTATTATGAAACAGACAAAGGTACAGG 420
DB 504 CATGAAGATTGTAAGAGGCGCAGTGAAGATTTATTATGAAACAGACAAAGGTACAGG 563
QY 421 ACAGCCAGCGCTCATCTGCTTGTGACGTGAGAACTCCATGAAAGTCTCTTTTCTAT 480
DB 564 ACAGCCAGCGCTCATCTGCTTGTGACGTGAGAACTCCATGAAAGTCTCTTTTCTAT 623
QY 481 TCAGAGAGGAGGCTAATAGGCTCGAGATCTTGTCATATGTTTACTGTGTGTGTG 540
DB 624 TCAGAGAGGAGGCTAATAGGCTCGAGATCTTGTCATATGTTTACTGTGTGTGTG 683
QY 541 AAGATTTCATGAGACACAGCTGGCCCGAATTCGCGACAGTAAGATCAATGTGTTCC 600
DB 684 AAGATTTCATGAGACACAGCTGGCCCGAATTCGCGACAGTAAGATCAATGTGTTCC 743
QY 601 GTGAATACGCGCTTTCAGGCTTCGAAAGGATTCATCACTCAATTTGAAAGAGTCTG 660
DB 744 GTGAATACGCGCTTTCAGGCTTCGAAAGGATTCATCACTCAATTTGAAAGAGTCTG 803
QY 661 ATGAATTTAGAGGCTGAACCATCCACATATGTGAGAGAGTCAATTCAGTGTG 720
DB 804 ATGAATTTAGAGGCTGAACCATCCACATATGTGAGAGAGTCAATTCAGTGTG 863
QY 721 GTGAGAGAAACGCGCTTCGACATGCCCGCAACGTGACAGAGGTCTTCGAGCTTCA 780
DB 864 GTGAGAGAAACGCGCTTCGACATGCCCGCAACGTGACAGAGGTCTTCGAGCTTCA 923
QY 781 ATCAATACCTGCTGACATCAATGAAAGCCCTTTTCTGTGAAAGACCTTATTACTG 840
DB 924 ATCAATACCTGCTGACATCAATGAAAGCCCTTTTCTGTGAAAGTACTTATTACTG 983
QY 841 TGTCAGAGCGCTATCTTAAAGAGTGGCATGAAAGTGCATCCAGGTGAGATGAC 900
DB 984 TGTCAGAGCGCTATCTTAAAGAGTGGCATGAAAGTGCATCCAGGTGAGATGAC 1043
QY 901 GATGAGCTCTCTTTATCTCCAGTTCGTGATCAATCAACACACACTGTTCTGACGT 960
DB 1044 GATGAGCTCTCTTTATCTCCAGTTCGTGATCAATCAACACACACTGTTCTGACGT 1103

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QY 961 TCCATCTGAGCATGCGCCCTGCTGATCTCTTCTGCTCTAGACCTGCTCTCTG 1020
DB 1104 TCCATCTGAGCATGCGCCCTGCTGATCTCTTCTGCTCTAGACCTGCTCTCTG 1163
QY 1021 TGGTTCTGCGCCCTGCTGCTGCTGATGATTATGAAAGAGTCTCTCCACCCCTGCGAG 1080
DB 1164 TGGTTCTGCGCCCTGCTGCTGCTGATGATTATGAAAGAGTCTCTCCACCCCTGCGAG 1223
QY 1081 GAGAGTGAAGAAA 1094
DB 1224 GAGAGTGAAGAAA 1237

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RESULT 5

ABX72029 standard; DNA; 5540 BP.

ABX72029;

12-MAR-2003 (first entry)

XX DNA encoding human tumour endothelial marker TEM 19.

XX Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;

KW Tumour endothelial marker; normal endothelial marker; PEM;

KW pan-endothelial marker; polycystic kidney disease; psoriasis;

KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;

KW neovascularization; immune response; cytoskeletal; antidiabetic; gene;

XX ophthalmological; antirheumatic; antirheumatic; antipsoriatic; ds.

OS Homo sapiens.

XX W0200283874-A2.

XX 24-OCT-2002.

PF 10-Apr-2002; 2002WO-US008253.

XX 11-APR-2001; 2001US-0282850P.

PR 06-FEB-2002; 2002US-0354262P.

XX (UJJO) UNIV JOHNS HOPKINS.

XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;

DR WPI; 2003-093016/08.

XX P-PSDB; ABUS4457.

PT New purified human transmembrane protein, designated as tumor endothelial

PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,

PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or

PT psoriasis.

XX Disclosure; Page 223-225; 374pp; English.

XX The present invention relates to a novel method for the isolation of

XX endothelial cells (ECs), and the identification of genes expressed in

XX normal and tumour ECs. Tumour endothelial marker (TEM), normal

XX endothelial marker (NEM), and pan-endothelial marker (PEM) genes are

XX identified in human ECs. The human EC marker proteins and the

XX polynucleotide sequences encoding them are useful for detecting,

XX diagnosing or treating tumours as well as polycystic kidney disease,

XX diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also

XX useful for inhibiting neovascularization or tumour angiogenesis, for

XX inducing an immune response to tumour endothelial cells in a patient, or

XX for identifying candidate drugs for treating tumours. The present

XX sequence represents a human TEM or NEM gene of the invention

XX

XX Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;

XX Query Match 98.8%; Score 1090.8; DB 10; Length 5540;

XX Best Local Similarity 99.8%; Pred. No. 0;

XX Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 ATGGCCACGGCGAGGAGAGCCCTGCGCATGCGCTTCAGTGGCTCTCTTTGGCCACT 60
DB 144 ATGGCCACGGCGAGGAGAGCCCTGCGCATGCGCTTCAGTGGCTCTCTTTGGCCACT 203
QY 61 CTGGTCTCATCTGCGCCCGGCGAAGGGGGAACGAGAGAGATGGGGTCCAGCTCTGAC 120
DB 204 CTGGTCTCATCTGCGCCCGGCGAAGGGGGAACGAGAGAGATGGGGTCCAGCTCTGAC 263
QY 121 GGGGATTTGACCTGATCTTCAATTTTGGACAAATTCAGGAAGTGTGTCGACCACTGGAAT 180
DB 264 GGGGATTTGACCTGATCTTCAATTTTGGACAAATTCAGGAAGTGTGTCGACCACTGGAAT 323
QY 181 GAAATCTAATTAATTTTGGAAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAATG 240
DB 324 GAAATCTAATTAATTTTGGAAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAATG 383
QY 241 TCTTTTATTTGTTTTTCTCCACCGGAGAAACACTTAATGAAATGACAGAGACAGAA 300
DB 384 TCTTTTATTTGTTTTTCTCCACCGGAGAAACACTTAATGAAATGACAGAGACAGAA 443
QY 301 CAAATCCGTCAAGGCGCTAGAGAACTCCAGAAAGTTCTGCGAGAGAGACCTTACATG 360
DB 444 CAAATCCGTCAAGGCGCTAGAGAACTCCAGAAAGTTCTGCGAGAGAGACCTTACATG 503
QY 361 CATGAAGATTTTGAAGGCGCAGTGAAGATTTATTAAGAAACAGACAGGGTACAG 420
DB 504 CATGAAGATTTTGAAGGCGCAGTGAAGATTTATTAAGAAACAGACAGGGTACAG 563
QY 421 ACAGCCAGGCTCATCTTGTCTTGAATGAGAACTCCATGAAAGTCTCTTTTCTAT 480
DB 564 ACAGCCAGGCTCATCTTGTCTTGAATGAGAACTCCATGAAAGTCTCTTTTCTAT 623
QY 481 TCAGAGAGGAGGCTAATAGTCTGAGATCTTGGTGAATGTTTACTGTGTGTGTG 540
DB 624 TCAGAGAGGAGGCTAATAGTCTGAGATCTTGGTGAATGTTTACTGTGTGTGTG 683
QY 541 AAAGATTTCAATAGACACAGCTGCGCCGAGATTCGAGACAGTAAGATCATGTGTTCC 600
DB 684 AAAGATTTCAATAGACACAGCTGCGCCGAGATTCGAGACAGTAAGATCATGTGTTCC 743
QY 601 GTGAATGACGGCTTCAAGCTCTGCAAGGATCATCACTCAATTTTGAAGAGTCTG 660
DB 744 GTGAATGACGGCTTCAAGCTCTGCAAGGATCATCACTCAATTTTGAAGAGTCTG 803
QY 661 ATGGAATTTCTAGCAGCTGAACCATGACCATATGTGACAGGAAGTCAATTCAGTTGTC 720
DB 804 ATGGAATTTCTAGCAGCTGAACCATGACCATATGTGACAGGAAGTCAATTCAGTTGTC 863
QY 721 GTGAGAGAAACGGCTTCCGACATGCGCCGCAACGTGAGACAGGCTCTCTGACAGTTCAAG 780
DB 864 GTGAGAGAAACGGCTTCCGACATGCGCCGCAACGTGAGACAGGCTCTCTGACAGTTCAAG 923
QY 781 ATCAATGATCGGCTCACTCAATGAGAAAGCTTTTCTGTGAAAGCACTTATTTACTG 840
DB 924 ATCAATGATCGGCTCACTCAATGAGAAAGCTTTTCTGTGAAAGCACTTATTTACTG 983
QY 841 TGTCCAGCGCTTCTTAAAGAAAGTGGGATGAAAGCTGCACTCCAGGTCACATGAAC 900
DB 984 TGTCCAGCGCTTCTTAAAGAAAGTGGGATGAAAGCTGCACTCCAGGTCACATGAAC 1043
QY 901 GATGAGCTCTCTTTTATCTCAGTTCTGTCATCATCAACACACAGACTGTTTGAAGCT 960
DB 1044 GATGAGCTCTCTTTTATCTCAGTTCTGTCATCATCAACACACAGACTGTTTGAAGCT 1103
QY 961 TCCATCTGCGCATCGCGCTGCTGATCTGTCTCTGCTCTAGCCCTGCTCTCTG 1020
DB 1104 TCCATCTGCGCATCGCGCTGCTGATCTGTCTCTGCTCTAGCCCTGCTCTCTG 1163
QY 1021 TGGTTCGCGCCCTCTGCTGCACTGATATCAAGAGAGTCCCTCAACCCCTGCGAG 1080
DB 1164 TGGTTCGCGCCCTCTGCTGCACTGATATCAAGAGAGTCCCTCAACCCCTGCGAG 1223
```

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QY 1081 GAGAGTGAGAAAA 1094
DB 1224 GAGAGTGAGAGAA 1237

RESULT 6
ABX72003
ID ABX72003 standard; DNA; 5540 BP.
XX
AC ABX72003;
XX
DT 12-MAR-2003 (first entry)
XX
DE DNA encoding human tumour endothelial marker TEM 8.
XX
KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
KW Tumour endothelial marker; normal endothelial marker; PEM;
KW pan-endothelial marker; polycystic kidney disease; psoriasis;
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
KW neovascularization; immune response; cystostatic; antidiabetic; gene;
KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic; db.
XX
OS Homo sapiens.
XX
PN WO200283874-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US008253.
XX
PR 11-APR-2001; 2001US-0282850P.
XX
PR 06-FEB-2002; 2002US-0354262P.
XX
PA (UYPD ) UNIV JOHNS HOPKINS.
XX
PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
XX
DR WPI; 2003-093016/08.
XX
DR P-PSDB; ABUS4430.
XX
PT New purified human transmembrane protein, designated as tumor endothelial
PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
PT psoriasis.
XX
PS Disclosure; Page 117-120; 374pp; English.
XX
CC The present invention relates to a novel method for the isolation of
CC endothelial cells (ECs), and the identification of genes expressed in
CC normal and tumour ECs. Tumour endothelial marker (TEM), normal
CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
CC identified in human ECs. The human EC marker proteins and the
CC polynucleotide sequences encoding them are useful for detecting,
CC diagnosing or treating tumours as well as polycystic kidney disease,
CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
CC useful for inhibiting neovascularization or tumour angiogenesis, for
CC inducing an immune response to tumour endothelial cells in a patient, or
CC for identifying candidate drugs for treating tumours. The present
CC sequence represents a human TEM or NEM gene of the invention
XX
SQ Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
XX
Query Match 98.8%; Score 1090.8; DB 10; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGCCACGGCGAGGAGAGCCCTGCGCATGCGCTTCAGTGGCTCTCTTTGGCCACT 60
DB 144 ATGGCCACGGCGAGGAGAGCCCTGCGCATGCGCTTCAGTGGCTCTCTTTGGCCACT 203
QY 61 CTGGTCTCATCTGCGCCCGGCGAAGGGGGAACGAGAGAGATGGGGTCCAGCTCTGAC 120
DB 204 CTGGTCTCATCTGCGCCCGGCGAAGGGGGAACGAGAGAGATGGGGTCCAGCTCTGAC 263
```

Qy	121	GGCGGATTTGA	CTGTA	ACTTCA	TTTGGACA	AAATCAGGA	ATGTCG	GCAC	CTGGAA	180
Db	264	GGCGGATTTGA	CTGTACTT	CA	TTTGGACA	AAATCAGGA	ATGTCG	GCAC	CTGGAA	323
Qy	181	GAAATCTAT	CTTCTGTGGA	CAGTGG	CTCA	AAATTCAT	CAGCCCA	CAGTTG	GAGATG	240
Db	324	GAAATCTAT	CTTGTGTGGA	CA	GTTGGCTCA	AAATTCAT	CAGCCCA	CAGTTG	GAGATG	383
Qy	241	TCCTTTATG	TTTTCTCCA	CCGAGAA	CAACTT	ATGAA	CTGAC	GAAGA	CA	300
Db	384	TCCTTTATG	TTTTCTCCA	CCGAGAA	CAACTT	ATGAA	CTGAC	GAAGA	CA	443
Qy	301	CAATCCG	CTCAAGG	CTGAA	GAATCCAGA	AAGTCTG	CCAGAG	AGGACA	CTTA	360
Db	444	CAATTCG	CTCAAGG	CTGAA	GAATCCAGA	AAGTCTG	CCAGAG	AGGACA	CTTA	503
Qy	361	CATGAAG	ATTGAA	AGGSCAG	TGACAG	ATTTAT	TGAAA	CAGCA	AGGTAC	420
Db	504	CATGAAG	ATTGAA	AGGSCAG	TGACAG	ATTTAT	TGAAA	CAGCA	AGGTAC	563
Qy	421	ACAAGC	AGCTCAT	TGCTTTGA	CTGATG	AGAACTCC	ATGA	AGATCT	CTTTTCTAT	480
Db	564	ACAAGC	AGCTCAT	TGCTTTGA	CTGATG	AGAACTCC	ATGA	AGATCT	CTTTTCTAT	623
Qy	481	TCAGA	GAGGAGG	GCAT	AAGGCTG	GAGATCT	TGGTGC	AACTTGT	TACTG	540
Db	624	TCAGA	GAGGAGG	GCAT	AAGGCTG	GAGATCT	TGGTGC	AACTTGT	TACTG	683
Qy	541	AAAGATT	CAATG	AACA	CAGCTGG	CCGGAT	TGGGGA	CAGTAA	AGATCAT	600
Db	684	AAAGATT	CAATG	AACA	CAGCTGG	CCGGAT	TGGGGA	CAGTAA	AGATCAT	743
Qy	601	GTGA	ATGACGG	CTTCA	GCTCTG	CAAGG	CATATCC	CACTAA	TTTGA	660
Db	744	GTGA	ATGACGG	CTTCA	GCTCTG	CAAGG	CATATCC	CACTAA	TTTGA	803
Qy	661	ATCG	AAATTTCT	TA	GAGAGCTG	AAACCA	TCCATATG	TGAGAG	AGATCA	720
Db	804	ATCG	AAATTTCT	TA	GAGAGCTG	AAACCA	TCCATATG	TGAGAG	AGATCA	863
Qy	721	GTGA	GAGAA	ACGG	CTTCCGA	CATGCCG	CAACGTG	GA	CAGG	780
Db	864	GTGA	GAGAA	ACGG	CTTCCGA	CATGCCG	CAACGTG	GA	CAGG	923
Qy	781	ATCA	ATGACTCG	GTCA	CACTCA	TATAGA	AGCCCTTT	CTGTG	GAAGA	840
Db	924	ATCA	ATGACTCG	GTCA	CACTCA	TATAGA	AGCCCTTT	CTGTG	GAAGA	983
Qy	841	TGTC	CAGGGCC	CTATCT	TAA	AAGA	GTGG	AGTGA	AGCTG	900
Db	984	TGTC	CAGGGCC	CTATCT	TAA	AAGA	GTGG	AGTGA	AGCTG	1043
Qy	901	GATG	GCCTCT	CTTTAT	CTCCAG	TCTGT	CATCAT	CA	CCAC	960
Db	1044	GATG	GCCTCT	CTTTAT	CTCCAG	TCTGT	CATCAT	CA	CCAC	1103
Qy	961	TCAT	TCCTG	GCATG	GCCTGT	GTATCT	GTTCCT	GTCT	CTA	1020
Db	1104	TCAT	TCCTG	GCATG	GCCTGT	GTATCT	GTTCCT	GTCT	CTA	1163
Qy	1021	TGGT	CTG	GCCTCT	GTG	CTG	CACTG	ATAT	CA	1080
Db	1164	TGGT	CTG	GCCTCT	GTG	CTG	CACTG	ATAT	CA	1223
Qy	1081	GAG	AGTGA	GAAAA	1094					
Db	1224	GAG	AGTGA	GAAAA	1237					

XX	AC	ADR48215;
XX	DT	18-NOV-2004 (first entry)
XX	DE	Human tumour endothelial marker 8 precursor encoding cDNA SEQ:3.
XX	KM	pancreatic cancer-associated transcript; pancreatic cancer; human;
XX	KW	cytostatic; gene therapy; protein therapy;
XX	KW	tumour endothelial marker 8 precursor; TEM8; gene; ss.
OS	OS	Homo sapiens.
XX	FT	Key Location/Qualifiers
XX	FT	CDS 144..1838
XX	FT	/tag= a
XX	FT	/product= "tumour endothelial marker 8 precursor (TEM8)"
XX	PX	WO2004074510-A1.
PD	PD	02-SEP-2004.
XX	PF	18-FEB-2004; 2004MO-AU000194.
XX	PR	18-FEB-2003; 2003AU-00900747.
XX	PA	(GARV-) GARVAN INST MEDICAL RES.
PI	PI	Blankin A, Segara D, Henshall S, Sutherland R;
XX	DR	WPI: 2004-635591/61.
PT	PT	P-PSDB; ADR48216.
XX	CC	Detecting pancreatic cancer-associated transcript in a biological sample,
XX	CC	useful for diagnosing or treating the disease, comprises contacting the
XX	CC	sample with a polynucleotide that selectively hybridizes to a specific
XX	CC	sequence.
XX	PS	Claim 70; SEQ ID NO 3; 263bp; English.
XX	CC	The present invention describes a method for detecting a pancreatic
XX	CC	cancer-associated transcript in a biological sample. The method comprises
XX	CC	contacting the biological sample with a polynucleotide that selectively
XX	CC	hybridizes to a sequence at least 80% identical to a sequence as shown in
XX	CC	any one of Tables 3 to 25 in the specification or having the Genbank
XX	CC	Accession Number AF279145. Also described: (1) diagnosing pancreatic
XX	CC	cancer in a human or animal subject being tested, determining the
XX	CC	likelihood that a subject having a pancreatic cancer will survive, or
XX	CC	determining the suitability of a subject having a pancreatic cancer for
XX	CC	surgical resection therapy; (2) detecting a pancreatic cancer-associated
XX	CC	polypeptide in a biological sample; (3) determining the likelihood that a
XX	CC	subject having a pancreatic cancer will survive; and (4) monitoring the
XX	CC	efficacy of a therapeutic treatment of pancreatic cancer. A pancreatic
XX	CC	cancer-associated transcript has cytostatic activity, and can be used in
XX	CC	gene and protein therapy. A pancreatic cancer-associated transcript
XX	CC	polynucleotide, a vector comprising the polynucleotide, an isolated
XX	CC	polypeptide or an antibody that binds to the isolated polypeptide can be
XX	CC	used for diagnosing or prognosing pancreatic cancer or for preparing a
XX	CC	medicament for the treatment of pancreatic cancer. The prognostic or
XX	CC	diagnostic methods are useful for the early detection of pancreatic
XX	CC	cancer or its metastases, and for monitoring the progress of disease such
XX	CC	as during remission or following surgery or chemotherapy. The present
XX	CC	sequence encodes human tumour endothelial marker 8 precursor (TEM8),
XX	CC	which is used in the exemplification of the present invention.
XX	SO	Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
XX	Query Match	98.8%; Score 1090.8; DB 13; Length 5540;
XX	Best Local Similarity	99.8%; Pred. No. 0;
XX	Matches 1092; Conservative	0; Mismatches 2; Indels 0; Gaps 0

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1 ATGGCAGCGGCGAGCGAGGCCCTTGGCAATGCCTTCATTGGCCACT
|||||

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Db 144 ATGGCCACGGCGGAGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTTGGCCACT 203
Oy 61 CTGGTCTCATCTGCGCCGGGACGAAGGAGGAGATGGGGGTCCAGCTGCTAC 120
Db 204 CTGGTCTCATCTGCGCCGGGACGAAGGAGGAGATGGGGGTCCAGCTGCTAC 263
Oy 121 GGGGATTTGACCTGACTTCAATTTTGAACAAATCAGAAAGTGTGTGCAACAATGGAAAT 180
Db 264 GCGGATTTGACCTGACTTCAATTTTGAACAAATCAGAAAGTGTGTGCAACAATGGAAAT 323
Oy 181 GAAATCTATTAATTTTGTGAAACAGTTGGTCAAAATTCATGACCCCAAGTTGAAAG 240
Db 324 GAAATCTATTAATTTTGTGAAACAGTTGGTCAAAATTCATGACCCCAAGTTGAAAG 383
Oy 241 TCCCTTATTTGTTTCTCCACCCGAGGAACAACTTAATGAAAATGACAGAAAGAGAA 300
Db 384 TCCCTTATTTGTTTCTCCACCCGAGGAACAACTTAATGAAAATGACAGAAAGAGAA 443
Oy 301 CAAATCCGTCAGAGGCTAGAAAGACTCCAGAAAATTCTGCGAGAGAGAACACTTACATG 360
Db 444 CAAATCCGTCAGAGGCTAGAAAGACTCCAGAAAATTCTGCGAGAGAGAACACTTACATG 503
Oy 361 CATGAAGATTTGAAAGGCGCAATGAGCAATTTATTAAGAAAACGAAGAAGGTCAAG 420
Db 504 CATGAAGATTTGAAAGGCGCAATGAGCAATTTATTAAGAAAACGAAGAAGGTCAAG 563
Oy 421 ACAGCAGCGTCATCATTTGCTTGAATGAGAACTCCATGAAGATCTCTTTTCTAT 480
Db 564 ACAGCAGCGTCATCATTTGCTTGAATGAGAACTCCATGAAGATCTCTTTTCTAT 623
Oy 481 TCAGAGAGGAGGCTAATAGTCTGAGATCTTGTGCAATTTGTTTACTGTGTGTGTG 540
Db 624 TCAGAGAGGAGGCTAATAGTCTGAGATCTTGTGCAATTTGTTTACTGTGTGTGTG 683
Oy 541 AAAAGATTTCAATGAGACACAGCTGCGCCGGAATGGGACAGTGAAGATCATGTGTTCCC 600
Db 684 AAAAGATTTCAATGAGACACAGCTGCGCCGGAATGGGACAGTGAAGATCATGTGTTCCC 743
Oy 601 GTGAATGACGGCTTTGAGGCTTGCAAGGATCATCACTCAATTTTGAAGAAGTCTGCG 660
Db 744 GTGAATGACGGCTTTGAGGCTTGCAAGGATCATCACTCAATTTTGAAGAAGTCTGCG 803
Oy 661 ATCGAATTTCTAGCAGCTGAAACCATCAATATGTGCAAGAGAGTCAATTTCAAGTTGTC 720
Db 804 ATCGAATTTCTAGCAGCTGAAACCATCAATATGTGCAAGAGAGTCAATTTCAAGTTGTC 863
Oy 721 GTGAGAGGAAACGGCTTCCGACATGCGCCGCAAGTGAAGAGGTCTCTGCAAGCTTCAAG 780
Db 864 GTGAGAGGAAACGGCTTCCGACATGCGCCGCAAGTGAAGAGGTCTCTGCAAGCTTCAAG 923
Oy 781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTTCTGTGGAAGACCTTATTTACTG 840
Db 924 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTTCTGTGGAAGATTTATTTACTG 983
Oy 841 TGTCCAGCGCTATCTTAAAGAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAAC 900
Db 984 TGTCCAGCGCTATCTTAAAGAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAAC 1043
Oy 901 GATGGCTCTCTTTTATCTTCAATTTCTGATCATATCAACCAACCAACATGTTTGACGCT 960
Db 1044 GATGGCTCTCTTTTATCTTCAATTTCTGATCATATCAACCAACCAACATGTTTGACGCT 1103
Oy 961 TCCATCTGACCAATGCGCCCTGCTGATCTGTTCTGTGCTCTTACGCTGCTCTCTCTG 1020
Db 1104 TCCATCTGACCAATGCGCCCTGCTGATCTGTTCTGTGCTCTTACGCTGCTCTCTCTG 1163
Oy 1021 TGGTCTTGCCCTCTGCTGCACTGATGATTAATCAGAGAGTCCCTCAACCCCTGCGAG 1080
Db 1164 TGGTCTTGCCCTCTGCTGCACTGATGATTAATCAGAGAGTCCCTCAACCCCTGCGAG 1223
Oy 1081 GAGAGTGAGGAAAA 1094
Db 1224 GAGAGTGAGGAAAA 1237

RESULT 8
AD270742
ID AD270742 standard; cDNA; 5540 BP.
XX
AC AD270742;
XX
AC AD270742;
XX
DE 14-JUL-2005 (first entry)
XX
DE Tumor endothelial marker 8 precursor (Tem8) cDNA.
XX
KW osteopathic; antiarthritic; gene expression; differentiation;
KW transcription; bone disease; osteoarthritis; antiarthritic; osteopathic;
KW musculoskeletal disease; tumor endothelial marker 8 precursor; Tem8; gene;
KW ss.
XX
OS Homo sapiens.
XX
PN WO2005038022-A1.
XX
PN 28-APR-2005.
XX
PF 20-OCT-2004; 2004WO-JP015879.
XX
XX 20-OCT-2003; 2003JP-00359172.
XX
PA (TEIJ-) TEIJIN PHARMA LTD.
XX
PA (KOMORI) KOMORI T.
XX
PI Komori T, Kanatani N, Yoshida CA, Zama A, Kobayashi S, Yamana K;
XX
DR WPI; 2005-322866/33.
XX
DR P-PSDB; AD270743.
XX
PT Acquiring chondrogenic differentiation control related gene Runx2/Cbfa1,
PT by forcibly expressing transcriptional factor related to pathological
PT condition in cell strain lacking transcriptional factor and screening for
PT gene.
XX
XX
PS Claim 15; SEQ ID NO 27; 357bp; Japanese.
XX
CC The invention describes acquiring (M1) a pathological condition related
CC gene, preferably chondrogenic differentiation control related gene
CC Runx2/Cbfa1, comprising forcibly expressing a transcriptional factor
CC related to pathological condition, preferably Runx2/Cbfa1 in a cell
CC strain or a primary culture cell lacking the transcriptional factor, and
CC screening for the gene whose expression is induced or suppressed (M1) is
CC useful for acquiring a pathological condition related gene, preferably
CC chondrogenic differentiation control related gene Runx2/Cbfa1.
CC Polynucleotides detailed in the invention are useful for screening a
CC preventive and/or therapeutic agent of bone and/or articular disease such
CC as osteoarthritis. This sequence encodes tumor endothelial marker 8
CC precursor (Tem8) associated with isolation of a pathological condition
CC related gene.
XX
SQ Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
XX
Query Match 98.8%; Score 1090.8; DB 14; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 ATGGCCACGGCGGAGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTTGGCCACT 60
Db 144 ATGGCCACGGCGGAGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTTGGCCACT 203
Oy 61 CTGGTCTCATCTGCGCCGGGACGAAGGAGGAGATGGGGGTCCAGCTGCTAC 120
Db 204 CTGGTCTCATCTGCGCCGGGACGAAGGAGGAGATGGGGGTCCAGCTGCTAC 263
Oy 121 GGGGATTTGACCTGACTTCAATTTTGAACAAATCAGAAAGTGTGTGCAACAATGGAAAT 180
Db 264 GCGGATTTGACCTGACTTCAATTTTGAACAAATCAGAAAGTGTGTGCAACAATGGAAAT 323

QY 181 GAAATCTATTACTTTGGGAAAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGAAATG 240
 DB 324 GAAATCTATTACTTTGGGAAAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGAAATG 383
 QY 241 TCCCTTATTGTTTTCTCCACCCGAGAAACAACCTTAATGAAATGACAGAAAGAA 300
 DB 384 TCCCTTATTGTTTTCTCCACCCGAGAAACAACCTTAATGAAATGACAGAAAGAA 443
 QY 301 CAAATCCGTCGAAGCCCTGAGAAAGCTCCAGAAAGTTCTGCGAGAGAGACATTTACATG 360
 DB 444 CAAATCCGTCGAAGCCCTGAGAAAGCTCCAGAAAGTTCTGCGAGAGAGACATTTACATG 503
 QY 361 CATGAAGGATTTGAAAGGGCCAGTGAAGCAGATTTATATGAAAGAAACAAGGTTACAG 420
 DB 504 CATGAAGGATTTGAAAGGGCCAGTGAAGCAGATTTATATGAAAGAAACAAGGTTACAG 563
 QY 421 ACAGCCAGCTCATCATTTGCTTGAATGATGAGAACTCCATGAAAGATCTCTTTTCTAT 480
 DB 564 ACAGCCAGCTCATCATTTGCTTGAATGATGAGAACTCCATGAAAGATCTCTTTTCTAT 623
 QY 481 TCAGAGAGGAGGCTAATAGCTCTCGAGATCTTGTCGAATTTGTTTACTGTGTGGTGTG 540
 DB 624 TCAGAGAGGAGGCTAATAGCTCTCGAGATCTTGTCGAATTTGTTTACTGTGTGGTGTG 683
 QY 541 AAAGATTTCAATGAGACAGAGCTGGCCCGGATTTGCGGACAGTAAAGATCAATGTTTCCC 600
 DB 684 AAAGATTTCAATGAGACAGAGCTGGCCCGGATTTGCGGACAGTAAAGATCAATGTTTCCC 743
 QY 601 GTGAATGACGGCTTTCAAGCTCTGCAAGGATCATCATCAATTTTGAAGAAGTCTGCG 660
 DB 744 GTGAATGACGGCTTTCAAGCTCTGCAAGGATCATCATCAATTTTGAAGAAGTCTGCG 803
 QY 661 ATCGAATTTAGACAGTGAACCATCCATATGTGCAAGAGATCATTTCAAGTTGTC 720
 DB 804 ATCGAATTTAGACAGTGAACCATCCATATGTGCAAGAGATCATTTCAAGTTGTC 863
 QY 721 GTGAGAGGAAACGGCTTCCGACATGCCCCGGAAGCTGGAACAGGGTCTCTGCAAGCTTCAAG 780
 DB 864 GTGAGAGGAAACGGCTTCCGACATGCCCCGGAAGCTGGAACAGGGTCTCTGCAAGCTTCAAG 923
 QY 781 ATCAATGACTCGGTCACTCAATGAGAAACCTTTTCTGTGAAAGACACTTAATTTACTG 840
 DB 924 ATCAATGACTCGGTCACTCAATGAGAAACCTTTTCTGTGAAAGACTTAATTTACTG 983
 QY 841 TGTCCAGCGGCTTATCTTAAAGAAAGTTGGAGTGAAGCTGCACTCCAGGTCAAGTGAAC 900
 DB 984 TGTCCAGCGGCTTATCTTAAAGAAAGTTGGAGTGAAGCTGCACTCCAGGTCAAGTGAAC 1043
 QY 901 GATGGCTCTCTTTTATCTGCAATGCTGATCATCATCAACCAACAACCTGTTGAGAGGT 960
 DB 1044 GATGGCTCTCTTTTATCTGCAATGCTGATCATCATCAACCAACAACCTGTTGAGAGGT 1103
 QY 961 TCCATCTCGGCAATCGGCTGCTGATCTGTTCTGCTGCTGAGCCCTGAGCTCTCTCTG 1020
 DB 1104 TCCATCTCGGCAATCGGCTGCTGATCTGTTCTGCTGCTGAGCCCTGAGCTCTCTCTG 1163
 QY 1021 TGGTCTTGCCCTCTCTGCTGCACTGTGATTAATCAAGAGAGTCCCTCCACCCCTGCGAG 1080
 DB 1164 TGGTCTTGCCCTCTCTGCTGCACTGTGATTAATCAAGAGAGTCCCTCCACCCCTGCGAG 1223
 QY 1081 GAGAGTGAAGGAAA 1094
 DB 1224 GAGAGTGAAGGAAA 1237

RESULT 9
 ID AEA29804 standard; DNA; 5540 BP.
 AC AEA29804;
 XX
 DT 11-AUG-2005 (first entry)

XX DE DNA encoding a human tumor endothelial marker 8 protein.
 XX KW synergistic induction; tumor-associated antigen; vaccine;
 XX tumor endothelial marker 8; immune stimulation; cytostatic; gene; da.
 XX OS Homo sapiens.
 XX FT Key Location/Qualifiers
 FT CDS 144..1838
 FT /tag= a
 FT /product= "Human tumor endothelial marker 8 protein"
 XX
 PN MO2005048943-A2.
 XX
 PD 02-JUN-2005.
 XX
 PF 15-NOV-2004; 2004WO-US038022.
 XX
 PR 13-NOV-2003; 2003US-0519498P.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX
 PI Gregor P. Houghton A. Concetti A. Venanzi FM;
 XX
 DR WPI: 2005-395941/40.
 DR P-PSDB; AEA29805.
 XX
 PT New composition useful as a vaccine for inducing anti-tumor immune
 PT response and having a vector with a nucleic acid sequence encoding a
 PT tumor-associated antigen and/or encoding a tumor endothelial marker 8.
 XX
 PS Claim 6; SEQ ID NO 4; 54bp; English.
 XX
 CC The invention relates to novel compositions and methods for the
 CC synergistic induction of antitumor immunity. The invention discloses a
 CC synergistic effect between vaccines encoding a tumor-associated antigen
 CC and vaccines encoding a tumor endothelial marker 8 (TEM8). The invention
 CC further includes a method of inducing anti-tumor immune responses in an
 CC individual, comprising administering to the individual a composition
 CC cited above or dendritic cells comprising a nucleic acid or protein
 CC selected from the composition cited above and proteins encoded by the
 CC vectors of the composition. The methods and compositions of the present
 CC invention are useful in the field of anti-tumor immunity, in particular
 CC for inducing an anti-tumor immune response by targeting both tumor-
 CC associated antigens and tumor endothelia, hence have cytostatic activity.
 CC This polynucleotide sequence represents the DNA encoding a human tumor
 CC endothelial marker 8 protein of the invention.
 XX
 SQ Sequence 5540 BP; 1601 A; 1306 C; 1187 G; 1446 T; 0 U; 0 Other;
 Query Match 98.8%; Score 1090.8; DB 14; Length 5540;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGGCCACGGCGGAGGAGAGCCCTCGGATGAGGCTTCAGAGGCTCTCTTTGGCCACT 60
 DB 144 ATGGCCACGGCGGAGGAGAGCCCTCGGATGAGGCTTCAGAGGCTCTCTTTGGCCACT 203
 QY 61 CTGGTCTCATCTGCGCCGCGGCAAGGGGACGCGAGGAGATGGGGTCCAGCTGCTAC 120
 DB 204 CTGGTCTCATCTGCGCCCGGCAAGGGGACGCGAGGAGATGGGGGTCCAGCTGCTAC 263
 QY 121 GCGGATTTGACCTGTACTTCAATTTTGAACAATTCAGAAAGTGTGTCACCACTGGAAT 180
 DB 264 GCGGATTTGACCTGTACTTCAATTTTGAACAATTCAGAAAGTGTGTCACCACTGGAAT 323
 QY 181 GAAATCTATTACTTTGGGAAAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGAAATG 240
 DB 324 GAAATCTATTACTTTGGGAAAGTTGGCTCACAAATTCATCAGCCCAAGTTGAGAAATG 383
 QY 241 TCCCTTATTGTTTTCTCCACCCGAGAAACAACCTTAATGAAATGACAGAAAGAA 300

D 384 TCCTTATTGTTTTCACCCGAGAACACCTTAATGAACTGACAGAGACAGAGAA 443
Q 301 CAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 360
D 444 CAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 503
Q 361 CATGAAGATTGTAAGAGGCGCAGTAGACAGATTTATTAATGAAACAGACAGAGGTAACAG 420
D 504 CATGAAGATTGTAAGAGGCGCAGTAGACAGATTTATTAATGAAACAGACAGAGGTAACAG 563
Q 421 ACAGCCAGGCTCATCTTGTCTGACTGATGAGAACTCCAGAAATCTCTTTTCTAT 480
D 564 ACAGCCAGGCTCATCTTGTCTGACTGATGAGAACTCCAGAAATCTCTTTTCTAT 623
Q 481 TCAGAGAGGAGGCTAATAGAGTCTCGAGATCTTGAGTCAATGTTTACTGTGTGTG 540
D 624 TCAGAGAGGAGGCTAATAGAGTCTCGAGATCTTGAGTCAATGTTTACTGTGTGTG 683
Q 541 AAAGATTTCATAGACACAGCTGAGCCCGGATTGCGAGACGTAAAGATCATGTGTTCC 600
D 684 AAAGATTTCATAGACACAGCTGAGCCCGGATTGCGAGACGTAAAGATCATGTGTTCC 743
Q 601 GTGAATGAGCGGCTTCAAGGCTCTGCAAGGATATCTCACTCAATTTTGAAGAGTCTTC 660
D 744 GTGAATGAGCGGCTTCAAGGCTCTGCAAGGATATCTCACTCAATTTTGAAGAGTCTTC 803
Q 661 ATCGAATTTCTAGCAGCTGAAACCATCATATGTGCAAGAGTCAATTTCAAGTTGTC 720
D 804 ATCGAATTTCTAGCAGCTGAAACCATCATATGTGCAAGAGTCAATTTCAAGTTGTC 863
Q 721 GTGAGAGAAACGGCTTCCGACATGCCCCGACATGAGACAGGCTCTGCAAGTTCAAG 780
D 864 GTGAGAGAAACGGCTTCCGACATGCCCCGACATGAGACAGGCTCTGCAAGTTCAAG 923
Q 781 ATCGAATTTCTAGCAGCTGAAACCATCATATGTGCAAGAGTCAATTTCAAGTTGTC 840
D 924 ATCGAATTTCTAGCAGCTGAAACCATCATATGTGCAAGAGTCAATTTCAAGTTGTC 983
Q 841 TGTCAGAGCCTTCTTAAAGAGTTGGCATGAAAGCTGCACTCCAGGTGACATGAAC 900
D 984 TGTCAGAGCCTTCTTAAAGAGTTGGCATGAAAGCTGCACTCCAGGTGACATGAAC 1043
Q 901 GATGCGCTCTCTTTATCTTCAGATTCTGTCATATGACACACACAGACTGTTTCAAGGT 960
D 1044 GATGCGCTCTCTTTATCTTCAGATTCTGTCATATGACACACACAGACTGTTTCAAGGT 1103
Q 961 TCATCTCTGCGCATGCGCCTGCTGATCTCTTCTGCTCTGAGCCTGCTCTCTCTG 1020
D 1104 TCATCTCTGCGCATGCGCCTGCTGATCTCTTCTGCTCTGAGCCTGCTCTCTCTG 1163
Q 1021 TGGTTCGAGCCCTCTGCTGCACTGTGATATGAGAGGTCCTCCACCCCTGCGAG 1080
D 1164 TGGTTCGAGCCCTCTGCTGCACTGTGATATGAGAGGTCCTCCACCCCTGCGAG 1223
Q 1081 GAGAGTGAGGAAAA 1094
D 1224 GAGAGTGAGGAAAA 1237
RESULT 10
AAD05303
ID AAD05303 standard; cDNA; 2447 BP.
XX
AC AAD05303;
XX
DT 17-JUL-2001 (first entry)
XX
DE Human secreted protein-encoding gene 4 cDNA clone HMLFR02, SEQ ID NO:14.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;

KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiogenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder; infection; wound healing; vulnerability; cell culture;
KW chemotaxis; food additive; gene therapy; binding partner identification;
KW chromosome 19; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 140..1351
FT /tag= a
FT /product= "Human secreted protein"
FT sig_peptide 140..220
FT /tag= b
FT mat_peptide 221..1348
FT /tag= c
FT /product= "Mature human secreted protein"
XX
PN MO200134626-A1.
XX
PD 17-MAY-2001.
XX
PF 01-NOV-2000; 2000MO-US030045.
XX
PR 05-NOV-1999; 99US-0163581P.
XX 30-JUN-2000; 2000US-0215133P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Komatsoulis GA, Moore PA, Birse CE, Ni J,
PI MPI: 2001-308778/32.
XX P-PSDB; AAE01439.
DR
DR New nucleic acid molecules encoding 28 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
PS Claim 1; Page 425-426; 562pp; English.
XX
XX AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE01436-AAE01513 represent the proteins they encode.
CC AAB01514-AAE01544 represent human secreted protein fragments or variants.
CC The genes and their secreted proteins are useful for preventing, treating
CC or ameliorating medical conditions, e.g., by protein or gene therapy.
CC Pathological conditions can be diagnosed by determining the amount of the
CC new protein in a sample or by determining the presence of mutations in
CC the new genes. Specific uses are described for each of the 28 genes,
CC based on the tissues in which they are most highly expressed, and include
CC developing products for the diagnosis or treatment of proliferative
CC disorders, cancer, tumours, foetal and developmental abnormalities,
CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
CC pregnancy-related disorders, endocrine disorders, and infections. The
CC proteins can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues, to identify their cognate ligands or binding
CC partners, and in chemotaxis, and can be used as a food additive or a
CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
CC present sequence represents a human secreted protein-encoding cDNA of the
CC invention
XX
SQ Sequence 2447 BP; 673 A; 562 C; 587 G; 625 T; 0 U; 0 Other;

AAE01514-AAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 28 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of the invention

Sequence 2086 BP; 544 A; 491 C; 538 G; 501 T; 0 U; 12 Other;

Query Match 98.7%; Score 1089.4; DB 4; Length 2086;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 1090; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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QY 1 ATGCGCACCGCGGAGCGGAGAGCCCTCGGATCGGCTTCAGTGGCTCTTTGGCCACT 60
DB 166 ATGCGCACCGCGGAGCGGAGAGCCCTCGGATCGGCTTCAGTGGCTCTTTGGCCACT 225
QY 61 CTGGTGTCTATCTGCGCGCGGGAAGGAGGAGATGGGGGTCCAGGCTGTAC 120
DB 226 CTGGTGTCTATCTGCGCGCGGGAAGGAGGAGATGGGGGTCCAGGCTGTAC 285
QY 121 GGGGGAATTTGACCTGTACTTTCATTTTGGACAAATCAGAAAGTGTGTCACCACTGGAAT 180
DB 286 GGGGGAATTTGACCTGTACTTTCATTTTGGACAAATCAGAAAGTGTGTCACCACTGGAAT 345
QY 181 GAAATCTATTAATCTTTGTGGAACAGTTGGCTCACAATTTCAAGCCCAAGTTGAGAAAG 240
DB 346 GAAATCTATTAATCTTTGTGGAACAGTTGGCTCACAATTTCAAGCCCAAGTTGAGAAAG 405
QY 241 TCCTTATTTGTTTTCACCGGAGGACAACTTATATGAAATGACAGAGACAGAGA 300
DB 406 TCCTTATTTGTTTTCACCGGAGGACAACTTATATGAAATGACAGAGACAGAGA 465
QY 301 CAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCGCAGAGAGACACTTACATG 360
DB 466 CAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCGCAGAGAGACACTTACATG 525
QY 361 CATGAAGATTTGAAAAGGCGCAGTGAACAGATTATTTAGAAAACGACAGGGTACAG 420
DB 526 CATGAAGATTTGAAAAGGCGCAGTGAACAGATTATTTAGAAAACGACAGGGTACAG 585
QY 421 ACAGCAGGTCATCATTTGCTTGAATGAGAACTCATGAAATGCTCTTTTCTAT 480
DB 586 ACAGCAGGTCATCATTTGCTTGAATGAGAACTCATGAAATGCTCTTTTCTAT 645
QY 481 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCATTTTACTGTGTGTGTG 540
DB 646 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCATTTTACTGTGTGTGTG 705
QY 541 AAAGATTTCAATAGACACAGCTGGCCGGATTCGGACAGTAAGATCATGTGTTCCC 600
DB 706 AAAGATTTCAATAGACACAGCTGGCCGGATTCGGACAGTAAGATCATGTGTTCCC 765

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QY 601 GTGAATGACGGGCTTTCAGGCTCTGCAAGGACATCATCTCAATTTTGAAAGATCCTGC 660
DB 766 GTGAATGACGGGCTTTCAGGCTCTGCAAGGACATCATCTCAATTTTGAAAGATCCTGC 825
QY 661 ATCGAAATTTTACGACGCTGGAACCATCCATATGTGACAGAGAGTCAATTTCAAGTTGTC 720
DB 826 ATCGAAATTTTACGACGCTGGAACCATCCATATGTGACAGAGAGTCAATTTCAAGTTGTC 885
QY 721 GTGAGAGGAAACGGCTTCGACATGCGCGCAACGTGACAGGGTCTCTGACGTTCAAG 780
DB 886 GTGAGAGGAAACGGCTTCGACATGCGCGCAACGTGACAGGGTCTCTGACGTTCAAG 945
QY 781 ATCAATGACTCGGTGACACTCAATGAGAGCCCTTTCTGTGGAAGACACTTATTTACTG 840
DB 946 ATCAATGACTCGGTGACACTCAATGAGAGCCCTTTCTGTGGAAGATCTTATTTACTG 1005
QY 841 TGTCCAGGCGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCATCGAGTCAAGTCAAG 900
DB 1006 TGTCCAGGCGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCATCGAGTCAAGTCAAG 1065
QY 901 GATGAGCTCTCTTTATCTGCAATGTCATCATCACACACACACTGTCTGACGCT 960
DB 1066 GATGAGCTCTCTTTATCTGCAATGTCATCATCACACACACTGTCTGACGCT 1125
QY 961 TCCATCTGAGCCATGCGCCCTGCTGATCTGTTCTGCTCTTACGCCCTGCTCTCTG 1020
DB 1126 TCCATCTGAGCCATGCGCCCTGCTGATCTGTTCTGCTCTTACGCCCTGCTCTCTG 1185
QY 1021 TGTGTTGCGCCCTCTGCTGCACTGTGATTTCAAGAGAGTCCCTCCACCCCTGCGAG 1080
DB 1186 TGTGTTGCGCCCTCTGCTGCACTGTGATTTCAAGAGAGTCCCTCCACCCCTGCGAG 1245
QY 1081 GAGAGTGAAGAAATTA 1097
DB 1246 GAGAGTGAAGTAACTGA 1262

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RESULT 12

AD100549
AD100549 standard; DNA; 1674 BP.

AC AD100549;

DT 22-APR-2004 (first entry)

DE Human TANGO 197 Ig fusion mutated DNA - plasmid p0610.

KW fusion; von Willebrand factor A-like domain; vWF; antibacterial;

KW cutaneous; inhalation anthrax; human; TANGO 197 Ig fusion; mutant;

KW plasmid p0610; ds; gene.

OS Homo sapiens.

OS Synthetic.

PN US2003144193-A1.

PD 31-JUL-2003.

PF 24-JUL-2002; 2002US-00201292.

PR 20-DEC-2001; 2001US-00038307.

PA (ROTT/) ROTTMAN J B.

PA (OKER/) O'KEEFE T L.

PA (OZKA/) OZKAYNAK E.

PA (HEAL/) HEALEY J J.

PI Rotman JB, O'keefe TL, Ozkaynak E, Healey JJ;

DR WPI; 2003-720708/68.

DR P-PSDB; AD100550.

PT New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or
PT ameliorating symptoms of anthrax comprises a von Willebrand factor A-like
PT domain (vWF) amino acid sequence and an amino acid sequence heterologous
PT to the vWF.

XX Example; SEQ ID NO 17; 86bp; English.

CC The invention relates to a novel fusion polypeptide comprising a von
CC Willebrand factor A-like domain (vWF) amino acid sequence and an amino
CC acid sequence heterologous to the vWF. The polypeptide of the invention
CC demonstrates antibacterial activities whilst the composition and method
CC may be useful in preventing or ameliorating the symptoms of cutaneous
CC and/or inhalation anthrax. The current sequence is that of the human
CC TANGO 197 Ig mutated fusion DNA of the invention.

XX Sequence 1674 BP; 433 A; 461 C; 424 G; 356 T; 0 U; 0 Other;

Query Match 87.0%; Score 960.8; DB 10; Length 1674;
Best Local Similarity 99.8%; Pred. No. 4,4e-284;
Matches 962; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCACGGCGGAGCGGAGAGCCCTCGGATCGGCTTCAGTGGCTCTTTGGCCACT 60
DB 13 ATGGCCACGGCGGAGCGGAGAGCCCTCGGATCGGCTTCAGTGGCTCTTTGGCCACT 72
QY 61 CTGCTGCTCATCTGCGCGCGGCAAGGGGAGCGCAGGAGAGATGGGGTCCAGCTGTGAC 120
DB 73 CTGCTGCTCATCTGCGCGCGGCAAGGGGAGCGCAGGAGAGATGGGGTCCAGCTGTGAC 132
QY 121 GGGGAGATTGACCTGTACTCTATTTTGGACAAATCAGGAAGTGTGCGACCACTGGAAT 180
DB 133 GGGGAGATTGACCTGTACTCTATTTTGGACAAATCAGGAAGTGTGCGACCACTGGAAT 192
QY 181 GAAATCTATTACTTGTGAAACAGTTGGCTCACAAATTCACAGCCCAAGTTGAGATG 240
DB 193 GAAATCTATTACTTGTGAAACAGTTGGCTCACAAATTCACAGCCCAAGTTGAGATG 252
QY 241 TCCCTTATTTGTTTCTCCACCCGAGAAACAACCTTATATGAAACAGACAAAGGTAAG 300
DB 253 TCCCTTATTTGTTTCTCCACCCGAGAAACAACCTTATATGAAACAGACAAAGGTAAG 312
QY 301 CAATCCGTCAGGCGCTAGAAAGAACTCCAGAAAGTTCTGCGAGGAGAGACCTTACATG 360
DB 313 CAATCCGTCAGGCGCTAGAAAGAACTCCAGAAAGTTCTGCGAGGAGAGACCTTACATG 372
QY 361 CATGAAGATTGTAAGAGGCGCAGTGAACAGATTATTATGAAACAGACAAAGGTAAG 420
DB 373 CATGAAGATTGTAAGAGGCGCAGTGAACAGATTATTATGAAACAGACAAAGGTAAG 432
QY 421 ACAGCCAGCGTCATCTGTTGATGATGAGAACTCCATGAAGATCTTTTCTTAT 480
DB 433 ACAGCCAGCGTCATCTGTTGATGATGAGAACTCCATGAAGATCTTTTCTTAT 492
QY 481 TCAGAGGAGGAGGTATAGGTCTCGAGATCTTGATGATGATGATGATGATGATGATG 540
DB 493 TCAGAGGAGGAGGTATAGGTCTCGAGATCTTGATGATGATGATGATGATGATGATG 552
QY 541 AAGATTTCATGAGACACAGCTGGCCCGATGCGGACAGTAAGATCAATGTTTCCC 600
DB 553 AAGATTTCATGAGACACAGCTGGCCCGATGCGGACAGTAAGATCAATGTTTCCC 612
QY 601 GTGAATACGGGCTTTCAGGCTTCGACAGGATTCATCACTCAATTTGAAAGAGTCTTGC 660
DB 613 GTGAATACGGGCTTTCAGGCTTCGACAGGATTCATCACTCAATTTGAAAGAGTCTTGC 672
QY 661 ATGAAATTTCTAGACGTGAACCATCCACCTATATGAGAGAGATGATTTCAAGTTGTC 720
DB 673 ATGAAATTTCTAGACGTGAACCATCCACCTATATGAGAGAGATGATTTCAAGTTGTC 732
QY 721 GTGAGAGAAACGGCTTCCGACATGCCGCAACGTGACAGAGGATCTCTGACGTTCAAG 780
DB 733 GTGAGAGAAACGGCTTCCGACATGCCGCAACGTGACAGAGGATCTCTGACGTTCAAG 792

QY 781 ATCAATGATCGGTGCACACTCAATGAGAAAGCCCTTCTGTGGAGACACTTATTACTG 840
DB 793 ATCAATGATCGGTGCACACTCAATGAGAAAGCCCTTCTGTGGAGACACTTATTACTG 852
QY 841 TGTCCAGCGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAC 900
DB 853 TGTCCAGCGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAC 912
QY 901 GATGCGCTCTCTTTTATCTTCACATTTCTGTCAATCATACACACACACACTGTTGACGGT 960
DB 913 GATGCGCTCTCTTTTATCTTCACATTTCTGTCAATCATACACACACACACTGTTGACGGT 972
QY 961 TCCA 964
DB 973 CCGA 976

RESULT 13

ADM64575
ID ADM64575 standard; DNA; 1674 BP.

XX ADM64575;

XX 03-JUN-2004 (first entry)

XX Mouse TANGO197-immunoglobulin (Ig) fusion protein DNA.

XX antibacterial; gene therapy;

XX von Willebrand factor A-like domain amino acid sequence;

XX vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;

XX inhalation anthrax; mouse; TANGO197; immunoglobulin; Ig; fusion protein;

XX gene; ds.

XX Mus sp.

XX Synthetic.

XX US2003134786-A1.

XX 17-JUL-2003.

XX 20-DEC-2001; 2001US-00038307.

XX 20-DEC-2001; 2001US-00038307.

XX (ROTT/) ROTTMAN J B.

XX (OKEE/) O'KEEFE T L.

XX (OZKA/) OZKAYNAK E.

XX (HEAL/) HEALEY J J.

XX Rottman JB, O'Keefe TL, Ozkaynak E, Healey JJ;

XX WPI; 2003-829643/77.

XX P-PSDB; ADM64576.

XX New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or

XX ameliorating symptoms of anthrax comprises a von Willebrand factor A-like

XX domain (vWF) amino acid sequence and an amino acid sequence heterologous

XX to the vWF.

XX Example; SEQ ID NO 17; 64bp; English.

XX The invention describes a fusion polypeptide comprising a von Willebrand

XX factor A-like domain (vWF) amino acid sequence and an amino acid sequence

XX heterologous to the vWF. Also described are: a method of preventing or

Query Match 87.0%; Score 960.8; DB 11; Length 1674;
 Best Local Similarity 99.8%; Pred. No. 4.4e-284;
 Matches 962; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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1  ATGGCCACGGCGGAGAGAGCCCTCGGCATCGGCTTCAGTGAGCTCTCTTTGGCCACT 60
13  ATGGCCACGGCGGAGAGAGCCCTCGGCATCGGCTTCAGTGAGCTCTCTTTGGCCACT 72
61  CTGGGCTCATCTGCGCCGGGCAAGGGGACGAGGAGAGATGGGGGTCCACCTGCTAC 120
73  CTGGGCTCATCTGCGCCGGGCAAGGGGACGAGGAGAGATGGGGGTCCACCTGCTAC 132
121  GCGGATTTGACCTGACTTCAATTTTGGCAAAATCAGAAAGTGCTGTGACCACTGGAA 180
133  GCGGATTTGACCTGACTTCAATTTTGGCAAAATCAGAAAGTGCTGTGACCACTGGAA 192
181  GAAATCTATTACTTTGTGGAACAGTTGGCTCACAATTCATCAGCCCAAGTTGAGATG 240
193  GAAATCTATTACTTTGTGGAACAGTTGGCTCACAATTCATCAGCCCAAGTTGAGATG 252
241  TCCCTTATTTGTTTCTCCACCCGAGAGACAACTTTAATGAACTGACAGAAAGACAGAA 300
253  TCCCTTATTTGTTTCTCCACCCGAGAGACAACTTTAATGAACTGACAGAAAGACAGAA 312
301  CAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 360
313  CAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 372
361  CATGAAGATTGAAAAGGGCCAGTAGACAGATTTATTATGAAAACAGACAGAGGTACAG 420
373  CATGAAGATTGAAAAGGGCCAGTAGACAGATTTATTATGAAAACAGACAGAGGTACAG 432
421  AACAGCCAGGCTATCATTTGCTTGTGATGATGAGAACTCCATGAGAAATCTCTTTTCTAT 480
433  AACAGCCAGGCTATCATTTGCTTGTGATGATGAGAACTCCATGAGAAATCTCTTTTCTAT 492
481  TCAGAGAGGAGGCTAATAGAGTCTCGAGATCTTGTGTCATTTGTTACTGTGTGCTG 540
493  TCAGAGAGGAGGCTAATAGAGTCTCGAGATCTTGTGTCATTTGTTACTGTGTGCTG 552
541  AAGATTTCAATGAGACAGAGCTGCGCCGAGATTGCGAGACAGTAAAGATCATGTGTTCC 600
553  AAGATTTCAATGAGACAGAGCTGCGCCGAGATTGCGAGACAGTAAAGATCATGTGTTCC 612
601  GTGAATGAGAGGCTTTAGAGGCTCTGCAAGGACATCATCTCAATTTTGAAGAAGTCCGC 660
613  GTGAATGAGAGGCTTTAGAGGCTCTGCAAGGACATCATCTCAATTTTGAAGAAGTCCGC 672
661  ATCGAATTTCTAGCAGCTGACCATCCACATATGTGCGAGAGAGTCAATTTCAAGTTGTC 720
673  ATCGAATTTCTAGCAGCTGACCATCCACATATGTGCGAGAGAGTCAATTTCAAGTTGTC 732
721  GTGAGAGGAAAAGCGCTTCCGACATGCGCCGACAGTGAACAGGCTCTCTGACGCTTCAAG 780
733  GTGAGAGGAAAAGCGCTTCCGACATGCGCCGACAGTGAACAGGCTCTCTGACGCTTCAAG 792
781  ATCAATGATCTCGGTCACTGCAATGAGAGCCCTTTTCTGTGGAACAACCTTATTACG 840
793  ATCAATGATCTCGGTCACTGCAATGAGAGCCCTTTTCTGTGGAACAACCTTATTACG 852
841  TGTCCAGCGCCTATCTTTAAAGAAAGTGGCATGAAAGTGCATCCAGGTCAGCATGAAC 900
853  TGTCCAGCGCCTATCTTTAAAGAAAGTGGCATGAAAGTGCATCCAGGTCAGCATGAAC 912
901  GATGCGCTCTCTTTTATCTTCAGATTTGTTCATCATCAACACACAGCTGTTCTGACGT 960
913  GATGCGCTCTCTTTTATCTTCAGATTTGTTCATCATCAACACACAGCTGTTCTGACGT 972
961  TGCA 964
973  CCA 976
  
```

RESULT 14
 AD100545
 ID AD100545 standard; DNA; 1650 BP.
 XX
 AC AD100545;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human TANGO 197 Ig FcR mutated fusion DNA - plasmid pUKTOK127.
 XX
 XX fusion; von Willebrand factor A-like domain; vWF; antibacterial;
 KW cutaneous; inhalation anthrax; human; TANGO 197 Ig FcR fusion; mutant;
 KW plasmid pUKTOK127; de; gene.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US2003144193-A1.
 XX
 PD 31-JUL-2003.
 XX
 PF 24-JUL-2002; 2002US-00201292.
 XX
 PR 20-DEC-2001; 2001US-00038307.
 XX
 PA (ROTT/) ROTTMAN J B.
 PA (OKEB/) O'KEEFE T L.
 PA (OZKA/) OZKAYNAK E.
 PA (HEAL/) HEALEY J J.
 PI Rotman JB, O'keefe TL, Ozkaynak E, Healey JJ;
 XX
 DR MPI: 2003-720708/68.
 DR P-PSDB: AD100546.
 XX
 PT New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or
 PT ameliorating symptoms of anthrax comprises a von Willebrand factor A-like
 PT domain (vWF) amino acid sequence and an amino acid sequence heterologous
 PT to the vWF.
 XX
 PS Example; SEQ ID NO 13; 86pp; English.
 XX
 CC The invention relates to a novel fusion polypeptide comprising a von
 CC Willebrand factor A-like domain (vWF) amino acid sequence and an amino
 CC acid sequence heterologous to the vWF. The polypeptide of the invention
 CC demonstrates antibacterial activities whilst the composition and method
 CC may be useful in preventing or ameliorating the symptoms of cutaneous
 CC and/or inhalation anthrax. The current sequence is that of the human
 CC TANGO 197 Ig FcR mutated fusion DNA of the invention.
 XX
 SO Sequence 1650 BP; 427 A; 454 C; 419 G; 350 T; 0 U; 0 Other;

Query Match 86.3%; Score 952.4; DB 10; Length 1650;
 Best Local Similarity 99.4%; Pred. No. 1.7e-281;
 Matches 956; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

1  ATGGCCACGGCGGAGAGAGCCCTCGGCATCGGCTTCAGTGAGCTCTCTTTGGCCACT 60
13  ATGGCCACGGCGGAGAGAGCCCTCGGCATCGGCTTCAGTGAGCTCTCTTTGGCCACT 60
61  CTGGGCTCATCTGCGCCGGGCAAGGGGACGAGGAGAGATGGGGGTCCACCTGCTAC 120
63  CTGGGCTCATCTGCGCCGGGCAAGGGGACGAGGAGAGATGGGGGTCCACCTGCTAC 120
121  GCGGATTTGACCTGACTTCAATTTTGGCAAAATCAGAAAGTGCTGTGACCACTGGAA 180
133  GCGGATTTGACCTGACTTCAATTTTGGCAAAATCAGAAAGTGCTGTGACCACTGGAA 180
181  GAAATCTATTACTTTGTGGAACAGTTGGCTCACAATTCATCAGCCCAAGTTGAGATG 240
181  GAAATCTATTACTTTGTGGAACAGTTGGCTCACAATTCATCAGCCCAAGTTGAGATG 240
  
```

QY 241 TCCTTATTGTTTCTCCACCCGAGGACCACTTAATGAACTGACAGAAAGACAGAA 300
 XX |||||
 Db 241 TCCTTATTGTTTCTCCACCCGAGGACCACTTAATGAACTGACAGAAAGACAGAA 300
 QY 301 CAAATCCGTCAGGCTTGAAGAACTTCAGAAAGTTCTGCCAGAGAGACACTTACATG 360
 XX |||||
 Db 301 CAAATCCGTCAGGCTTGAAGAACTTCAGAAAGTTCTGCCAGAGAGACACTTACATG 360
 QY 361 CATGAAGAGATTGAAAGGGCCAGTGAAGCATTATTAATGAAACAGAAAGGTTACAG 420
 XX |||||
 Db 361 CATGAAGAGATTGAAAGGGCCAGTGAAGCATTATTAATGAAACAGAAAGGTTACAG 420
 QY 421 ACAGCAGAGCTCATCATTTGCTTGAAGTGAAGAACTCCATGAAGATCTCTTTTCTAT 480
 XX |||||
 Db 421 ACAGCAGAGCTCATCATTTGCTTGAAGTGAAGAACTCCATGAAGATCTCTTTTCTAT 480
 QY 481 TCAGAGAGGAGGCTAATAGGTTCTCGAGATCTTGGTCAATTGTTTACATGTTGGTGTG 540
 XX |||||
 Db 481 TCAGAGAGGAGGCTAATAGGTTCTCGAGATCTTGGTCAATTGTTTACATGTTGGTGTG 540
 QY 541 AAGGATTTCAATGACACAGCTGGCCCGGATTTGCCGACAGTAAGATCATGTTTCCC 600
 XX |||||
 Db 541 AAGGATTTCAATGACACAGCTGGCCCGGATTTGCCGACAGTAAGATCATGTTTCCC 600
 QY 601 GTGATGACGAGCTTTCAGGCTTCGAAAGGATCATCACTCAATTTTGAAGAGTCTGCG 660
 XX |||||
 Db 601 GTGATGACGAGCTTTCAGGCTTCGAAAGGATCATCACTCAATTTTGAAGAGTCTGCG 660
 QY 661 ATCGAAATTCCTAGCAGTGAACCATCCACATATGTCAGAGAGATCATTTCAAGTTGTC 720
 XX |||||
 Db 661 ATCGAAATTCCTAGCAGTGAACCATCCACATATGTCAGAGAGATCATTTCAAGTTGTC 720
 QY 721 GTGAGAGGAAACGGCTTCCGACATGCCCGAAGCTGACAGGGTCTCTGACCTTCAAG 780
 XX |||||
 Db 721 GTGAGAGGAAACGGCTTCCGACATGCCCGAAGCTGACAGGGTCTCTGACCTTCAAG 780
 QY 781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGGAAGACCTTATTTACTG 840
 XX |||||
 Db 781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGGAAGACCTTATTTACTG 840
 QY 841 TGTCCAGCGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAAAC 900
 XX |||||
 Db 841 TGTCCAGCGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAAAC 900
 QY 901 GATGGCTCTCTTTTATCTCAAGTTCTGTATCATACCAACACACTGTTCTGAGAGT 960
 XX |||||
 Db 901 GATGGCTCTCTTTTATCTCAAGTTCTGTATCATACCAACACACTGTTCTGCCAAA 960
 QY 961 TC 962
 XX |||||
 Db 961 TC 962
 XX |||||

RESULT 15
 ADI00547
 ID ADI00547 standard; DNA; 1650 BP.
 AC ADI00547;

22-APR-2004 (first entry)
 Human TANGO 197 Ig FCR WT fusion DNA - plasmid pLTKOK129.
 fusion; von Willebrand factor A-like domain; vWF; antibacterial;
 cutaneous; inhalation anthrax; human; TANGO 197 Ig FCR fusion; wild-type;
 plasmid pLTKOK129; de; gene.

OS Homo sapiens.
 XX
 XX US2003144193-A1.
 PN
 XX
 PD 31-JUL-2003.
 XX

PF 24-JUL-2002; 2002US-00201292.
 XX
 PR 20-DEC-2001; 2001US-00038307.
 XX
 PA (ROTT/) ROTTMAN J B.
 PA (OKEE/) O'KEEFE T L.
 PA (OZKA/) OZKAYNAK E.
 PA (HEAL/) HEALEY J J.
 XX
 PI Rottman JB, O'keefe TL, Ozkaynak E, Healey JJ,
 DR WPI; 2003-720708/68.
 DR P-PSDB; ADI00548.
 XX
 PT New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or
 PT ameliorating symptoms of anthrax comprises a von Willebrand factor A-like
 PT domain (vWF) amino acid sequence and an amino acid sequence heterologous
 PT to the vWF.
 XX
 PS Example; SEQ ID NO 15; 86bp; English.
 CC The invention relates to a novel fusion polypeptide comprising a von
 CC Willebrand factor A-like domain (vWF) amino acid sequence and an amino
 CC acid sequence heterologous to the vWF. The polypeptide of the invention
 CC demonstrates antibacterial activities whilst the composition and method
 CC may be useful in preventing or ameliorating the symptoms of cutaneous
 CC and/or inhalation anthrax. The current sequence is that of the human
 CC TANGO 197 Ig FCR wild-type fusion DNA of the invention.
 XX
 SQ Sequence 1650 BP; 427 A; 453 C; 419 G; 351 T; 0 U; 0 Other;
 QY Query Match 86.3%; Score 952.4; DB 10; Length 1650;
 Best Local Similarity 99.4%; Pred. No. 1.7e-281;
 Matches 956; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 ATGGCCACGCGCGAGGAGGAGCCCTCGGATGCGCTTCAGTGGCTCTTTGGCCACT 60
 Db 1 ATGGCCACGCGCGAGGAGGAGCCCTCGGATGCGCTTCAGTGGCTCTTTGGCCACT 60
 QY 61 CTGGTGCTCATCTGCGCCGGGCAAGGGGACGACGAGAGATGGGGGTCCAGCTGTAC 120
 Db 61 CTGGTGCTCATCTGCGCCGGGCAAGGGGACGACGAGAGATGGGGGTCCAGCTGTAC 120
 QY 121 GCGGATTTGACCTGTACTTATTTGGAACAATCGAAGTGTCTGACCACTGGAAT 180
 Db 121 GCGGATTTGACCTGTACTTATTTGGAACAATCGAAGTGTCTGACCACTGGAAT 180
 QY 181 GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCAGCCACAGTTGAGAAATG 240
 Db 181 GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCAGCCACAGTTGAGAAATG 240
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 Db 301 CAAATCCGTCAGGCTTGAAGAACTTCAGAAAGTTCTGCCAGAGAGACACTTACATG 360
 QY 361 CATGAAGAGATTGAAAGGGCCAGTGAAGCATTATTAATGAAACAGAAAGGTTACAG 420
 Db 361 CATGAAGAGATTGAAAGGGCCAGTGAAGCATTATTAATGAAACAGAAAGGTTACAG 420
 QY 421 ACAGCAGAGCTCATCATTTGCTTGAAGTGAAGAACTCCATGAAGATCTCTTTTCTAT 480
 Db 421 ACAGCAGAGCTCATCATTTGCTTGAAGTGAAGAACTCCATGAAGATCTCTTTTCTAT 480
 QY 481 TCAGAGAGGAGGCTAATAGGTTCTCGAGATCTTGGTCAATTGTTTACATGTTGGTGTG 540
 Db 481 TCAGAGAGGAGGCTAATAGGTTCTCGAGATCTTGGTCAATTGTTTACATGTTGGTGTG 540
 QY 541 AAGGATTTCAATGACACAGCTGGCCCGGATTTGCCGACAGTAAGATCATGTTTCCC 600
 Db 541 AAGGATTTCAATGACACAGCTGGCCCGGATTTGCCGACAGTAAGATCATGTTTCCC 600

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Db      541 AAAGATTTCATAGAGACACAGCTGGCCCGAATTGCGGACGTAAGGATCAGTGTTCCTCC 600
QY      601 GTGAATGACGGCTTTCAAGGCTCTGCAAGGCTATCCACTCAATTTTGAAGAAGTCCTGC 660
Db      601 GTGAATGACGGCTTTCAAGGCTCTGCAAGGCTATCCACTCAATTTTGAAGAAGTCCTGC 660
QY      661 ATCGAAATTCTAGCAGCTGACCATCCACATATGTGAGAGAGTCAATTCAGTTGTC 720
Db      661 ATCGAAATTCTAGCAGCTGACCATCCACATATGTGAGAGAGTCAATTCAGTTGTC 720
QY      721 GTGAGAGGAAACGGCTTCGACATGCCCCGCAACGTGACAGGTCCTCTGCAGCTTCAG 780
Db      721 GTGAGAGGAAACGGCTTCGACATGCCCCGCAACGTGACAGGTCCTCTGCAGCTTCAG 780
QY      781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGGAAGACATTATTACTG 840
Db      781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGGAAGATATTATTACTG 840
QY      841 TGTCCAGCGCTATCTTAAAGAAAGTTGGCATGAAGCTGCACTCCAGGTCAAGCATGAAC 900
Db      841 TGTCCAGCGCTATCTTAAAGAAAGTTGGCATGAAGCTGCACTCCAGGTCAAGCATGAAC 900
QY      901 GATGGCTCTCTTTTATCTCCAGTTCTGTCAATCATCACACACACACTGTTCTGACGCT 960
Db      901 GATGGCTCTCTTTTATCTCCAGTTCTGTCAATCATCACACACACACTGTTCTGACGCT 960
QY      961 TC 962
Db      961 TC 962

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Search completed: December 17, 2005, 19:23:03
 Job time : 739.269 secs

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OM nucleic - nucleic search, using sw model

Run on: December 18, 2005, 07:01:39 ; Search time 4989.04 Seconds
(without alignments)
10353.271 Million cell updates/sec

Title: US-09-970-076-1_COPY_104_1207
Perfect score: 1104
Sequence: 1 atgcgcacggcgagcgagcgag.....gtcgaggaataataataaaa 1104

Scoring table: IDENTIFY NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST :
1: gb_ests1:
2: gb_ests2:
3: gb_ests3:
4: gb_hic:
5: gb_ests4:
6: gb_ests5:
7: gb_ests6:
8: gb_ests7:
9: gb_ests8:
10: gb_ests9:
11: gb_ests10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	949.4	86.0	1957	4	CR601167 full-length
2	853.4	77.3	3161	4	AK031465 Mus muscu
3	689.2	62.4	1006	1	AL542724
4	684.6	62.0	878	3	BI823853
5	681.4	61.7	1614	4	AK013005 Mus muscu
6	662	60.0	1054	3	BM800898
7	658.8	59.7	833	7	CO245219
8	637.8	57.8	725	2	BE741333
9	614	55.6	744	8	CX872420
10	585	53.0	963	2	EG326444
11	582.6	52.8	820	2	BG281561
12	552	50.0	641	6	CF132432
13	541.4	49.0	780	6	CF126791
14	534	48.4	823	5	BU131302
15	531.4	48.3	564	6	CD664532
16	531.4	48.1	877	5	EX364961
17	526.2	47.7	682	6	CF540285
18	520.2	47.1	727	6	CA324840
19	507.4	46.0	522	6	CD664533
20	498.4	45.1	600	6	CD664531
21	482	43.7	964	2	BG281831
22	480	43.5	1409	8	DN659443

23	468	42.4	672	8	DN993680	DN993680 TC13711
24	467.4	42.3	3178	4	AK048637	AK048637 Mus muscu
25	466.6	42.3	473	7	CV028654	CV028654 7224 Full
26	464.6	42.1	642	7	CN461036	CN461036 UI-M-HB0
27	461	41.8	600	7	CN262102	CN262102 170005326
28	451.6	40.9	643	5	BU632284	BU632284 UI-H-FE1
29	447.4	40.5	638	2	BE369415	BE369415 601220816
30	446.8	40.5	582	5	BK470942	BK470942 DKF26861
31	441.8	40.0	805	6	CB990959	CB990959 AGENCOURT
32	432.6	39.2	892	8	DN063003	DN063003 JGI CABD1
33	427.4	38.7	793	5	BK369960	BK369960 BK369960
34	421.2	38.2	867	5	BK337000	BK337000 BK337000
35	420.4	38.1	513	2	BE146084	BE146084 MR0-HT020
36	420.4	38.1	542	2	BE146075	BE146075 MR0-HT020
37	416.4	37.7	602	3	BP456257	BP456257 BP456257
38	409.6	37.1	524	6	CA945449	CA945449 UI-M-F00
39	408.2	37.0	776	7	CK787494	CK787494 AGENCOURT
40	399.8	36.2	465	2	BE145958	BE145958 MR0-HT020
41	384.8	34.9	487	2	BE146355	BE146355 MR0-HT020
42	382	34.6	775	5	BU363718	BU363718 603788453
43	381.2	34.5	539	1	AI466645	AI466645 mg81d04.Y
44	376.4	34.1	693	2	BG323538	BG323538 602422195
45	373.6	33.8	554	1	AI084806	AI084806 0280d12.X

ALIGNMENTS

RESULT 1
LOCUS CR601167 1957 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0D1035YA13 of Placenta Cot 25-normalized
of Homo sapiens (human).

ACCESSION CR601167.1 GI:50481974
VERSION CR601167.1
KEYWORDS HTC; CDS; CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1957)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1957)

REFERENCE 2 (bases 1 to 1957)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
1..1957
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1035YA13"
/issue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 86.0%; Score 949.4; DB 4; Length 1957;
Best Local Similarity 99.9%; Pred. No. 2.6e-270;
Matches 950; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCCACGGCGGAGCGGAGAGCCCTCGGAGTCGGCTTCACAGTGGCTCTCTTTGGCCACT 60
DB 195 ATGGCCACGGCGGAGCGGAGAGCCCTCGGAGTCGGCTTCACAGTGGCTCTCTTTGGCCACT 254
QY 61 CTGGTCTCATCTGCGCCCGGGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTCTCTAC 120
DB 255 CTGGTCTCATCTGCGCCCGGGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTCTCTAC 314
QY 121 GGGGATTTGACCTGTACTTCAATTTGGAACAATTCAGAAAGTGTGTGACCACTGGAAAT 180
DB 315 GGGGATTTGACCTGTACTTCAATTTGGAACAATTCAGAAAGTGTGTGACCACTGGAAAT 374
QY 181 GAAATCTATTACTTTGTGGAACAAGTGGCTCAAAATTCATCAGCCCAAGTTGAGATG 240
DB 375 GAAATCTATTACTTTGTGGAACAAGTGGCTCAAAATTCATCAGCCCAAGTTGAGATG 434
QY 241 TCTTTTATTGTTTCTTCACCCGAGAGAACCTTATGAAACTGACAGAGACAGAGAA 300
DB 435 TCTTTTATTGTTTCTTCACCCGAGAGAACCTTATGAAACTGACAGAGACAGAGAA 494
QY 301 CAAATCCGTCAAGGCGCTAGAGAACTCCAGAAAGTTCTGCGAGGAGAGACACTTACATG 360
DB 495 CAAATCCGTCAAGGCGCTAGAGAACTCCAGAAAGTTCTGCGAGGAGAGACACTTACATG 554
QY 361 CATGAAGATTGGAAGGGCCAGTGAAGCAAGTTATTATGAAACAGACAGAGGTACAGG 420
DB 555 CATGAAGATTGGAAGGGCCAGTGAAGCAAGTTATTATGAAACAGACAGAGGTACAGG 614
QY 421 ACAGCCAGGCTCATCTTGTCTTGTGATGAGAACTCCATGAGATCTCTTTTCTAT 480
DB 615 ACAGCCAGGCTCATCTTGTCTTGTGATGAGAACTCCATGAGATCTCTTTTCTAT 674
QY 481 TCAGAGAGGAGGCTATATGATGCTTCAGAACTTGTGTCGAATTTGATGTTGTGTG 540
DB 675 TCAGAGAGGAGGCTATATGATGCTTCAGAACTTGTGTCGAATTTGATGTTGTGTG 734
QY 541 AAAGATTTCAATGAGACACAGCTGCGCCGGATTGCGAGACAGTAAGATCATGTGTTCC 600
DB 735 AAAGATTTCAATGAGACACAGCTGCGCCGGATTGCGAGACAGTAAGATCATGTGTTCC 794
QY 601 GTGAATGAGGCGCTTTCAGGCTTCGCAAGGATCATCTCAATTTTGAAGAAGTCTGCG 660
DB 795 GTGAATGAGGCGCTTTCAGGCTTCGCAAGGATCATCTCAATTTTGAAGAAGTCTGCG 854
QY 661 ATCGAATTTCTAGCAGCTGAAACCATCAACATATGTCAGAGAGATCATTTCAAGTTGTC 720
DB 855 ATCGAATTTCTAGCAGCTGAAACCATCAACATATGTCAGAGAGATCATTTCAAGTTGTC 914
QY 721 GTGAGAGAAACGGCTTCCGACATGCGCCGCAAGTGGAGACAGGCTCTCTGCAAGTTCAAG 780
DB 915 GTGAGAGAAACGGCTTCCGACATGCGCCGCAAGTGGAGACAGGCTCTCTGCAAGTTCAAG 974
QY 781 ATCAATGACTCGGTCACTCACTGATGAGAGCCCTTTTCTGTGGAAGACACTTATTACG 840
DB 975 ATCAATGACTCGGTCACTCACTGATGAGAGCCCTTTTCTGTGGAAGACACTTATTACG 1034
QY 841 TGTCCAGCGCTATCTTTAAAGAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAAC 900
DB 1035 TGTCCAGCGCTATCTTTAAAGAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAAC 1094
QY 901 GATGCGCTCTCTTTTATCTCCAGTTCTGTGATGATGACCAACACAGACTGT 951
DB 1095 GATGCGCTCTCTTTTATCTCCAGTTCTGTGATGATGACCAACACAGACTGT 1145

RESULT 2
LOCUS AK031465 3161 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:6030436P19 product:ANTHRAX TOXIN RECEPTOR
PRECURSOR (TUMOR ENDOTHELIAL MARKER 8) homolog [Mus musculus], full
insert sequence.
ACCESSION AK031465

VERSION AK031465.1 GI:26082340
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Carninci, P., and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
AUTHORS
TITLE
JOURNAL
PUBMED 11042159
AUTHORS
REFERENCE
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Komno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system-384-format
JOURNAL sequencing pipeline with 384 multicapillary sequencer
PUBMED Genome Res. 10 (11), 1757-1771 (2000)
11076861
AUTHORS
TITLE
JOURNAL
PUBMED 11076861
AUTHORS
REFERENCE
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
5
TITLE
JOURNAL
PUBMED 11076861
AUTHORS
REFERENCE
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
JOURNAL of 60,770 full-length cDNAs
PUBMED Nature 420, 563-573 (2002)
6 (bases 1 to 3161)
AUTHORS
REFERENCE
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
Holt, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, D., Kojima, Y., Kondo, S., Komno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M., and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Sueni-cho, Tsukuba, Ibaraki, Japan,
Kanagawa 230-0045, Japan [E-mail: genome-res@gscl.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216]
COMMENT
cdna library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
FEATURES
source location/Qualifiers
1. 3161


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/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="6030436P19"
/sex="male"
/issue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="13 days embryo"
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MARKER 8) homolog [Mus musculus] (SWISSPROT|Q9CZ55,
evidence: PASTY, 100%ID, 84.6%length, match=1428) "
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ORIGIN

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Query Match      77.3%; Score 853.4; DB 4; Length 3161;
Best Local Similarity 87.3%; Pred. No. 1.2e-241;
Matches 935; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

24 CCTCGGCAATGCGCTTCAGTGGCTCTTTGGCCACTCTGCTCATCTGCGCGGCA 83
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401 CGGGGCGCGCGGAGATGGGGGACCACTGCTGCTAGCGGATTCGACTCTGATCAT 460
144 TTGGACAAATACAGAAATGCTGCTGCACTGCACTGCAATGAAATCTATTCTTTGGAACA 203
461 CTTGGACAAATGCAAGAAATGCTGCTGCACTGCAATGAAATCTATTCTTTGGAACA 520
204 GTTGGCTCACAATTCATCAGCCCACTGGAATGCTCTTATTTGTTTCTCCACCG 263
521 GTTGGCTCACAATTCATCAGCCCACTGGAATGCTCTTATTTGTTTCTCTACTCG 580
264 AGGAACAACCTTATGAACTGACAGAAAGACAGAAACAATCCGTCAAGGCTGAGAA 323
581 AGGACAACTTATGAACTGAACTGAGAGAGGAAAGAACTGACAAAGGCTGAGAA 640
324 ACTCCAGAAAGTTCTGCGAGAGAGACACTTACATCATGAAAGATTTGAAAGGCGAG 383
641 GCTCCAGAAAGTTCTGCGAGAGAGACACTTACATCATGAAAGATTTGAGAGGCGAG 700
384 TGAGCAGATTTATGTAAGAAACAGACAGAGGTAAGACAGCCGCTCATCTGCTTT 443
701 TGAGCAGATTTATGTAAGAAACAGTCAAGATACAGACGCGCTCATCTGCTTT 760
444 GACTGAGAGAACTCATGAAAGTCTTTTCTTATTCAGAGAGGAGGCTATAGGTC 503
761 GACGAGATGGGAGCTGACGAGGACTCTTCTTACTCAGAGAGGAGGCTAACGATC 820
504 TCGAGATCTTGGTCAATTTGTTTCTGTTGTTGTAAGAAATTTCAATGACACAGCT 563
821 CCGAGACTCTGGTGGCAATTTGTTTCTGTTGTTGTAAGAAATTTCAATGACAGTT 880
564 GGGCGGATTTGCGAGAGTAAGATCATGTGTTTCCGTAATGACGCGCTTCAAGCTCT 623
881 GGGCTCGGATTTGCAACAGTAAGACCAAGTCTTCTGTAAGACGCGCTTCAAGCTCT 940
624 GCAAGGATCATTCATCAATTTGTAAGAAAGTCTGATGTAAGAAATTTAGAGAGTAAAC 683
941 CCAAGGATTTATTCATCAATTTTAAAGAAATCTGATGTAAGAAATTTGAGGCGCTGAAAC 1000
684 ATCCACATATGTCAGAGAGAGTCAATTTCAAGTTGCTGAGAGAAACGCGCTTCCGACA 743
1001 ATCCACATATGTCAGAGAGAGTCTTTCAAGTTGCTGTAAGAGAAATGCGCTTCCGACA 1060
744 TGCCCGCAACGTGACAGAGGCTCTGCGAGCTTCAAGATCAATGATCTGCTGACACTGAA 803
1061 TGCCCGCAATGTGACAGAGGCTCTGCGAGCTTCAAGATCAATGATCTGCTGACACTGAA 1120
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Db 1121 TGAGAGCCCTTGTGTGGAAGACATTAATTTGTGTGCGCCAGACCAATCTTGAAGA 1180
Qy 864 AGTTGGCATGAAAGCTGCACTCCAGTCCAGACAGAAAGAGGCTCTTTATCTCCAG 923
Db 1181 AGTTGGCATGAAAGCTGCACTCCAGTCCAGACAGAAAGAGGCTCTTTATCTCCAG 1240
Qy 924 TTGTGTCATCATCAGCAGCAGACACTGTTGTGAGGTTCCATCTGAGCCATCCGCTGCT 983
Db 1241 TTGTGTCATCATCAGCAGCAGACACTGTTGTGAGGTTCCATCTGAGCCATCCGCTGCT 1300
Qy 984 GATCTGTTCTCTGCTCTGAGCCCTGAGCTCTCTGAGGTTGAGCCCTCTGCTGAC 1043
Db 1301 GGTCTCTCTCTGCTCTGAGCCCTGAGCTCTCTGAGGTTGAGCCCTCTGCTGAC 1360
Qy 1044 TGTGATTTATCAGAGAGTCCCTCCAGCCCTGCGAGAGAGTGAAGAAA 1094
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RESULT 3
AL542724 1006 bp mRNA linear EST 24-MAR-2004
LOCUS AL542724 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE011Y109
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION AL542724 GI:45718299
VERSION AL542724.3 GI:45718299
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1..(bases 1 to 1006)
AUTHORS Li,W.B., Gruber,C., Jesse,J., and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:30548161.
Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Creteil, CP 5706 - 91057 Evry cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1660.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?as=CS0DE011CR05QPLc=1660.f.
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FEATURES

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/clone="CS0DE011Y109"
/tissue_type="PLACENTA"
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/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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ORIGIN

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Query Match      62.4%; Score 689.2; DB 1; Length 1006;
Best Local Similarity 99.0%; Pred. No. 5.2e-193;
Matches 703; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

Qy 1 ATGGCCACGGCGGAGCGGAGAGCCCTGCGCATGCGCTTCCAGTGGCTCTTTGGCACT 60
Db 293 ATGGCCACGGCGGAGCGGAGAGCCCTGCGCATGCGCTTCCAGTGGCTCTTTGGCACT 352
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QY 61 CTGTGCTCATCTGCGCCGGGCGAAGGGGACGCGAGGAGATGGGGTCCAGCTGTAC 120
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|
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Db 353 CTGGTCTCATCTGCGCCGGGCGAAGGGGACGCGAGGAGATGGGGTCCAGCTGTAC 412
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|
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QY 121 GCGGATTTGACCTGTACTTCTTCTTGGCAAAATCGAGAGTGTGTGACCACTGGAT 180
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Db 413 GGGGATTTGACCTGTACTTCTTCTTGGCAAAATCGAGAGTGTGTGACCACTGGAT 472
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|
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QY 181 GAAATCTATTAATCTTGTGGCAAGTTGGCTCAAAATTCATCCAGCCACAGTTGAGATG 240
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|
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Db 473 GAAATCTATTAATCTTGTGGCAAGTTGGCTCAAAATTCATCCAGCCACAGTTGAGATG 532
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QY 241 TCTTTATTTGTTTCTTCCACCCGAGAACACTTAATGAACTGACAGAAACAGAGAA 300
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Db 533 TCTTTATTTGTTTCTTCCACCCGAGAACACTTAATGAACTGACAGAAACAGAGAA 592
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QY 301 CAAATCCGTCAGAGCCTTAGAAGAACTCCGAAAGTTCTCCAGAGAGACACTTTCAG 360
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Db 593 CAAATCCGTCAGAGCCTTAGAAGAACTCCGAAAGTTCTCCAGAGAGACACTTTCAG 652
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QY 361 CATGAGATTTGAAAGGCGCAGTACAGATTATTTATGAAACAGACAGGTTACAG 420
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Db 653 CATGAGATTTGAAAGGCGCAGTACAGATTATTTATGAAACAGACAGGTTACAG 712
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QY 421 ACAGCCAGCGTCATCTTGTCTTGTGATGAGAACTCCATGAGATCTTTTCTAT 480
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|
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Db 713 ACAGCCAGCGTCATCTTGTCTTGTGATGAGAACTCCATGAGATCTTTTCTAT 772
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QY 481 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTGCAATTTTAACTGTGTGTG 540
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Db 773 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTGCAATTTTAACTGTGTGTG 832
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QY 541 AAAGATTTCAATGAGACACAGCTGCGCCGATTCGAGACAGTAAGATCATGTGTTCC 600
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Db 833 AAAGATTTCAATGAGACACAGCTGCGCCGATTCGAGACAGTAAGATCATGTGTTCC 892
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QY 601 GTGAATGACGGCTTTCAAGCTCTGCAAGGATCATCTCAATTTTGAAGAGTCTTC 660
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Db 893 GTGAATGACGGCTTTCAAGCTCTGCAAGGATCATCTCAATTTTGAAGAGTCTTC 952
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QY 661 ATCGAATTTCTAGCACTGACATCCATATGTGCGAGAGATCAT 710
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|
|
Db 953 ATCGAATTTCTAGCA--CTGAACATCCATATGTGCGAGAGATCAT 1000
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|
|
RESULT 4
B1823853 878 bp mRNA linear EST 04-OCT-2001
LOCUS 603039031F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:517974 5',
DEFINITION mRNA sequence.
ACCESSION B1823853
VERSION B1823853.1 GI:15935416
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 878)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph. D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L14M1448 row: n column: 07
High quality sequence stop: 804.

FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:517974"
/lab_host="DH10B"
/clone_11b="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC library."

Query Match 62.0%; Score 684.6; DB 3; Length 878;
Best Local Similarity 95.1%; Pred. No. 1.2e-191;
Matches 783; Conservative 0; Mismatches 29; Indels 11; Gaps 7;

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Db 57 ATGGCCACGGCGGAGCGGAGAGCCTTCGCGATCGGCTTCAGTGGCTCTCTTTGGCCACT 116
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QY 61 CTGGTCTCATCTGCGCCGGGCGAAGGGGACGCGAGGAGATGGGGTCCAGCTGTAC 120
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Db 117 CTGGTCTCATCTGCGCCGGGCGAAGGGGACGCGAGGAGATGGGGTCCAGCTGTAC 176
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QY 121 GCGGATTTGACCTGTACTTCTTCTTGGCAAAATCGAGAGTGTGTGACCACTGGAT 180
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Db 177 GCGGATTTGACCTGTACTTCTTCTTGGCAAAATCGAGAGTGTGTGACCACTGGAT 236
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QY 181 GAAATCTATTAATCTTGTGGCAAGTTGGCTCAAAATTCATCCAGCCACAGTTGAGATG 240
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Db 237 GAAATCTATTAATCTTGTGGCAAGTTGGCTCAAAATTCATCCAGCCACAGTTGAGATG 296
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QY 241 TCTTTATTTGTTTCTTCCACCCGAGAACACTTAATGAACTGACAGAAACAGAGAA 300
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Db 297 TCTTTATTTGTTTCTTCCACCCGAGAACACTTAATGAACTGACAGAAACAGAGAA 356
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QY 301 CAAATCCGTCAGAGCCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 360
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Db 357 CAAATCCGTCAGAGCCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 416
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QY 361 CATGAGATTTGAAAGGCGCAGTACAGATTTATTTAAGAAACAGACAGAGGTACAG 420
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Db 417 CATGAGATTTGAAAGGCGCAGTACAGATTTATTTAAGAAACAGACAGAGGTACAG 476
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QY 421 ACAGCCAGCGTCATCTTGTGCTTGA CTGATGAGAACTCATGAAGATCTTTTCTAT 480
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Db 477 ACAGCCAGCGTCATCTTGTGCTTGA CTGATGAGAACTCATGAAGATCTTTTCTAT 536
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QY 481 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTGCAATTTTAACTGTGTGTG 540
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Db 537 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTGCAATTTTAACTGTGTGTG 595
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QY 541 AAAGATTTCAATGAGACACAGCTGCGCCGATTCGAGACAGTAAGATCATGTGTTCC 600
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Db 596 AAAGATTTCAATGAGACACAGCTGCGCCGATTCGAGACAGTAAGATCATGTGTTCC 655
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QY 601 GTGAATGACGGCTTTCAAGCTCTGCAAGGATCATCTCAATTTTGAAGAGTCTTC 659
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Db 656 GTGAATGACGGCTTTCAAGCTCTGCAAGGATCATCTCAATTTTGAAGAGTCTTC 715
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QY 660 CATC-GAAATTTCTAGACGCTGAAACATCCACATATGTGCGAGAGTCT-ATTCAAGTT 717
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Db 716 CATCGAATTTCTAGACGCTGAAACATCCACATATGTGCGAGAGTCAATTCGAAGTT 775
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QY 718 GTGTGAGAGG--AAAGGCTTCCGATGATCCCG--CAACGTGACAGAGG--TCTCTGTG 770
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Db	776	GTCTGTGAGAGGAAACGGGTTTCCGACATGGCGGCAACCTGTGACCAAGGTCCTTGG	835
Qy	771	CAGCTTCAGATCAATGACTGCTGGTCACACTCAATGAGAGCC	813
Db	836	AGGTTCCAGATCAATGACTGCTGGTCACACTTCATGAAAAAGCC	878
RESULT 5			
LOCUS	AK013005		
DEFINITION	AK013005	1614 bp	mRNA
			linear
			HTC 03-APR-2004
			Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
			enriched library, clone:2810405N18 product:ANTPAX TOXIN RECEPTOR
			PRECURSOR (TUMOR ENDOTHELIAL MARKER 8) homolog [Mus musculus], fulll
			insert sequence.
ACCESSION	AK013005		
VERSION	AK013005.1	GI:12850099	
KEYWORDS	HTC, CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;		
	Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	Carninci, P. and Hayashizaki, Y.		
AUTHORS	1		
	High-efficiency full-length cDNA cloning		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
	Itch, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and substructure of cap-trapper-selected cDNAs to		
	prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itch, M., Aizawa, K., Nagaoke, S., Sasaki, N., Carninci, P.,		
	Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Teshiro, H., Itch, M.,		
	Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,		
	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K.,		
	Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,		
	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,		
	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format		
	sequencing pipeline with 384 multichannel sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the		
	FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409, 685-690 (2001)		
PUBMED	5		
REFERENCE	The FANTOM Consortium and the RIKEN Genome Exploration Research		
AUTHORS	Group Phase I & II team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation		
	of 60,770 full-length cDNAs		
JOURNAL	Nature 420, 563-573 (2002)		
PUBMED	6 (bases 1 to 1614)		
REFERENCE	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,		
AUTHORS	Araiawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,		
	Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,		
	Hirooka, T., Hori, F., Imotani, K., Ishii, Y., Itch, M., Izawa, M.,		
	Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Koda, M.,		
	Koye, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,		
	Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Ose, C.,		
	Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,		
	Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y.,		
	Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,		
	Tejima, Y., Toyu, T., Yamamura, T., Yasunishi, A., Yoshida, K.,		
	Yoshino, M., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Direct Substitution		
JOURNAL	Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of		

COMMENT
Please visit our web site (<http://genome.gsc.riken.jp/>) for further
Fax: 81-45-503-9216
URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222,
Kanagawa 230-0045, Japan (E-mail: genome-isa@gsc.riken.jp,
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

FEATURES

GAGAGAGAGATTCGAGATTAAATTAATATCCCCCCCCCCC 3', cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
Host: SOLR.

Location/Qualifiers
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feature(1614..1615) "3' UTR"

CDS

polyA_signal
polyA_site

/note="unnamed protein product; ANTRAX TOXIN RECEPTOR
PACRINOR8 (TUMOR ENDOTHELIAL MARKER 8) homolog [Mus
musculus] (SWISSPROT|Q9CZ52, evidence: FASTA, 100%ID,
84.6%length, match=1428)
putative"
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/db_xref="xgi:12850100"
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QGYRASYATIALTGDELHEDLFYSEBANSROLGAIIVYCVGKRDNETLOLAIBS
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DRVCSFKNIDSVTLNEKRFPAVEDYITLCPAIPILKEKMGKALQVNSNDGFSIFSSS
IITTHCGDGSIIAIALVILFLALLIMFMPLCTGVIIKEVPPVSESEEDYE
GLPKKKMPTDVAAYVGGCGNGCIRKMEYVMEKSTEGALILEKXANARVYMPDEYVE
FPEPRLNNNNRRPSSPRKWTSPITKGKLDALVTLIRKGYDRVSNRQPGDTRRGMR
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1592..1597
/note="putative"
1614
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ORIGIN

Query Match	Similarity	81.7%	Score 601.4	DB 4	Length 1614
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				Indels	0
				Gaps	0
QY	268	ACAACTTAAATGAACTGACAGAAAGACAGAAACAATCCGTCAAGCCCTTGAAGAACTC	327		
DB	2	ACAACCTTAAATGAAACTTAATGAGAGACAGAGAAACAGATCCCAAGAGCCCTTGAAGAGCTTC	61		
QY	328	CAGAAAGTCTGCCAGAGGAGAGACACTTAATGCATGATGAAGATTGAAGAGGCCAGTAG	387		
DB	62	CAGAAAGTCTGCCAGAGGAGAGACACTTAATGCAGAGGAATTCGAAGAGGCCAGTAG	121		
QY	388	CAGATTATTATGAAACAGACAAAGGGTACAGACAGCCAGTCGTATCATTTGCTTGA	447		
DB	122	CAGATTACTATGAGAAACAGTCAGAGATACAGAGAGCGTCATCATCGCGTTGACG	181		
QY	448	GATGAGAACTCCATGAAGATCTCTTTTCTATTACAGAGAGAGAGGCTTAATAGGCTCTGSA	507		

DB 182 GATGGGAGCTGACACAGGACCTCTTCTACTCAGAGAGGAGGCTAACGATCCCA 241
QY 508 GATCTTGGGCAATGTTTACTGTGTGTGGAAGATTTCATAGACACAGCTGGCC 567
DB 242 GACCTTGGGCGATTTTACTGCGTTGGCGTGAATTTTCATGAATCTCAGTTGGCT 301
QY 568 CGGATTCGCGAGAGTAAGATCATGTGTTCCTCGTGAATGACGGCTTTCAGGCTGCA 627
DB 302 CGGATTCGAGACGTAAGACACGATGTTTCTGTGAACGACGGCTTTCAGGCTGCA 361
QY 628 GGCATATCATCTCAATTTTGAAGAAGTCTGATGAATTTCTAGCAGTGAACATCC 687
DB 362 GGCATATCATCTCAATTTTGAAGAAGTCTGATGAATTTCTAGCAGTGAACATCC 421
QY 688 ACCATATGTCAGGAGAGTCAATTTCAAGTTGTGTGAGAGGAAAGGCTTCCGACATGCC 747
DB 422 ACCATATGTCAGGAGAGTCTTTCATAGTGTGTGAAGAAATGGCTTCCGACATGCC 481
QY 748 CGCAACGTGAGACGGGTCTCTGACAGCTTCAAGATCAATGACTCGTCACTCATATGAG 807
DB 482 CGCAATGTGAGACGGGTCTCTGACAGCTTCAAAATCAATGACTCACTCATATGAG 541
QY 808 AAGCCTTTTCTGTGGAAGACACTTATTTACTGTGTGACGGCTTATTTAAAGAAGTT 867
DB 542 AAGCCTTTTCTGTGGAAGACACTTATTTACTGTGTGACGGCTTATTTAAAGAAGTT 601
QY 868 GGCATGAAGCTGCACTCCAGGTGACATGAAGATGAGGCTCTTTTATTCACATGTC 927
DB 602 GGCATGAAGCTGCACTCCAGGTGACATGAAGATGAGGCTCTTTCATCTCAGATGTC 661
QY 928 GTTCATCATCACACACACACTGTTCTGACGGTTCATCTGACATGCGCTGCTGATC 987
DB 662 GTTCATCATCACACACACTGTTCTGACGGTTCATCTGACATGCGCTGCTGATG 721
QY 988 CTGTTCTGCTCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1047
DB 722 CTGTTCTGCTCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 781
QY 1048 ATTATCAAGAGAGTCCCTCACCCCTGTTGAGAGAGTGAAGAA 1094
DB 782 ATCATCAAGAGAGTCCCTCACCCCTGTTGAGAGAGTGAAGAA 828

RESULT 6
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LOCUS BM800898
DEFINITION AGENCOURT_6420797 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5541228
5', mRNA sequence.
ACCESSION BM800898
VERSION BM800898.1 GI:19117721
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1054)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DICP/dnp
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
<http://image.llnl.gov>
Plate: LLAM12238 row: j column: 13
High quality sequence stop: 595.
Location/Qualifiers

FEATURES

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/db_xref="taxon:9606"
/clone="IMAGE:5541228"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-Sport6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 60.0%; Score 662; DB 3; Length 1054;
Best Local Similarity 97.5%; Pred. No. 6.6e-185;
Matches 704; Conservative 0; Mismatches 15; Indels 3; Gaps 3;

QY 1 ATGGCCACGGCGGAGCGGAGAGCCCTCGGATCGGCTTCAGTGCTCTCTTTGGCCACT 60
DB 97 ATGGCCACGGCGGAGCGGAGAGCCCTCGGATCGGCTTCAGTGCTCTCTTTGGCCACT 156
QY 61 CTGGTGCTCATCTGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
DB 157 CTGGTGCTCATCTGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 216
QY 121 GCGGATTTGACCTGTACTTCAATTTTGGACAATGAGAGTGTGTCGACCACTGGAAT 180
DB 217 GCGGATTTGACCTGTACTTCAATTTTGGACAATGAGAGTGTGTCGACCACTGGAAT 276
QY 181 GAAATCTATTAATTTGTGGAACAGTTGGCTCAAAATTCATACGCCACAGTTGAGATG 240
DB 277 GAAATCTATTAATTTGTGGAACAGTTGGCTCAAAATTCATACGCCACAGTTGAGATG 336
QY 241 TCCCTTATTTGTTTCTCCACCGGAGGAACAACCTTAATGAATGAGAGAGAGAGAG 300
DB 337 TCCCTTATTTGTTTCTCCACCGGAGGAACAACCTTAATGAATGAGAGAGAGAGAG 396
QY 301 CAATTCCTGCAAGGCTTAGAAGAACTCCAGAAAGTCTGCGAGAGAGAGAGAGAGAG 360
DB 397 CAATTCCTGCAAGGCTTAGAAGAACTCCAGAAAGTCTGCGAGAGAGAGAGAGAGAG 456
QY 361 CATGAAGATTTGAAAGGGCCAGTGAAGAGATTTATGAAACAGACAGAGGTAAGG 420
DB 457 CATGAAGATTTGAAAGGGCCAGTGAAGAGATTTATGAAACAGACAGAGGTAAGG 516
QY 421 AAGGCAAGGCTATCATTTGCTGATGATGAGAACTCCAGAAAGTCTCTTTTCTAT 480
DB 517 AAGGCAAGGCTATCATTTGCTGATGATGAGAACTCCAGAAAGTCTCTTTTCTAT 576
QY 481 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTGCAATGTTTACTGTGTGTGTG 540
DB 577 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTGCAATGTTTACTGTGTGTGTG 636
QY 541 AAGATTTCAATGAGACACAGCTGCGCGGATTCGGAACAGTAAGGATCATGTGTTCC 600
DB 637 AAGATTTCAATGAGACACAGCTGCGCGGATTCGGAACAGTAAGGATCATGTGTTCC 696
QY 601 GTGAATGAGGCTTTCAAGGCTCTGCAAGGAGCATCATCTCAATTTTGAAGAAGTCTG 660
DB 697 GTGAATGAGGCTTTCAAGGCTCTGCAAGGAGCATCATCTCAATTTTGAAGAAGTCTG 755
QY 661 ATCGAAATTTAGACAGTGAACATCAACCAT-ATGTGCA-GGAGAGTCAATTTCAAGTTG 718
DB 756 ATCGAAATTTAGACAGGTTGAACATCCCATGATGTGCAAGGAGAGAGATTTCCAGGTG 815
QY 719 TC 720
DB 816 TC 817

RESULT 7
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LOCUS	833 bp	mRNA	linear	EST 23-JUN-2004
DEFINITION	AGENCOURT_26524177 NIH_MGC_212 Homo sapiens cDNA clone			
ACCESSION	IMAGE:30924322 5', mRNA sequence.			
VERSION	CO245219			
KEYWORDS	CO245219.1 GI:49108057			
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
TITLE	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
JOURNAL	Homidae; Homo.			
COMMENT	1 (bases) to 833)			
	NIH-MGC http://mgc.nci.nih.gov/ .			
	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Daniela S. Gerhard, Ph.D.			
	Office of Cancer Genomics			
	National Cancer Institute / NIH			
	Bldg. 31 Rm10A07 Bethesda, MD 20892			
	Email: cgapbs-remail.nih.gov			
	Tissue Procurement: Mary Hendrix			
	cDNA Library Preparation: M. Bento Soares, University of Iowa			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
	DNA Sequencing by: Agencourt Bioscience Corporation			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LNL at:			
	http://image.llnl.gov			
	Plate: NDAM1166	row: 3	column: 11	
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FEATURES	Location/Qualifiers
SOURCE	1. .833

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/clone_image="30924322"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/lab_host="DH10B (T1 phage resistant)"
/clone_idb="NH_MGC_212"
/notes="Organ: Lung; Vector: pYX-Abc; Site 1: EcoR I; Site 2: Not I; The library was constructed according Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pYX-Abc vector. The library tag sequence located between the Not I site and the polyA tail is GATAGGCCA. Tissue was provided by Mary Hendrix."

```

ORIGIN

Query Match	Similarity	59.7%	Score 658.8	DB 7	Length 833
Best Local	Conservative	97.9%	Pred. No. 5,4e-184	Matches 12	Indels 3
Matches	689	0			Gaps 2
QY	1	ATGGCCACGCGGAGCGAGAGAGCCCTCGCATCGGCTTCAGTGGCTCTTTTGGCACT	60		
Db	100	ATGGCCACGCGGAGCGAGAGAGCCCTCGCATCGGCTTCAGTGGCTCTTTTGGCACT	159		
QY	61	CTGGTCTCTATCTGGCGCGGGGCAAGGGGACGACGAGAGAGTGGGGTCCACCTGGTAC	120		
Db	160	CTGGTCTCTATCTGGCGCGGGGCAAGGGGACGACGAGAGAGTGGGGTCCACCTGGTAC	219		
QY	121	GGCGATTTGACCTGTACTTCAATTTTGGCAAAATCAGAAAGTGTGTGACCATCTGAAT	180		
Db	220	GGCGATTTGACCTGTACTTCAATTTTGGCAAAATCAGAAAGTGTGTGACCATCTGAAT	279		
QY	181	GAATATTAATCTTTTGGGACAGTTGGCTCACAATTTATACAGCCCAAGTTGGAAATG	240		
Db	280	GAATATTAATCTTTTGGGACAGTTGGCTCACAATTTATACAGCCCAAGTTGGAAATG	339		
QY	241	TGCTTATATGTTTCTCCACCGGAGAACACTTATGAAACTGACAGAAACAGAGAA	300		

Db 340 TCCTTTATTTGTTTCTCCACCCGAGAAACAACCTTAATGAACCTGACGAGAACAGAGAA 399

Qy 301 CAAATCCGTCAGGCGCTTAGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG 360

Db 400 CAAATCCGTCAGGCGCTTAGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG 459

Qy 361 CATGAGGATTTGAAAGGGCCAGTGAGACAGATTTATATGAAAACAGACAAAGGTCACAG 420

Db 460 CATGAGGATTTGAAAGGGCCAGTGAGACAGATTTATATGAAAACAGACAAAGGTCACAG 519

Qy 421 ACAGCGAGCGTCATCATTTGCTTTAGCTAGTAGAGAACTCCATGAAGATCTCTTTTCTAT 480

Db 520 ACAGCGAGCGTCATCATTTGCTTTAGCTAGTAGAGAACTCCATGAAGATCTCTTTTCTAT 579

Qy 481 TCAGAGAGGAGGCGTAATAGGTCCTCGAGATCTTGAGTCAGTAATGTTTACTGTGTTGTGTG 540

Db 580 TCAGAGAGGAGGCGTAATAGGTCCTCGAGATCTTGAGTAATGTTTACTGTGTTGTGTG 639

Qy 541 AAAGATTTCAATGAGACACACAGCTGCGCCGGATTGGCGACAGTAAGGATCATGTGTTTCCC 600

Db 640 AAAGATTTCAATGAGACACACAGCTGCGCCGGATTGGCGACAGTAAGGATCATGTGTTTCCC 699

Qy 601 GTGAATGACGGCTTTCAGGCTCTGTGCAAGGCAATCATCTCAATTTTGAATAAGTCCGCGC 660

Db 700 GTGAATGACGGCTTTCAGGCTCTGTGCAAGGCAATCATCTCAATTTTGAATAAGTCCGCGC 759

Qy 661 ATCGAAATTCAGAGCGTGAACCAATCCACCACTATGTGACAGAGA 704

Db 760 ATCGAAA-TCTAGACAGCTGAAC--ATCCACCATATGTGACAGAGA 800

RESULT	8
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LOCUS	
DEFINITION	BE741333 725 bp mRNA linear EST 15-SEP-2000 601594179P1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:394814 5', mRNA sequence.
ACCESSION	BE741333
VERSION	BE741333.1 GI:10155325
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 725) NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1998)
AUTHORS	Contact: Robert Strausberg, Ph.D.
JOURNAL	
COMMENT	

```

FEATURES
    source
        CDNA Library Preparation: Ling Hong/Rubin Laboratory
        DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
        DNA Sequencing by: Incyte Genomics, Inc.
        Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LNLN at: image.jnl.gov
        plate: L10CM810 row: n column: 19
        High quality sequence stop: 711.
        Location/Qualifiers
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                /lab_host="DH10B (phage-resistant)"
                /clone_1lb="NH MGC 9"
                /note="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dt priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCATCAG(G). Size-selected >500bp for average
                insert size 1.8kb. Library constructed by Ling Hong in

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QY 361 CATGAAGATTGAAAAGGCGCAGTACAGATTTATTATGAAAACAGACAGGCTACAG 420
DB 491 CATGAAGATTGAAAAGGCGCAGTACAGATTTATTATGAAAACAGACAGGCTACAG 550
QY 421 ACAGCAGCGCTCATCTTGTGCTGATGAGAACTCCATGAAGATCTTTTCTTAT 480
DB 551 ACAGCAGCGCTCATCTTGTGCTGATGAGAACTCCATGAAGATCTTTTCTTAT 610
QY 481 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCATTTGTTTACTGTGTGTG 540
DB 611 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCATTTGTTTACTGTGTGTG 670
QY 541 AAAGATTTCAATAGACACAGCTGGCCCGGATTCGAGACAGTAAAGTCACTGTTC 600
DB 671 AAAGATTTCAATAGACACAGCTGGCCCGGATTCGAGACAGTAAAGTCACTGTTC 720
QY 601 GTGAATGAGCGCTT 614
DB 731 GTGAATGAGCGCTT 744

RESULT 10
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LOCUS 602425082P1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4563020 5',
DEFINITION mRNA sequence.

ACCESSION BG326444
VERSION BG326444.1 GI:13132881
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Homidae; Homo.
COMMENT 1 (bases 1 to 963)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straube, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM276 row: c column: 21
High quality sequence stop: 718.
Location/Qualifiers

FEATURES
Source
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/issue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_14"
/note="Organ: kidney; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 53.0%; Score 585; DB 2; Length 963;
Best Local Similarity 96.3%; Pred. No. 5.2e-162;
Matches 621; Conservative 0; Mismatches 20; Indels 4; Gaps 2;

QY 1 ATGCCACGGCGGAGGAGAGCCCTCGGCATGCGCTTCAGTGGCTCTCTTGGCCACT 60
DB 114 ATGCCACGGCGGAGGAGAGCCCTCGGCATGCGCTTCAGTGGCTCTCTTGGCCACT 173
QY 61 CTGGTCTCATCTGCCCGGGCAAGGGGAGCGAGGAGAGTGGGCTCCAGCTGTAC 120
DB 174 CTGGTCTCATCTGCCCGGGCAAGGGGAGCGAGGAGAGTGGGCTCCAGCTGTAC 233
QY 121 GGGGATTGACCTGTACTTCAATTTTGGACAAATTCAGAAAGTGTCTGACCACTGGAAT 180
DB 234 GGGGATTGACCTGTACTTCAATTTTGGACAAATTCAGAAAGTGTCTGACCACTGGAAT 293
QY 181 GAAATCTATCTTGTGGAAAGTGGCTCAAAATTCAGCCACAGTGGAGATG 240
DB 294 GAAATCTATCTTGTGGAAAGTGGCTCAAAATTCAGCCACAGTGGAGATG 353
QY 241 TCCCTTATGTTTCTCCACCCGAGAAACAACCTTAATGAACAGAAACAGAGAA 300
DB 354 TCCCTTATGTTTCTCCACCCGAGAAACAACCTTAATGAACAGAAACAGAGAA 413
QY 301 CAAATCCGTACAGCCTTAGAAAGATTCAGAAAGTGTCTGACAGAGAGACACTTACATG 360
DB 414 CAAATCCGTACAGCCTTAGAAAGATTCAGAAAGTGTCTGACAGAGAGACACTTACATG 473
QY 361 CATGAAGATTGAAAAGGCGCAGTACAGATTTATTATGAAAACAGACAGGCTACAG 420
DB 474 CATGAAGATTGAAAAGGCGCAGTACAGATTTATTATGAAAACAGACAGGCTACAG 533
QY 421 ACAGCAGCGCTCATCTTGTGCTGATGAGAACTCCAGTAAAGATCTTTTCTAT 480
DB 534 ACAGCAGCGCTCATCTTGTGCTGATGAGAACTCCAGTAAAGATCTTTTCTAT 593
QY 481 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCATTTGTTTACTGTGTGTG 540
DB 594 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCATTTGTTTACTGTGTGTG 653
QY 541 AAAGATTTCAATAGACACAGCTGGCCCGGATTCGAGACAGTAAAGATCACTGTTC 600
DB 654 AAAGATTTCAATAGACACAGCTGGCCCGGATTCGAGACAGTAAAGATCACTGTTC 711
QY 601 GTGAATGAGCGCTTTCAGGCTTCGAAAGGATCATCTCAATT 645
DB 712 GTGAATGAGCGCTTTCAGGCTTCGAAAGGATCATCTCAATT 754

RESULT 11
BG281561 820 bp mRNA linear EST 21-FEB-2001
LOCUS 602402412P1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4544691 5',
DEFINITION mRNA sequence.

ACCESSION BG281561
VERSION BG281561.1 GI:13030486
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Homidae; Homo.
COMMENT 1 (bases 1 to 820)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straube, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
Plate: LNCM228 row: h column: 04
High quality sequence stop: 815.
Location/Qualifiers

FEATURES

source

1. .820
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:454691"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH MGC 20"
/note="Organ: skin; Vector: pOT7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG (G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 52.8%; Score 582.6; DB 2; Length 820;
Best Local Similarity 96.1%; Pred. No. 2,5e-161;
Matches 663; Conservative 0; Mismatches 19; Indels 9; Gaps 8;

QY 1 ATGGCCACGCGGAGAGAGCCCTCGGCATCGCTTCAGTGGCTCTCTTTGGCCACT 60
DB 112 ATGGCCACGCGGAGAGAGCCCTCGGCATCGCTTCAGTGGCTCTCTTTGGCCACT 171
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DB 172 CTGGTCTCATCTGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 231
QY 121 GCGGATTTGACCTGACTTCACTTTTGGCAAAATCAGAAAGTGTCTGACCACTGGAA 180
DB 232 GCGGATTTGACCTGACTTCACTTTTGGCAAAATCAGAAAGTGTCTGACCACTGGAA 291
QY 181 GAAATCTATTACTTTGTGAAACAGTT-GGCTCAAAATTCATAGCCACAGTTGGAA 239
DB 292 GAAATCTATTACTTTGTGAAACAGTTGGTGTTCACAAATTCATAGCCACAGTTGGAA 351
QY 240 GTCCCT--TATGTGTTTCTCCACCGAGAAACCTTATGAAATGACAGAGACAG 297
DB 352 GTCCCTATATGTGTTTCTCCACCGAGAAACCTTATGAAATGACAGAGACAG 411
QY 298 GAACAATCCGTCAGAGCCCTAGAAAGATCTCAGAAAGTTCTCCAGAGAGAGACCTTAC 357
DB 412 GAACAATCCGTCAGAGCCCTAGAAAGATCTCAGAAAGTTCTCCAGAGAGAGACCTTAC 471
QY 358 ATGCATGAAGAGATTGAAAGGCGCAGTGAAGCAGATTATT-ATGAAACAGACAGGTA 416
DB 472 ATGCATGAAGAGATTGAAAGGCGCAGTGAAGCAGATTATTATGAAACAGACAGGTA 531
QY 417 CAGGACAGCAGGCTATCATTTGCTTGAATGAGAACTCCATGAAGATCTCTTTT 476
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QY 477 CTATTCAGAGAGAGAGCTTATAGTCTCGAGATCTTTGGTCAATTTTACTGTGTTG 536
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QY 537 TGTGA-AGATTTCATAGACACAGCTGCGCGGATTCGAGACAGT-AAAGATCATGTG 594
DB 652 TGTGAACAGATTTCATAGACACAGCTGCGCGGATTCGAGACAGT-AAAGATCATGTG 711
QY 595 TTTCCCGTGAATACGCTTTCAGGCTTCGAGAGAGATTCACATCAATTTTGAAGAAG 654
DB 712 TTTCCCGTGAATACG-TTTCAAGGCTTCG-AGGATCATCAATCAATTTTGAAGAAG 769
QY 655 TCTGCATCGAAATTCAGAGCTGAACCATCCACATATGTGACAGAGAG 705
DB 770 TCTGCATCGAAATTCAGAGCTGAACCATTACA-CATATGTGACAGAGAG 819

RESULT 12
CF132432

LOCUS CF132432 641 bp mRNA linear EST 05-AUG-2003
DEFINITION UI-HF-PQ0-awo-m-16-0-UI.r1 NIH MGC_215 Homo sapiens cDNA clone
IMAGE:30560079 5', mRNA sequence.
ACCESSION CF132432
VERSION CF132432.1 GI:33215693
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 641)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
COMMENT 8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Mary Hendrix
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/humanfl.html
Seq primer: pyx-5.
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location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30560079"
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/lab_host="DH10B (71 phage resistant)"
/clone_1ib="NIH MGC 215"
/note="Organ: Lung; Vector: pYX-Absc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Absc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATTAAGGCCA. Tissue was provided by Mary Hendrix."

ORIGIN

Query Match 50.0%; Score 552; DB 6; Length 641;
Best Local Similarity 99.8%; Pred. No. 2,9e-152;
Matches 563; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGGCCACGCGGAGAGAGCCCTCGGCATCGCTTCAGTGGCTCTCTTTGGCCACT 60
DB 79 ATGGCCACGCGGAGAGAGCCCTCGGCATCGCTTCAGTGGCTCTCTTTGGCCACT 138
QY 61 CTGGTCTCATCTGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 139 CTGGTCTCATCTGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 198
QY 121 GCGGATTTGACCTGACTTCACTTTTGGCAAAATCAGAAAGTGTCTGACCACTGGAA 180
DB 199 GCGGATTTGACCTGACTTCACTTTTGGCAAAATCAGAAAGTGTCTGACCACTGGAA 258
QY 181 GAAATCTATTACTTTGTGAAACAGTTGGCTCAAAATTCATAGCCACAGTTGAGATG 240
DB 259 GAAATCTATTACTTTGTGAAACAGTTGGCTCAAAATTCATAGCCACAGTTGAGATG 318

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Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

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1. 823
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
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/notes="Organ: trunk; Vector: pBluescript II KS(+);
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II KS(+) [Stratagene] vector to accommodate cDNA produced
with the T-primed protocol (Construction of
uni-directionally cloned cDNA libraries from messenger RNA
for improved 3' end DNA sequencing by Glenn Fu, et al.
U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with
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containing BglI and BamHI sites
[5'ggcgcgtgcagcccgccgacccgaataaaagc]
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ORIGIN

Query Match 48.4%; Score 534; DB 5; Length 823;

Best Local Similarity 80.4%; Pred. No. 7.3e-147;

Matches 650; Conservative 0; Mismatches 155; Indels 3; Gaps 2;

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3 CAGATTGGCTTAAAGTGTCTCTTGGACTTTCTGCTGCTGTGTGATGGGCAAG 62
85 GGGGAGCAGCAGGAGATGGGGGCTCCAGCTCTACGGCGATTTGACCTGATCTT 144
63 TGGGAAGAGAGAGAGACGGGGCTCTGCTCTACGGAGGTTTATTTGATCTTCA 122
145 TTGGCAAAATCAGAAAGTGTCTGCAACCACTGGAATGAATCTATTACTTTGG 204
123 CTGGCAAAATCAGAAAGTGTCTGCAACCACTGGAATGAATCTATTACTTTGG 182
205 TTGGCTCAAAATTCATCGCCCAAGTTGGAATGCTTTATTTCTCCACCGCA 264
183 TTGGCCCGCAAGTTCATAGCCCTCAGCTGAGGATGCTTCACTGTTCTCAAC 242
265 GGAACAACCTTATGAAGTGAAGAGACAGAAACAAATCCGTCAAGGCTTGAAGA 324
243 GGAACAATCTGATGATTAACAGAAAGACAGGAACAGTACTCAGGGTCTGAAGA 302
325 CTCCAGAAAGTGTGCGCAGAGAGACACTTACATCATGAGATTTGAAGGCGCAG 384
303 CTTCAGAAAGTCTTCAGAGAGGTGACACTACATCATGAGATTTGAAGGCGCA 362
385 GAGCAATTTATATATAAACAAGAGGTACAGACGCCGCTCATCTGTTTG 444
363 GAACAAATTTACTATGAAAATGTTCAATGTTTACAGAACTGCAAGTTCATTT 422
445 ACTGATGAGAACTCATGAAAGATCTTTTCTATTTCAGAGAGGAGCTAATAGT 504
423 ACAGATGAGAGAGTCCACGAAGACATATTTTCTACTGAGAGGAGGCAATCG 482
505 CGAGATCTTGTCGAATGTTTACTGTGTGTGTGAAGATTTCAATGAGACAGCT 564
483 AGAGAGCTGGAGCAACAGATATATGTGTGTGTGAAGACTTCAATGAACCACT 542
565 GCCCGATTCGCAAGTAAAGATCATGTGTTCCTCGTGAATGACGGCTTTCAGG 624
543 GCGAAGATTCGTCAGCAAGCAAGATCATGTCTTCTGTGATGATGATGATTTG 602
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QY 685 TCCACCAATATGTCAGAGAGATCAATTTCAAGTGTGTGAGAGGAAACGGCTTCGACAT 744
DB 663 TCCAGTAAATATGTCAGAGAGATCAATTTCAAGTGTGTGAGAGGAAATGATTTGACAT 722
QY 745 GCCCGCAAGTGCAGAGAGTCTCTGCACTTCAAGATCAATGATCTCGTCACTCAAT 804
DB 723 GCTGTAAAGTGCAGAGAGTACTCTGACGCTTCAAGATC-ATGACACACTCACTCAAT 781
QY 805 GAGAAGCCCTTTTCTGTGGAAGACACTT 832
DB 782 GAGAAGCCCTTTTGTGTGGAAGAGATT 809
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RESULT 15
CD664532 564 bp mRNA linear EST 30-MAR-2005
LOCUS CD664532
DEFINITION g2b4 IMR32_SSH Homo sapiens cDNA, mRNA sequence.
ACCESSION CD664532
VERSION CD664532.1 GI:40546157
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE
1 (bases 1 to 564)
De Preter, K., Pattyn, F., Bex, G., Strueman, K., Mente, B., Van
Roy, F., De Paep, A., Speleman, F., and Vandesompele, J.
Combined subtractive cDNA cloning and array CGH: an efficient
approach for identification of overexpressed genes in DNA amplicons
BMC Genomics 5 (1), 11 (2004)
15018647

COMMENT
Contact: Speleman, F.
Center for Medical Genetics
Ghent University Hospital
De Pintelaan 185, Medical Research Building, 2nd floor, 9000 Ghent,
Belgium
Tel: 3292406549
Fax: 3292404970
Email: franki.speleman@ugent.be.

FEATURES

source

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1. 564
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/cell_line="Neuroblastoma"
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ORIGIN

Query Match 48.3%; Score 533.4; DB 6; Length 564;

Best Local Similarity 96.6%; Pred. No. 9.4e-147;

Matches 545; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

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QY 416 ACAGACAGCCAGCTCATCTTGTGACTGATGAGAACTCATGAAAGATCTCTTT 475
DB 1 ACAGACAGCCAGCTCATCTTGTGACTGATGAGAACTCATGAAAGATCTCTTT 60
QY 416 TCTATTCAAGAGGAGGCTAATAGGCTTCGAGATCTTGTCATTTGTTTACTGTG 535
DB 61 TCTATTCAAGAGGAGGCTAATAGGCTTCGAGATCTTGTCATTTGTTTACTGTG 120
QY 536 GTGTAAAGATTTCAATGAGACAGCTGGCCGGAATTCGCAAGTAAAGATCATGTGT 595
DB 121 GTGTAAAGATTTCAATGAGACAGCTGGCCGGAATTCGCAAGTAAAGATCATGTGT 180
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QY 596 TTCCCGTGAATGACGGCTTTCAGGCTCTGCAAGGATCATCACTCAATTTTGAAGAGT 655
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QY 656 CCTGCATCGAAATTTTACGAGCTGAACCATCCACATATGTGCAAGAGTCAATTTCAAG 715
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Db 241 CCTGCATCGAAATTTTACGAGCTGAACCATCCACATATGTGCAAGAGTCAATTTCAAG 300
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QY 716 TTGTCGTGAGAGGAAACGGCTTCCGACATGCGCGCAACGTGACAGGGTCTCTGCAGCT 775
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Db 301 TTGTCGTGAGAGGAAACGGCTTCCGACATGCGCGCAACGTGACAGGGTCTCTGCAGCT 360
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Db 361 TCAAGATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAGAGATACATTATT 420
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using BW model

Run on: December 17, 2005, 10:16:44 ; Search time 207.822 Seconds
(Without alignments)
9442.828 Million cell updates/sec

Title: US-09-970-076-1_COPY_104_1207

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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	803.8	72.8	1609	US-09-620-312D-8	Sequence 8, Appl1
2	516.8	46.8	3981	US-09-799-451-250	Sequence 250, App
3	346.2	31.4	2234	US-10-104-047-669	Sequence 669, App
4	307.4	27.8	1492	US-09-774-528-297	Sequence 297, App
5	307.4	27.8	1492	US-10-120-988-297	Sequence 297, App
6	79.4	7.2	450	US-10-131-827-8330	Sequence 8330, App
7	47	4.3	7218	US-08-232-463-14	Sequence 14, Appl
8	42.4	3.8	399	US-09-621-976-8976	Sequence 8976, App
9	41.4	3.7	7218	US-08-232-463-14	Sequence 14, Appl
10	40.6	3.6	37822	US-09-806-7088-22	Sequence 22, Appl
11	40	3.6	37822	US-09-949-016-16291	Sequence 16291, A
12	37.6	3.4	1141	US-09-806-7088-22	Sequence 22, Appl
13	37.4	3.4	3489	US-08-728-323A-1	Sequence 1, Appl1
14	37.4	3.4	3489	US-09-298-568-1	Sequence 1, Appl1
15	37.4	3.4	3489	US-09-410-399-1	Sequence 1, Appl1
16	37.4	3.4	3489	US-09-894-273-1	Sequence 1, Appl1
17	37.4	3.4	32207	US-08-770-379-20	Sequence 20, Appl
18	37.4	3.4	32207	US-08-757-659A-20	Sequence 20, Appl
19	37.4	3.4	32207	US-08-230-371A-20	Sequence 20, Appl
20	37.2	3.4	488	US-09-385-982-368	Sequence 368, App
21	37	3.4	254366	US-09-822-871-3	Sequence 3, Appl1
22	37	3.4	1830121	US-09-557-884-1	Sequence 1, Appl1
23	37	3.4	1830121	US-09-643-990A-1	Sequence 1, Appl1
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C 25	36.8	3.3	387902	3	US-09-949-016-14543	Sequence 14543, A
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27	36.2	3.3	2198	3	US-09-533-559-842	Sequence 842, App
28	36.2	3.3	5299	3	US-09-902-540-645	Sequence 645, App
C 29	35.6	3.2	424	3	US-09-621-976-7975	Sequence 7975, App
C 30	35.6	3.2	2278	3	US-09-620-312D-1003	Sequence 1003, App
C 31	35.6	3.2	2278	3	US-09-148-545-78	Sequence 78, Appl
C 32	35.6	3.2	2278	3	US-09-148-545-131	Sequence 131, App
C 33	35.6	3.2	2278	3	US-09-621-011-78	Sequence 78, Appl
C 34	35.6	3.2	2278	3	US-09-621-011-131	Sequence 131, App
C 35	35.6	3.2	2368	3	US-09-999-833A-471	Sequence 471, App
C 36	35.6	3.2	2368	3	US-10-020-445A-471	Sequence 471, App
C 37	35.2	3.2	1440	2	US-07-882-202A-3	Sequence 3, Appl1
C 38	35.2	3.2	1440	2	US-08-021-615A-3	Sequence 3, Appl1
C 39	35.2	3.2	1440	2	US-08-321-777-3	Sequence 13, Appl
C 40	35.2	3.2	1440	2	US-09-009-217-13	Sequence 13, Appl
C 41	35.2	3.2	1440	6	US-09-009-656-13	Sequence 13, Appl
C 42	35.2	3.2	1440	6	PCT-US93-04493-3	Sequence 3, Appl1
C 43	35.2	3.2	2138	3	US-10-030-203-12	Sequence 12, Appl
C 44	35.2	3.2	2409	3	US-09-949-016-2968	Sequence 2968, App
C 45	35.2	3.2	2422	2	US-08-475-845-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-620-312D-8
Sequence 8, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Lili, Chenghua
APPLICANT: Aesudi, Vinod
APPLICANT: Zhaudi, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Weinman, Tom
APPLICANT: Xue, Aildong J.
APPLICANT: Yang, Yongshong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghaast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_fl_genes Version 1.0
SEQ ID NO 8
LENGTH: 1609
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (309) ..(1202)
US-09-620-312D-8
Query Match 72.8%; Score 803.8; DB 3; Length 1609;
Best Local Similarity 99.8%; Pred. No. 9e-250;
Matches 805; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGCCACGGCGAGGAGAGGCCCTCGGATCGGCTTCAGTGGCTCTCTTGGCACT 60

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Qy 121 GCGCGATTGACCTGTACTTCAATTTTGA CAATCAGAAAGTGTGTGACCACTGGAA 180
Db 429 GCGCGATTGACCTGTACTTCAATTTTGA CAATCAGAAAGTGTGTGACCACTGGAA 488
Qy 181 GAAATCTATTACTTTGTGGAACAGTTGGCTCA CAATTCATCGCCCAAGTTGAGATG 240
Db 489 GAAATCTATTACTTTGTGGAACAGTTGGCTCA CAATTCATCGCCCAAGTTGAGATG 548
Qy 241 TCCCTTATTTGTTTCCCAACCGGAGAACACCTTAATGAATGAACAAGACAGAGA 300
Db 549 TCCCTTATTTGTTTCCCAACCGGAGAACACCTTAATGAATGAACAAGACAGAGA 608
Qy 301 CAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG 360
Db 609 CAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG 668
Qy 361 CATGAAGATTGAAAAGGCCAGTGAAGAGATTATTATGAACACAGACAGGATACAG 420
Db 669 CATGAAGATTGAAAAGGCCAGTGAAGAGATTATTATGAACACAGACAGGATACAG 728
Qy 421 AAGGCGAGGTCATCATTTGCTTGAAGTGAAGAACTCCAGTGAAGATCTTTTTCAT 480
Db 729 AAGGCGAGGTCATCATTTGCTTGAAGTGAAGAACTCCAGTGAAGATCTTTTTCAT 788
Qy 481 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTGCAATTGTTACTGTGTGTGTG 540
Db 789 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTGCAATTGTTACTGTGTGTGTG 848
Qy 541 AAGATTTCAATGAGACACAGCTGGGCCGAGATTGCCGACAGTAAAGATCATGTGTTCC 600
Db 849 AAGATTTCAATGAGACACAGCTGGGCCGAGATTGCCGACAGTAAAGATCATGTGTTCC 908
Qy 601 GTGAATGAGGCTTTCAGGCTCGCAAGGACATCATCTCAATTTTGAAGAAGTCTGCG 660
Db 909 GTGAATGAGGCTTTCAGGCTCGCAAGGACATCATCTCAATTTTGAAGAAGTCTGCG 968
Qy 661 ATCGAATTTCTAGCAGCTGAACCATCCATATGTGAGAGAGTCAATTTCAAGTTGTC 720
Db 969 ATCGAATTTCTAGCAGCTGAACCATCCATATGTGAGAGAGTCAATTTCAAGTTGTC 1028
Qy 721 GTGAGAGGAAAGGCTTCCGACATGCGCGCAACGTGGAACAGGCTCTGCAAGTTCAAG 780
Db 1029 GTGAGAGGAAAGGCTTCCGACATGCGCGCAACGTGGAACAGGCTCTCTGCAAGTTCAAG 1088
Qy 781 ATCAATGACTCGGTCACTCAATGAG 807
Db 1089 ATCAATGACTCGGTCACTCAATGAG 1115

RESULT 2
US-09-799-451-250
; Sequence 250, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yundong
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
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; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunxui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969: Nucleic Acids and
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pc_fl_genes Version 2.0
; SEQ ID NO 250
; LENGTH: 3981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (297)..(1118)
US-09-799-451-250

Query Match 46.8%; Score 516.8; DB 3; Length 3981;
Best Local Similarity 99.6%; Pred. No. 2,4e-156;
Matches 518; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 575 CGGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTTCAGGCTCGCAAGGCATCA 634
Db 1 CGGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTTCAGGCTCGCAAGGCATCA 60
Qy 635 TCCACTCAATTTTGAAGAAGTCTGTCATCGAAATTTAGACAGCTGAACCATCATAT 694
Db 61 TCCACTCAATTTTGAAGAAGTCTGTCATCGAAATTTAGACAGCTGAACCATCATAT 120
Qy 695 GTGCAAGAGATCATTTCAAGTGTGTGAGAGGAAAGGCTTCCGACATGCCCCGAAAG 754
Db 121 GTGCAAGAGATCATTTCAAGTGTGTGAGAGGAAAGGCTTCCGACATGCCCCGAAAG 180
Qy 755 TGGAAGAGGCTCTGCAAGCTTCAAGATCAATGATCTGGTCACTCAATGAGAGCCCT 814
Db 181 TGGAAGAGGCTCTGCAAGCTTCAAGATCAATGATCTGGTCACTCAATGAGAGCCCT 240
Qy 815 TTTCTGTGGAAGACATTAATTTACTGTGTGTCAGGCTTATCTTAAAGAGTTGGCATGA 874
Db 241 TTTCTGTGGAAGATTAATTTACTGTGTGTCAGGCTTATCTTAAAGAGTTGGCATGA 300
Qy 875 AAGCTGCACTCAGATCAGATGAAAGATGCGCTCTTTATCTTCAATTTCTGATCA 934
Db 301 AAGCTGCACTCAGATCAGATGAAAGATGCGCTCTTTATCTTCAATTTCTGATCA 360
Qy 935 TCACCACACACACATGTTCTGACGAGTTCCATCTGAGCAATCGCCCTGATCTGTGTC 994
Db 361 TCACCACACACACATGTTCTGACGAGTTCCATCTGAGCAATCGCCCTGATCTGTGTC 420
Qy 995 TGCTCTGAGCCCTGAGCTCTCTCTGTGTGTGAGCCCTCTGTCGACTGTGATTTACA 1054
Db 421 TGCTCTGAGCCCTGAGCTCTCTCTGTGTGTGAGCCCTCTGTCGACTGTGATTTACA 480
Qy 1055 AGGAGTCCCTTCAACCCCTGCGGAGAGAGTGAAGAAA 1094
Db 481 AGGAGTCCCTTCAACCCCTGCGGAGAGAGTGAAGAAA 520

RESULT 3
US-10-104-047-669
; Sequence 669, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241: full length cDNA
; FILE REFERENCE: H1-40105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
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; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 669
; LENGTH: 2234
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-669

Query Match      31.4%; Score 346.2; DB 3; Length 2234;
Best Local Similarity 58.3%; Pred. No. 3,7e-101;
Matches 628; Conservative 0; Mismatches 443; Indels 6; Gaps 1;

OY 1 ATGGCCAGCGGCGAGAGCCCTCGCATGGCTTCCAGTGGCTCTTTGGCCACT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 529 ATGGTGGCGGAGCGGTCCCGCGCCCGAGCCCGGAGCTGGCTGTTCCCGGGCTGTGG 588
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 61 CTGTGTCTCATCTGCGCGCGGCGAAGGGGAGCGAGAGAGATGGGGGTCCAGCTGTCTAC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 589 CTGTGTGTCTCATCTGCGCGCGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 648
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 121 GGGGATTTGACCTGTACTTCAATTTTGAACAAATCAGAAAGTGTGTGTGTGTGTGTGTGTGT 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 649 AGAGCTTTTATCTCTATCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 708
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 181 GAAATCTATTACTTTGTGAAACAGTTGGCTTCAAAATTCATCAGCCCAAGTTGAGAAATG 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 709 GAAATTTATATTTCGTACAGCAACTTGGAGAGATTTGTGAGCCCTGAAATGAGATTA 768
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 241 TCTCTTATTTTGTCTTCCACCCGAGAAACAACTTATAGAAACGACAGAAAGCAGAGAA 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 769 TCTTTCAATTTGTGTGTCTTCTCAAGCAACTTATTTTTCATTAAGTGTGTGTGTGTGTGT 828
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 301 CAATCCGTCAGAGGCTTGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 829 AATATCTGTAAAGGCTTGAAGATTTTAAACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 888
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 361 CATGAGGATTTGAAAGGCGCAGTACAGATTTTATATGAAACAGACAGAGGTCACAG 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 889 CATGAGGACTTAAAGTACGAAATGAAACAAAT-----TCAGAAAGCAGAGGCTTGAA 942
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 421 ACAGCCAGCTCATCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 943 ACCTCCAGTATCATTAATTTCTGTGACAGATGTGCAAGTTGACGCTGTGTGTGTGTGTGT 1002
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 481 TCAGAGAGGAGGCTTAATAGGTCTGAGATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1003 GCGAGAGAAAGGCAAAAGATATCCAGGTCACTTGGGCTAGTGTGTGTGTGTGTGTGTGTGT 1062
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 541 AAGATTTCAATGAGACACAGCTGCGCCGAGTTGCGGACAGTAAGATCATGTGTGTGTGT 600
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1063 CTGATTTTGAACAAGACACAGCTTGAAGAAATGCTGATTTCAAGAGCAAGTTTTCCT 1122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 601 GTGAATACGCGCTTTCAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1123 GTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 661 ATGCAATTTCTAGCAGCTGAAACATATCCATATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1183 ACTGAATTTCTGAATTTGTGACCTCTCAAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 721 GTGAGAGAAACGCGCTTCCGACATGCCGCAACGTGACAGGGTCTCTGTGACGCTTCAAG 780
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1243 TTAAATGGAAGAGATTCATCTGTGGGAGTGTGGAATGTGATGTCTGTGACATTAACAT 1302
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 781 ATCAATGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1303 GTAAATGAAACATATACACAGAGTGTAAACACAGTAAGTGTACAGCTTAATTTCTATGCTT 1362
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 841 TGTCCAGGCGCTTATCTTAAAGAGATTGGCATGAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1363 TGTCTGTGACCTTATCTGTATTAAGCTGTGAAAACTCTTGTGTGTGTGTGTGTGTGTGTGT 1422
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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OY 901 GATGCGCTCTCTTTTATCTTCCAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1423 GAGGAAATCTGTCTATTTTCAGATATTAATTTGTACAGCCAGACAAATGTTCTTAACGGG 1482
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 961 TCCATCTGTGCGCATCGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1483 ATGCAAGCATATTTTATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1542
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1021 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1077
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1543 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1599
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 4
US-09-774-528-297
; Sequence 297, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Kyle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aildong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: PL_FL_genes Version 2.0
; SEQ ID NO 297
; LENGTH: 1492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79)..(1434)
US-09-774-528-297

Query Match      27.8%; Score 307.4; DB 3; Length 1492;
Best Local Similarity 59.2%; Pred. No. 1.1e-88;
Matches 546; Conservative 0; Mismatches 371; Indels 6; Gaps 1;

OY 155 CAGGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 214
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2 CAGGCGCGCGGGGAGTAATGTGATTTGAATTTTATATTTGTGTGTGTGTGTGTGTGTGTGTGT 61
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 215 AATTCATGACCCCAAGTTGAGATGTCTTTATTTGTTTCTCAACCCGAGAAACCT 274
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 62 GATTTGTGAGCCCTGAAATGAGATTAATTTTCAATTTGTGTGTGTGTGTGTGTGTGTGTGTGT 121
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 275 TAATGAACCTGACAGAAAGAGAGAAACAATTCGTCAGAGGCTTGAAGAACTCCAGAAAG 334
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 122 TTTTGCATTAACTGTGAGACAGAGGCAAAATCAGTAAGGCTTGAAGAACTTAAACGTG 181
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 335 TTCTGCAAGAGAGACACTTAATCATGTAGTAAGATTTGAAGGCGCAGTGTGAGAGATTT 394
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 182 TTAGTCCAGTAGAGAGACATATATTCATGAAAGACTAAAGCTTGAAGAACTTAAT-- 239
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 395 ATTAATGAAACAGCAAGGCTAAGACAGCCAGCTCATCTTGTGTGTGTGTGTGTGTGTGTGT 454
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 240 -----TCAGAAAGCAGAGGCTTGAAGAACTTCCAGTATCATTAATTTGTGTGTGTGTGTGT 295
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Oy		455	AACGCCAAGAAAGATCTCTTTTTCATTGACAGAGGGAGCGTAATAAGCTCAGAATCTTG	514
Db		296	AGTTGGAACGCCTGTGGTCCCATCAITATGACAGAAAAGAGCAAAGATATCCAGGTCACTTG	355
Oy		515	GTCGAATTCGTTACTGTGTGGTGGTAGAAAGATTTCAATGAGACAACAGCTGACC	574
Db		356	GGGCTAGTCTTTATATGTGTGGGGGCTTGATTTTGAACAMGACACAGCTTGAAAGAAATTG	415
Oy		575	CGACACGTAAGGATCATGTGTTTTCCCCTGGAATGACGCGTTTCAGGCTTGTCAAGGCATCA	634
Db		416	CTGATTTCCMAAGAGACAGATTTTCCCTGCAAAAGGGAGATTTTCAGGCTCTTAAAGAAATA	475
Oy		635	TCCACTCAATTTTGMAGAAAGTCGTCGATCGAAATTCAGACGCTGAACATCCACATAT	694
Db		476	TTAATTTCTATCTAGCTACGATCACTGATCTGAATTCCTGAATTTGACGACCTTCMAAGTCT	535
Oy		695	GTCGACGAGAGTCAATTTCAAGTGTGCTGAGAGGAAACGAGCTTCGACATGCCGCAACG	754
Db		536	GTTGAGGGGGAAGAAATTTTCAGATTTGCTTAAGTGGAAAGAGATTCATGCTGGGCAGTCCGA	595
Oy		755	TGACACAGGGTCTCTGACGCTTCAAGATCAATGACTCGGTACACTCAATGAAAGCCCT	814
Db		596	ATGCGACAGGTCTCTGCACTTACACTGTAAATGAAACATATACAACGAGTGAACAAACGAG	655
Oy		815	TTTCTGTGGAGACACATTAATTACGTGTCCAGCGCCATCTCTAAANAAGTGGSCATGA	874
Db		656	TAAAGTACACACTTAATTTCTATGCTTTGTCTGACCTATCTGAAATTAACCTGGAGAA	715
Oy		875	AAGCTGCACTCCAGGTGACGATGAAAGCATGAGCCCTCTTTTATCTCCAGTCTGTCA	934
Db		716	CTCTTGATGTTTCACTGAGCTTTTAATGAGAGAAATCTGTCAATTCAGAGATCATTAATG	775
Oy		935	TCACCACACACACTGTTCTGACGGTTCATCTGGCCATCGCCCTGCTGATCTGTTC	994
Db		776	TCACAGCCACAGAAAGTTCTAAACGGGATCGACGCATCATGTTATTTTGGTGTATCGC	835
Oy		995	TGCTCTTACCCCTGGCTCTCCCTGTGTGTGTCTGTGGCCCCCTCTGCTGCACCTGTATATCA	1054
Db		836	TACTCTGTGGGATCGTGTGATGTGTGTGTGTGTGGCCCCCTTGTGCAAAAGTGTATTA	895
Oy		1055	AGGAGGTCCCTCCACCCCTGCGC	1077
Db		896	AGGATCTTCACACCAACCCCCC	918
 RESULT 5 US-10-120-988-297				
; Sequence 297, Application US/10120988				
; Patent No. 6919193				
; GENERAL INFORMATION:				
; APPLICANT: Tang, Y. Tom				
; APPLICANT: Goodrich, Ryle				
; APPLICANT: Liu, Chenghua				
; APPLICANT: Ren, Felyan				
; APPLICANT: Wang, Dunrui				
; TITLE OF INVENTION: No. 6919193el Nucleic Acids and				
; FILE REFERENCE: Polypeptides				
; CURRENT APPLICATION NUMBER: US/10/120,988				
; CURRENT FILING DATE: 2002-04-11				
; PRIOR APPLICATION NUMBER: 09/774,528				
; NUMBER OF SEQ ID NOS: 441				
; SOFTWARE: pc_FL_genes Version 2.0				
; SEQ ID NO 297				
; LENGTH: 1492				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
; FEATURE:				
; NAME/KEY: CDS				
; LOCATION: (79)..(1434)				
US-10-120-988-297				

Query Match	27.8%;	Score 307.4;	DB 3;	Length 1492;
Best Local Similarity	-59.2%;	Pred. No. 1.1e-88;		
Matches 546;	Conservative 0;	Mismatches 371;	Indels 6;	Gaps 1.

OY	155	AGGAAAGTGTCTCACCACTGGAAATGAAATCTTTTACTTTGTGGAAACAGTTGGCTCTCA	214
Db	2	CACGCCGCCGGCCGAAATACGTGAAATTTGAAATTTTATATTTTGGTACAGCAATCTGGGAGA	61
OY	215	AATTCAATCAGCCACAGTTGAGAAATGTCCTTATTTGTTTCTCCACCCGAGAACAACT	274
Db	62	GATTTGTAGCCCTGAAATAGATTTATCTTTCATGTGTTTCTTCTCAAGCACTATTA	121
OY	275	TAAATGAACTGACAGAAACAGAAACAAATCCCTCAAGGCTTAAAGAACTCCAGAAAG	334
Db	122	TTTTGCCCTTAACTGGAGACAGAGCCAAATCAGTAAAGGCTTGGAGATTAAACGTG	181
OY	335	TTCTGCCAGAGAGAGACACTTACATGCAATGAAAGATTGAAAGGGCCAGTGGAGATTT	394
Db	182	TTAGTCCAGTGGAGAGACATATTTCCATGAAAGCTAAAGCTACGAAATGAACAAAT--	239
OY	395	ATTATGAAACAGACAAAGGTACAGGACAGCCAGGCTCATTTGCTTTGACTGATGGAG	454
Db	240	----TCGAAAGCAGAGAGGCTTGAAAACTCCAGATCATATATTTCTCTGACAGATGGCA	295
OY	455	AATCCATGAAGATCTCTTTTCTTATTTCAATTCAGAGAGGAGGCTTAATATGTTCTCGAATCTTTG	514
Db	296	AGTTGAGACGGTCTGGTGCATCATATGACAGAAAGAGCAAAAGTATTCAGGTCACTTG	355
OY	515	GTGCAATTTGTTTACTCTGTGTGTGTGGAAAGATTTCAATGAGCAAGCTGGCCGGATTG	574
Db	356	GGGCTAGTGTATATGTGTGTGGGGCTCTTGATTTTGAACACAGCAAGCTTGAAAGAAATTG	415
OY	575	CGGACAGTAAAGATCATGTGTTTCCCGTGAATGACGGCTTTCAGGCTCTGCAAGGACATCA	634
Db	416	CTGATTCGAAGAGGAAGTTTCCCTGTCAAAAGGATTTCCAGGCTCTTAAAGAAATTA	475
OY	635	TCCACTCAATTTGAAAGATCTCTGCAATCGAAATTTCTGACAGCTAACCATCACCATAT	694
Db	476	TTAATTTCTATCTAGCTCAGTCACTGATCTGAATCTTGAATTTGACGCCCTCMAAGTCT	535
OY	695	GTGCAAGAGATCAATTTCAAGTGTGCGAGAGAAAGGCTTCCGACATGCCCGCAACG	754
Db	536	GTGTGGGGGAAGAAATTCAGATGTCTTAAAGTGAAGAGATTCATGCTGGCAAGTCGGA	595
OY	755	TGGAACAGGATCCTCTGCACTTCAAGATCAATGACTCGGTCACTCATATGAAAGCCCT	814
Db	596	ATGGCAGTGTCTCTGCACTTACCTGTAAATGAAACATATACACAGGTGTAAACAG	655
OY	815	TTTCTGTGAAGACACTTATTTTACTGTGTCCAGCGCCTATCTTAAAGAAAGTTGGCATCA	874
Db	656	TAAAGTGTCAACTTAAATCTATGCTTTTCTCTGCACTTACTGTAAATGAAGCTGGAGAA	715
OY	875	AAAGTGCACCTCAGGTGAGCAATGAACATAGGCTCTCTTTTATCTCCAGTTCTGTGCATCA	934
Db	716	CTCTTGATGTTTCACTGAGCTTAAATGAGAGAAATCTGTCACTTCCAGGATCATTAATTTG	775
OY	935	TCACCACACACACTGTTCTGACGGTTCCATCTGGCCATCGCCCTGCTGATCTGTGCC	994
Db	776	TCACAGCCACAGAAATTTCTAAACGGGATTCGACGATCATTTGTATTTTGGTGTAACTGC	835
OY	995	TGCTCTAGCCCTGGCTCTCCTCTGTGTGTCTGGCCCTCTGTCTGCTGACCTGTGATTTATCA	1055
Db	836	TACTCTGGGATCGGTTTGATGTGTGTGTGTGGCCCTTGTGCTGCAAAAGTGTATTA	895
OY	1055	AGGAGTCCCTTCACCCCTGCGC	1077
Db	896	AGGATCTTCACCAACCCCGC	918

RESULT 6
US-10-131-827-8330
; Sequence 8330, Application US/10131827


```
Patent No. 6905827
GENERAL INFORMATION:
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 50661200120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8330
LENGTH: 450
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-8330

Query Match
Best Local Similarity 7.2%; Score 79.4; DB 3; Length 450;
Matches 143; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 829 ACTATTATTAGTGTGTCAGGCGCCCTATCTTAAAGAGTTGGATGAAAGCTGACCTCCAG 888
DB 10 AATCTATGCTTGTCTCCGACCTATCTGTAATAAGCTGGAAGACTTGATGTTTCA 69
QY 889 GTGAGCATGAACGATGCGCTCTTTATATCTCCAGTTCTGTCATCATCACCACACAC 948
DB 70 GTGAGCTTTAATGAGGAAATCTGTCAATTCAGATCATTAATGTTCACAGCCACAGAA 129
QY 949 TGTTCGACGGTTCATCTGCGATGCGCCCTGCTGATCTGCTCTGCTCTAGCCCTG 1008
DB 130 TGTTCACAGGAGATCGACGACCATATGTTATTTTGGTGTTACTGCTACTCTGGGATC 189
QY 1009 GCTTCCTCTGTGTGTCTGTGCGCCCTCTGCTGACCTGATTAATCAAGAGTCCCTCA 1068
DB 190 GGTTCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 249
QY 1069 CCCCCTGCC 1077
DB 250 ACCCCCCC 258

RESULT 7
US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHREIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZSPC-Fls
US-08-232-463-14

Query Match
Best Local Similarity 4.3%; Score 47; DB 2; Length 7218;
Matches 26; Conservative 199; Mismatches 164; Indels 0; Gaps 0;

QY 689 CCATATGTGACGAGAGTCATTTCAAGTTGTCGTGAGAGAAAGCGCTTCCGACATGCC 748
DB 1011 CCATAGCTCAGAGAAATTAATTCGAGCTTGCTGAGAGTCGAGGAGCTTGGCATY 1070
QY 749 GCAACGTGACAGAGTCTCTGACGCTCAAGTCAATGATCTGGTCACCTGAATGAGA 808
DB 1071 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1130
QY 809 AGCCCTTCTGTGGAAGACATTAATTAATGTCGACGCGCTATTAAGAAAGTTG 868
DB 1131 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1190
QY 869 GCATGAAGCTGACCTCAGGTGACATGAGATGAGTGGCTCTTTATCTCCAGTTCTG 928
DB 1191 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1250
QY 929 TCATCATCACCACACACACTGTTCTGACGTTCCATCCCGCATGCGCCCTGATCC 988
DB 1251 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1310
QY 989 TGTTCCTGCTCTAGAGCCCTGCTCTGTTGTTCTGAGGCTCTGCTGCTGACATGTA 1048
DB 1311 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1370
QY 1049 TTAACAAGAGGTCCCTCCACCCCTGCC 1077
DB 1371 YYYYYYYYYYYYYYYYYYYYYYYYYYYY 1399

RESULT 8
US-09-621-976-8976/c
Sequence 8976, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J. B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J. Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 8976
LENGTH: 399
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TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-8976

Query Match 3.8%; Score 42.4; DB 3; Length 399;

Best Local Similarity 8.9%; Pred. No. 0.0046;
Matches 25; Conservative 142; Mismatches 113; Indels 0; Gaps 0;

QY 6 CACGCGAGCGAGCCCTCGGATCGGCTTCAGTGGCTCTTTGGCCCTCTGAT 65
DB 284 SRGSGTGRMSYRMMRGSMGSGSYRMAGRSSRWRYSAMRKKMTWKRRSSW 225
QY 66 GCTCATCTGCGCGGCGAGGAGGAGATGGGGTCCAGCTGCTTACGCGCG 125
DB 224 GSRSTGYAMMYKMSWCTSRKMYKRRKCTSTRTCYRGSTYKCMAYTTT 165
QY 126 ATTGACCTGATCTTATTTGACAAATAGAAAGTGTCTCACCCTGGAATGAAAT 185
DB 164 RMTATYTYYYKSYMCKTWRKKTAYTYWTKRMKTRTWTCTMCKCTTYMMAGTMY 105
QY 186 CTATATCTTTGTGAACAGTTGGCTCACAATTCATCAGCCAGTGGAGATGCTT 245
DB 104 RYRKYVYVYAKRAKMSKRCSTTCTCYCKTMAKCMGYSMSMKMGKSMWMTYTY 45
QY 246 TATGTTTCTCCAGCGAGAACACTTAATGAAACTG 285
DB 44 YMKMSKMTYMSWSCYARKCMRTYAKTYTMTCTMTGKR 5

RESULT 9
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367

GENERAL INFORMATION:

APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINER, F.

TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria
STATE: VA

COUNTRY: USA
ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,463
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/935,313
FILING DATE:

APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300

TELEFAX: (703)683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZgpc-Fls
US-08-232-463-14

Query Match 3.8%; Score 41.4; DB 2; Length 7218;

Best Local Similarity 6.8%; Pred. No. 0.07;
Matches 27; Conservative 198; Mismatches 174; Indels 0; Gaps 0;

QY 263 GAGAACAACTTAATGAACTGACAGAAAGACAGAAACAAATCCGTCAGAGCTTAGA 322
DB 1407 RRR 1348
QY 332 AACTCAGAAAGTTCTGCCAGAGAGACACTTACATGATGATTTGAAGGCGCA 382
DB 1347 RRR 1288
QY 383 GTGACAGATTTATATGAAACAGACAGAGGTACAGACAGCCGTCATCTTCTT 442
DB 1287 RRR 1228
QY 443 TGACTGATGAGAACTCCATGAAGATCTCTTTTATCAGAGAGGAGCTTAATAGT 502
DB 1227 RRR 1168
QY 503 CTCGAGATCTTGTCATTTGTTTACTGTGTGTGTGAAGATTTCAATGACACAGC 562
DB 1167 RRR 1108
QY 563 TGCCCGGATTCGACAGTAAAGATCATGTGTTTCCCTGAATAGCGCTTCAGGCTC 622
DB 1107 RRR 1048
QY 623 TGCAAGCATCATCCATCAATTTTGAAGAAGTCTGCA 661
DB 1047 TCGAGCAAGCTCGGAAATTAATCTGTGAGCGTATGCA 1009

RESULT 10
US-09-806-708B-22

Sequence 22, Application US/09806708B
Patent No. 6784342

GENERAL INFORMATION:

APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants

FILE REFERENCE: 4810-58741

CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03

PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04

NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patent In version 3.0

SEQ ID NO 22
LENGTH: 1141

TYPE: DNA
ORGANISM: Artificial sequence

FEATURE:
NAME/KEY: promoter

LOCATION: (1)..(1141)
OTHER INFORMATION: consensus sequence of A.c., L.a., and B.n. PAB1 promoters

US-09-806-708B-22

Query Match 3.7%; Score 40.6; DB 3; Length 1141;

Best Local Similarity 9.8%; Pred. No. 0.036;
Matches 68; Conservative 270; Mismatches 353; Indels 2; Gaps 1;

QY 226 CCACAGTTGAGATGCTTATTTATTTCTCCACCCGAGAACACTTAATGAAACTG 285
DB 98 YHARRKWKMTAYBMTMTMKGTGWRHRYWRBAMBDVDDHYVYVYANANNAATTCMDK 157
QY 286 ACAGAAAGACAGAAACAAATCCGTCAAGCCCTAGAAAGAACTCCAGAAATTCGCCAGGA 345
DB 158 DDKRTTMMKKNNATGMDDTKTHMMNNNGCBYTVMTVRYKTRDWSBKRNMYGMBMWK 217

QY 346 GGAGACACTTACATGCTAGTAAGATTGTAAGGCCGAGTGAAGATTTATTAAGAAC 405
DB 218 NMSYDVTYVWVDDMKRKYRRVWVTRGRNRVWVMBTAHRRYNNGTBMAAYRRMT 277
QY 406 AGACAAGGCTTACAGACAGCAGCGTATGCTTGTGA--CTGATGAGAACTCCATG 463
DB 278 MNNNNNNNAKMCRAKRWGNBVBVNSTCTTWSKTTKATVTSCHANNCRAGDANKHKWM 337
QY 464 AAGATCTTTTCTTATTCAGAGAGAGGCTTAATAGCTTCAGATCTTGTCGAATTG 523
DB 338 KMSAAMGVYNNNNNNNNMTYKARHBARDVMBVMSAKKMHANAHAHYSRKMTBYKKXTM 397
QY 524 TTTACTGTGTGGGTGTAAGATTTCAATGACACAGCTGGCCCGATGCGGACAGTA 583
DB 398 VNNNGTGTWKRMMWAMWYKMDMBGTYYNNNNNGRTYGTWTKNKKMTYKMKANCKW 457
QY 584 AGGATCATGTGTTCCCGTGAATGACGGCTTTCAGGCTTCGAAAGCATCATCACTCAA 643
DB 458 RANDBKTCNNNTTWMKTKTYNNNCYKSKMTNGSHBAAAVYTWYMMRRYAHANNNN 517
QY 644 TTTGAAGAAGCTTCGATCGAAATTCCTAGACGTAACCATCCATATGTCAGAG 703
DB 518 WDYWKACTWYKYBVCCKMNNNYAAWYTKSMYTSRYRWKTNNSWRMSDTRSMGRAN 577
QY 704 AGTCATTTCAAGTTGTCTGAGAGAAACGGCTCCGACATGCCCGCAAGCTGACAGG 763
DB 578 NYARABHYGYKMTNRMBWHSHTWBHRAGAHAYMBWMBYAKCHCMAMWKAKKYAGAG 637
QY 764 TCCTCTCAGCTTCAGATCATGACTCGGTGACACTCAATGAGAACCTTTTCTGTG 823
DB 638 SNNNNNNNNNNNNNNNNATCARDDYAAASRYAMAAKYYKBAANNAAYTHANNWGC 697
QY 824 AAGACCTTATTTACTGTCTCAGCGCTATCTTAAAGAAGTTGGCATAAGCTGCAC 883
DB 698 MNNATDTRMTWKKNNNNNAGTWKNNNNNNAKNAASAAKVAAYAAKAKKMRWAMKWM 757
QY 884 TCAGGTCAGCATGAAGATGCGCTCTCTTTA 916
DB 758 RGMHADAABRTDGRNNNGAYTKYTTNNNNNTYR 790

RESULT 11
US-09-949-016-16291/C
; Sequence 16291, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 16291
; LENGTH: 37822
; TYPE: DNA
; ORGANISM: Human
; FEATURES:
; NAME/KEY: misc feature
; LOCATION: (1)...(37822)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16291

Query March 3.6%; Score 40; DB 3; Length 37822;
Best Local Similarity 51.7%; Pred. No. 0.61;

Matches 91; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
QY 259 ACCCGAGGAACAACCTTAATGAACATGACAGAAAGACGAACAAATCCGTAGAGCCCTA 318
DB 8207 ATCCGAGAAACATAATTAACAAACAGAACGACAAATTAATTAATATGCTAAAAA 8148
QY 319 GAAGAATCCAGAAAGTTCTGCGAGAGAGACACTTAATGATGATGAAGATTGAAG 378
DB 8147 CAAGAAACCGAGTAGGAGAAAGATCTGAGTTCTAGAAATAGACATTAATTTAAATG 8088
QY 379 GCCAGTGACAGATTTATTAAGAAAAGACAAAGGTTACAGACAGCCAGCTCAT 434
DB 8087 TCAGGTTTTCAGCAAAACGATATAGACACAAAGAAAGAGAAAGATAGGCTCAT 8032

RESULT 12
US-09-806-708B-22/C
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAB1 promoters
US-09-806-708B-22

Query Match 3.4%; Score 37.6; DB 3; Length 1141;
Best Local Similarity 10.9%; Pred. No. 0.34;
Matches 89; Conservative 281; Mismatches 443; Indels 6; Gaps 1;

QY 286 ACAGAGACAGAGAAACAAATCCGTCAGAGCCCTGAGAGACTCCAGAAAGTTGCGACGA 345
DB 987 AAKKMAWMAWNN 928
QY 346 GGAGACACTTACATGCTAGTAAGATTGTAAGGCCGAGTGAAGATTTATTAAGAAC 405
DB 927 MKAANNNNNNNAAYTTACTNRAATNNKATTHMKHTGASHSRRTTRHTRTORRKYNNNNN 868
QY 406 AGACAAGGCTTACAGACAGCAGCGTATCATGCTTGTGAATGATGAGAACTCCATGAA 465
DB 867 NARTVYVYHHAARWMAWMTTRNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 808
QY 466 GATCTCTTTTCTTATTCAGAGAGAGGCTTAATAGCTTCGATGATCTGTGCAATTGT 525
DB 807 NNNNTWCHYTTAABDVRANNNNNAARMAKTCNNYMAAVTTTHDWCYKTMWNTWYWD 748
QY 526 TACTGTGTGTGTAAGATTCAATGAGACACAGCTGCCCGGATTTGGCAGATGAG 585
DB 747 MMTTMTTTRNNNTSTNN 688
QY 586 GATCATGTGTTCCCGTGAATGACGGCTTCAGGCTTCGAAAGCATATCACTCAAT 645
DB 687 RTNNNTTVMRBRWMTNTKTRWYSTTRRHVYGATNNNNNNNNNNNNNNNNNNNNNNNN 628
QY 646 TTGAAGAAGTCGCAATCGAAATTTCTAGAGCTGGAACCATCCACATATGAGAGAGAG 705
DB 627 RWTMKGDMTVRKVKVKKRDTTCTYVDWADSWWYTAANNRCKDVYTRNNYCKSYAHS 568
QY 706 TCATTTCAAGTTGCTGAGAGAGAAACGGCTTCGACATGCCGCAACGTGACAGGCTC 765

Db	567	1WYMSNNAMWYRRYSABRWSSMARITTTNNMMWSGBVAMRWAGTMMWHMNNNTDREYY	508
Qy	766	CTGCGACGCTTCAGATCATGACTCGGTCACACTCAATGAGAACCCCTTTTCTGTGGA	825
Db	507	WWWKMMABTITTVYDSMCAKSMFMGNWWRAMKMMWAAANNAGAMDHTYMMGNNTMMR	448
Qy	826	GACACTATTACTGTGTCCAGCGGCTATCTTAAAGAAGTTGGCATGAAGCTGCATCC	885
Db	447	RAMKMMNNAMCPRAYCCNNNNNNRACVWHKHK----MWRWTWKMMWGAACNNNNBKMY	394
Qy	886	CAGGTCAGCATGAACGATGGCCTCTTTTATCTTCAGGTTCTGTATCATCACACACA	945
Db	393	MRVAMMYSRDPTNTDMMWTSDBMHMYTYDYTMRLAMNNNNNNNNMBCKTSMWMMMD	334
Qy	946	CAGTGTTCGACGGTTCATCCTGGCCATCGCCCTGTGATTCCTGTTCCTGCTCCTAGCC	1005
Db	333	HMNTHCTYGNNTWGSAYBMAAASMAAGASBNVTYMCMRMTYMGKWTNNNNNNKAWY	274
Qy	1006	CTGGCTCTCCTCTGTGGTCTTGAGCCCTTCGTGCTCATGTGATTATCAAGAGGTCCCT	1065
Db	273	RTKTVAMCNRNYYDYTAVTBKRNNKYCYAABWYBMVTKGHMBWRBRABHRSNNMMWV	214
Qy	1066	CCACCCCTCGCGAGAGAGTGAAGAAATAATAATATAA	1104
Db	213	KCRNKTYMSHTYHAKRYKMBABVCCNNNNMKDRAAHHTM	175

RESULT 13
US-08-728-323A-1/c
; Sequence 1, Application US/08728323A

GENERAL INFORMATION:

1 APPLICANT: Chang, Yuan
 2 APPLICANT: Bohenzky, Roy A.
 3 APPLICANT: Russo, James J.
 4 APPLICANT: Edelman, Jidore S.
 5 APPLICANT: Moore, Patrick S.
 6 TITLE OF INVENTION: Immediate Early Protein From Kaposi's
 7 TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
 8 TITLE OF INVENTION: Encoding Same And Uses Thereof
 9 NUMBER OF SEQUENCES: 21
 10 CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.

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;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:

NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTIC
; LENGTH: 3489 base pa
; TYPE: nucleic acid

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;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
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; FEATURE:
; NAME/KEY: CDS

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LOCATION: 1..3489
US-08-728-323A-1

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1149 CTCCTGCATCTCTCTGTCATCTCTCTGTCATCTCTCTGTCATCTCTCTGTCATC 109

943 AACACACTGTTCTGACGGTTCATCCTGGCCATCGCCCTGTCGATCCTTCTCTCCCTCA 100

1089 CTCCTGTCATCTCCTCTCATCTCCCTGTCATCCTCCTGTCATC 103

1003 GCCCTGGCTCTCTCTGGTGGTTCGGCCCCCTGCTGCACCTGTGATTATCAAGAGGTC 106

1029 CTCTCGACCTCATCTGTCTCCTGCTCTCTCCATCATCTTATGTGATGTGATC 970

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505 C11 50 /

ESULT 14
S-09-298-568-1/C

Sequence 1, Application US/09298568
Patent No. 6322792

GENERAL INFORMATION:
APPLICANT: Kieff, Elliott D.

APPLICANT: Ballesstas, Mary E.
APPLICANT: Kaye, Kenneth M.

TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
 TITLE OF INVENTION: KHAJALU VIRUS LANA ACIDS IN IRANS ON A UNIT OF KHAJALU
 TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
 FIRM PRESENCE: 15613-100013

FILE REFERENCE: 1912-1001A
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21

EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19

NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1
LENGTH: 3489

TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
NO. OF NUC. ACID BASES: 162,000

Query Match 3.4% Score 37.4 DB 3 Length 3489
S-U3-298-368-1

Best Local Similarity	50.3%	Pred. No. 0.85;
Matches	92:	Conservative
	0:	Mismatches
	0:	Indels
	0:	Gaps

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1149 CTCCTGTCATCCTCTGTCATCCTCTGTCATCCTCTGTCATCCTCTGTCATC 1091

943 ACACACTGTCTGACGGTTCCATCCTGGCCATGCCCTGCTGATCTCTTCTCTCTTA 1003

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1003 GCCTGGCTCTCCTGATGGTTCGGCCCTCTGCTGCACGTGATTATCAAGAGATC 106

1029 CTCCTGCTCCTCATCTGTCTCCTGCTCCCTCATCATCTTATTTGTCATTGTGATTC 970

1063 CCT 1065

b 969 CTT 967

RESULT 15
00 410 200 1/2

S-03-410-399-1/C
Sequence 1, Application US/09410399
Patent No 6482587

GENERAL INFORMATION:

APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A. to Inhibit or Enhance the Binding of Viral DNA
TITLE OF INVENTION: Methods to Genomic Host DNA
FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ. ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 3489
TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-410-399-1

Query Match 3.4%; Score 37.4; DB 3; Length 3489;
Best Local Similarity 50.3%; Pred. No. 0.85;
Matches 92; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
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1149 CTCCTGTCATCCTCTGTCATCTCTGTCATCTCTGTCATCTCTGTCATCTCTGTCATC 1090
QY 943 ACACACTGTTCTGACGGTTCATCTGGCCATCGCCCTGATCTCTGTCCTCTCTA 1002
DB 1089 CTCCTGTCATCTCTGTCATCTCTGTCATCTCTGTCATCTCTGTCATCTCTGTCATC 1030
QY 1003 GCCCTGGCTCTCTCTGAGTGTGAGCCCTCTGTCGACTGTGATTTATCAAGAGGTC 1062
DB 1029 CTCCTGTCCTCTCTGTCATCTGTCTGTCCTCTCTCTCATCACTTATGTGATGTGATC 970
QY 1063 CCT 1065
DB 969 CTT 967

Search completed: December 17, 2005, 13:37:40
Job time : 215.822 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 17, 2005, 13:22:55 ; Search time 105.43 Seconds
(without alignments)
8990.628 Million cell updates/sec

Title: US-09-970-076-1_COPY_104_1207

Perfect score: 1104

Sequence: 1 atggccacggcgagcgag.....gtgaggaataataataaa 1104

Scoring table: IDENTITY_NUC

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1104	100.0	1414	10	US-11-047-278-1
2	1104	100.0	1454	6	US-10-133-937-58
3	1104	100.0	1454	6	US-10-159-563-58
4	1090.8	98.8	5540	3	US-09-918-715-176
5	1090.8	98.8	5540	3	US-09-918-715-231
6	1090.8	98.8	5540	6	US-10-301-822-198
7	1090.8	98.8	5540	8	US-10-474-794-176
8	1090.8	98.8	5540	9	US-10-474-794-231
9	1090.8	98.8	5540	9	US-10-979-159-176
10	1090.8	98.8	5540	9	US-10-979-159-231
11	1090.8	98.8	5540	10	US-11-047-278-5
12	960.8	87.0	1674	6	US-10-038-307-17
13	960.8	87.0	1674	6	US-10-201-292-17
14	952.4	86.3	1650	6	US-10-038-307-13
15	952.4	86.3	1650	6	US-10-038-307-15
16	952.4	86.3	1650	6	US-10-201-292-13
17	952.4	86.3	1650	6	US-10-201-292-15
18	950.8	86.1	1650	6	US-10-038-307-9
19	950.8	86.1	1650	6	US-10-201-292-9
20	949.4	86.0	1056	6	US-10-038-307-23
21	949.4	86.0	1056	6	US-10-201-292-23
22	949.4	86.0	1713	6	US-10-038-307-19
23	949.4	86.0	1713	6	US-10-201-292-19

24	949.4	86.0	2112	10	US-11-047-278-7	Sequence 7, Appl1
25	949.4	86.0	2272	3	US-09-796-753-11	Sequence 11, Appl1
26	949.4	86.0	2272	6	US-10-038-307-1	Sequence 1, Appl1
27	949.4	86.0	2272	6	US-10-201-292-1	Sequence 1, Appl1
28	949.4	86.0	2353	5	US-10-198-846-9957	Sequence 9957, Ap
29	949.4	86.0	1008	6	US-10-038-307-25	Sequence 25, Appl1
30	949.4	86.0	1008	6	US-10-201-292-25	Sequence 25, Appl1
31	912.4	82.6	1047	6	US-10-038-307-21	Sequence 21, Appl1
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33	892.6	80.9	1608	6	US-10-201-292-35	Sequence 35, Appl1
34	867.6	78.6	1623	6	US-10-038-307-11	Sequence 11, Appl1
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36	860	77.9	2397	6	US-10-062-674-1757	Sequence 1757, Ap
37	853.4	77.3	5220	3	US-09-918-715-300	Sequence 300, App
38	853.4	77.3	5220	3	US-09-918-715-300	Sequence 300, App
39	853.4	77.3	5220	8	US-10-474-794-186	Sequence 186, App
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41	853.4	77.3	5220	9	US-10-979-159-186	Sequence 186, App
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43	819	74.2	1534	6	US-10-201-292-33	Sequence 33, Appl1
44	803.8	72.8	1609	5	US-10-037-270-8	Sequence 8, Appl1
45	803.8	72.8	1609	6	US-10-117-722-8	Sequence 8, Appl1

ALIGNMENTS

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RESULT 1
US-11-047-278-1
; Sequence 1, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296, 97745
; CURRENT APPLICATION NUMBER: US/11/047, 278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970, 076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251, 481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)..(1207)
US-11-047-278-1
Query Match 100.0%; Score 1104; DB 10; Length 1414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCCACGGCGAGCGAGAGCCCTCGCATGCGCTTCAGTGGCTCTCTTTGGCCACT 60
DB 104 ATGGCCACGGCGAGCGAGAGCCCTCGCATGCGCTTCAGTGGCTCTCTTTGGCCACT 163
QY 61 CTGGTGCTCATCTGCGCGGCGCAAGCGAGCGAGCGAGATGGGGCTCCAGCTGCTAC 120
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QY 121 GGGCGATTTCACCTGATCTTTCATTTGGAACAATTCAGAGTGTGCTGCACCACTGGAAT 180
DB 224 GGGCGATTTCACCTGATCTTTCATTTGGAACAATTCAGAGTGTGCTGCACCACTGGAAT 283
QY 181 GAAATCTATTAATCTTTGGAACAGTTGGCTCACAATTCAGCCCAAGTTGAGATG 240
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Db 284 GAAATCTATTACTTTGTGTGAGACGTTGGCTCAAAATTCATGACCCACAGTTGGAATG 343
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Qy 301 CAAATCCGTCAGAGGCTAGAGAACTCCAGAAAGTTCTCCAGAGAGACACTTAATG 360
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Db 464 CATGAAGATTTGAAAGGGCCAGTGCAGATTTATTAAGAAACAGAAAGGTACAG 523
Qy 421 ACAGCAGGCTATCTATGCTTGTGATGAGAGAACTCATGAAGATCTCTTTCTAT 480
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RESULT 2
US-10-133-937-58
; Sequence 58, Application US/10133937
; Publication No. US20030207278A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,

; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; FILE OF INVENTION: OTHER BIOLOGICAL STATES
; FILE REFERENCE: 11613.56US01
; CURRENT APPLICATION NUMBER: US/10/133,937
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-937-58

Query Match 100.0%; Score 1104; DB 6; Length 1454;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCCGACGGCGGAGGAGGAGGCTTCGGCATCGGCTTCCAGTGGCTCTTTGGCACT 60
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Qy 121 GCGGATTTGACCTGACTTCAATTTTGAACAATGAGAAAGTGTGCTGCACCATGGAAT 180
Db 264 GCGGATTTGACCTGACTTCAATTTTGAACAATGAGAAAGTGTGCTGCACCATGGAAT 323
Qy 181 GAAATCTATTACTTTGTGGAACAGTTGGCTCAAAATTCATATGACCCACAGTTGAGAAATG 240
Db 324 GAAATCTATTACTTTGTGGAACAGTTGGCTCAAAATTCATATGACCCACAGTTGAGAAATG 383
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Qy 301 CAAATCCGTCAGAGGCTAGAGAACTCCAGAAAGTTCTCCAGAGAGACACTTAATGATG 360
Db 444 CAAATCCGTCAGAGGCTAGAGAACTCCAGAAAGTTCTCCAGAGAGACACTTAATGATG 503
Qy 361 CATGAAGATTTGAAAGGGCCAGTGCAGATTTATTAAGAAACAGAAAGGTACAG 420
Db 504 CATGAAGATTTGAAAGGGCCAGTGCAGATTTATTAAGAAACAGAAAGGTACAG 563
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Db 624 TCAGAGAGGAGGCTAATAGGTCCTGAGATCTTGTGCAATGTTTACTGTGTGTG 683
Qy 541 AAAGATTTCAATGACACACAGCTGGCCGAGATTGGGACAGTAAAGATCATGTGTTCC 600
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RESULT 3
US-10-159-563-58
; Sequence 58, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markue
; APPLICANT: Peterson, Carsten
; APPLICANT: Melzer, Paul
; TITLE OF INVENTION: SELECTIONS AND METHODS OF USING THE SAME FOR
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCCACGGCGGAGGAGAGCCCTCGGATCGGCTTCCAGTGGCTCTTTGGGCACT 60
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DB 144 ATGGCCACGGCGGAGGAGAGCCCTCGGATCGGCTTCCAGTGGCTCTTTGGGCACT 203
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QY 61 CTGGTCTCATCTGCGCCGGGGAAGGGGGAAGGAGGAGATGGGGGTCCAGGCTGCTAC 120
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DB 204 CTGGTCTCATCTGCGCCGGGGAAGGGGGAAGGAGGAGATGGGGGTCCAGGCTGCTAC 263
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|
DB 264 GGGGATTTGACCTGTACTTCAATTTTGGACAAATTCAGAAAGTGTGTCACCACTGGAAAT 323
|
|
|
QY 181 GAAATCTATTAATCTTTGGAAAGCTGGCTCAAAATTCATCAGCCCAAGTTGAAGATG 240
|
|
|
DB 324 GAAATCTATTAATCTTTGGAAAGCTGGCTCAAAATTCATCAGCCCAAGTTGAAGATG 383
|
|
|
QY 241 TCCCTTATGTTTCTTCCACCGGAGAAACCTTAATGAATGACAGAAAGACAGAA 300
|
|
|
DB 384 TCCCTTATGTTTCTTCCACCGGAGAAACCTTAATGAATGACAGAAAGACAGAA 443
|
|
|
QY 301 CAAATCGTCAAGGCTTAGAAGAACTTCAGAAAGTTCTGCGAGAGAGACACTTACATG 360
|
|
|
DB 444 CAAATCGTCAAGGCTTAGAAGAACTTCAGAAAGTTCTGCGAGAGAGACACTTACATG 503
|
|
|

QY 361 CATGAAGATTTGAAGGGCCAGTAGACAGATTTATATGAAGAAAGACAGAGGTAACAG 420
|
|
|
DB 504 CATGAAGATTTGAAGGGCCAGTAGACAGATTTATATGAAGAAAGACAGAGGTAACAG 563
|
|
|
QY 421 ACAGCAGGCTCATCATGCTTTGACTGATGAGAACTTCATGAAGATCTCTTTTCTAT 480
|
|
|
DB 564 ACAGCAGGCTCATCATGCTTTGACTGATGAGAACTTCATGAAGATCTCTTTTCTAT 623
|
|
|
QY 481 TCAAGAGGAGGCTTAATGATGCTGAGATCTTGGGCAATGTTTACTGTTGGTGG 540
|
|
|
DB 624 TCAAGAGGAGGCTTAATGATGCTGAGATCTTGGGCAATGTTTACTGTTGGTGG 683
|
|
|
QY 541 AAAAGATTTCAATGACACAGCTGCGCCGATTTGGGCAAGTAAGATCATGTTTCCC 600
|
|
|
DB 684 AAAAGATTTCAATGACACAGCTGCGCCGATTTGGGCAAGTAAGATCATGTTTCCC 743
|
|
|
QY 601 GTGAATGACGCTTTTCAGGCTCTGCAAGGATCATCATCAATTTTGAAGAACTCTGC 660
|
|
|
DB 744 GTGAATGACGCTTTTCAGGCTCTGCAAGGATCATCATCAATTTTGAAGAACTCTGC 803
|
|
|
QY 661 ATCGAAATTTCTAGCAGCTGGAACCATCCACCATATGTCAGAGAGCATTTCAAGTTGTC 720
|
|
|
DB 804 ATCGAAATTTCTAGCAGCTGGAACCATCCACCATATGTCAGAGAGCATTTCAAGTTGTC 863
|
|
|
QY 721 GTGAGAGAAAGGCTTCCGACATGCGCCGCAAGTGAAGAGGCTCTGCAAGCTTCAAG 780
|
|
|
DB 864 GTGAGAGAAAGGCTTCCGACATGCGCCGCAAGTGAAGAGGCTCTGCAAGCTTCAAG 923
|
|
|
QY 781 ATCAATGACTGCTGCTCACTCAATGAGAAAGCCCTTTCTGTGAGAGACATTAATTAATG 840
|
|
|
DB 924 ATCAATGACTGCTGCTCACTCAATGAGAAAGCCCTTTCTGTGAGAGACATTAATTAATG 983
|
|
|
QY 841 TGTCCAGGCGCTATCTTAAAGAGTTGGCATGAAAGCTGCATCCAGGTGACATGAAC 900
|
|
|
DB 984 TGTCCAGGCGCTATCTTAAAGAGTTGGCATGAAAGCTGCATCCAGGTGACATGAAC 1043
|
|
|
QY 901 GATGCGCTCTCTTTATCTCCAGTTCTGTCATCATCAGCAGACACATGTTCTGACGGT 960
|
|
|
DB 1044 GATGCGCTCTCTTTATCTCCAGTTCTGTCATCATCAGCAGACACATGTTCTGACGGT 1103
|
|
|
QY 961 TCCATCTGCGCCATCGCCCTGCTGATCTCTGTTCTCTGCTCTGACCTGCTCTCTCTG 1020
|
|
|
DB 1104 TCCATCTGCGCCATCGCCCTGCTGATCTCTGTTCTCTGCTCTGACCTGCTCTCTCTG 1163
|
|
|
QY 1021 TGGTCTGCGCCCTGCTGATCTGATGATTAATCAAGAGAGTCCCTGACCCCTGCGGAG 1080
|
|
|
DB 1164 TGGTCTGCGCCCTGCTGATCTGATGATTAATCAAGAGAGTCCCTGACCCCTGCGGAG 1223
|
|
|
QY 1081 GAGAGTGAGAAAATTAATAAATA 1104
|
|
|
DB 1224 GAGAGTGAGAAAATTAATAAATA 1247
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|
|
RESULT 4
US-09-918-715-176
; Sequence 176, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0

Db 984 TGTCCAGCGCTATCTTTAAAGAGTTGGCAGTGAAGCTGCACTCCAGGTCAAGTGAAC 1043
Qy 901 GATGCGCTCTCTTTATCTCCAGTTCTGTCATCATCAACACACACTGTTCTGACGT 960
Db 1044 GATGCGCTCTCTTTATCTCCAGTTCTGTCATCATCAACACACACTGTTCTGACGT 1103
Qy 961 TCCATCTGCGCCATCGCCCTGCTGATCTGTTCTGCTCTGAGCCTGCTCTCTG 1020
Db 1104 TCCATCTGCGCCATCGCCCTGCTGATCTGTTCTGCTCTGAGCCTGCTCTCTG 1163
Qy 1021 TGGTTGCGCCCTGCTGCACTGATATCAAGAGGTCCCTGACCCCTGCGAG 1080
Db 1164 TGGTTGCGCCCTGCTGCACTGATATCAAGAGGTCCCTGACCCCTGCGAG 1223
Qy 1081 GAGAGTGAAGAAA 1094
Db 1224 GAGAGTGAAGAAA 1237
RESULT 7
US-10-474-794-176
; Sequence 176, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-474-794-176
Query Match 98.8%; Score 1090.8; DB 8; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGGCCACGCGCGAGCGGAGAGCCCTCGGATCGGCTTCAGTGGCTCTTTGGCCACT 60
Db 144 ATGGCCACGCGCGAGCGGAGAGCCCTCGGATCGGCTTCAGTGGCTCTTTGGCCACT 203
Qy 61 CTGGTCTCATCTGCGCCCGGGAAGGGGACCGAGGAGAGAGGGGGTCCAGCTCTAC 120
Db 204 CTGGTCTCATCTGCGCCCGGGAAGGGGACCGAGGAGAGAGGGGGTCCAGCTCTAC 263
Qy 121 GGGGATTTGACCTGTACTTCTATTTGACAAATTCAGAAAGTGTGTCACCACTGAAAT 180
Db 264 GGGGATTTGACCTGTACTTCTATTTGACAAATTCAGAAAGTGTGTCACCACTGAAAT 323
Qy 181 GAAATCTATTAATCTTTGTGAAGAGTTGGCTCAAAATTCATCGCCCAAGTTGAGAAATG 240
Db 324 GAAATCTATTAATCTTTGTGAAGAGTTGGCTCAAAATTCATCGCCCAAGTTGAGAAATG 383
Qy 241 TCTTTATTTGTTTCTCCACCCGAGAACCACTTAATGAAATTCAGAAAGCAAGAA 300
Db 384 TCTTTATTTGTTTCTCCACCCGAGAACCACTTAATGAAATTCAGAAAGCAAGAA 443
Qy 301 CAAATCGTCAAGCCTAGAAAGTTCAGAAAGTTCGCGAGAGAGCACTTACATG 360
Db 444 CAAATCGTCAAGCCTAGAAAGTTCAGAAAGTTCGCGAGAGAGCACTTACATG 503
Qy 361 CATGAAGATTGAAAAGGCGCACTGAGCAGATTATATGAAAACAGACAAAGGTACAG 420

Db 504 CATGAAGATTGAAAAGGCGCACTGAGCAGATTATATGAAAACAGACAAAGGTACAG 563
Qy 421 ACAGCAGCGCTCATCTGCTTTGATGATGAGAACTCCATGAAGATCTCTTTCTAT 480
Db 564 ACAGCAGCGCTCATCTGCTTTGATGATGAGAACTCCATGAAGATCTCTTTCTAT 623
Qy 481 TCAGAGAGGAGGCTAATAGGTCTCGAATCTTGTGCAATTTGTTACTGTGTGTGTG 540
Db 624 TCAGAGAGGAGGCTAATAGGTCTCGAATCTTGTGCAATTTGTTACTGTGTGTGTG 683
Qy 541 AAAAATTTCAATGAAACACAGTGGCCCGGATTTGGGACAGTAAGATCATGTTTCCC 600
Db 684 AAAAATTTCAATGAAACACAGTGGCCCGGATTTGGGACAGTAAGATCATGTTTCCC 743
Qy 601 GTGAATGACGCGCTTCAAGCTCTGCAAGGATCATCTCAATTTTGAAGAGTCTG 660
Db 744 GTGAATGACGCGCTTCAAGCTCTGCAAGGATCATCTCAATTTTGAAGAGTCTG 803
Qy 661 ATCGAAATTTGAGAGCTGAACCATCAATATGTGAGAGAGTCAATTTGAAGTGTG 720
Db 804 ATCGAAATTTGAGAGCTGAACCATCAATATGTGAGAGAGTCAATTTGAAGTGTG 863
Qy 721 GTGAAGAGAAAGCGCTTCCGACATGCGCGCAACGTGACAGGCTCTGCAAGTTCAG 780
Db 864 GTGAAGAGAAAGCGCTTCCGACATGCGCGCAACGTGACAGGCTCTGCAAGTTCAG 923
Qy 781 ATCAATGACGCGCTGCACTCAATGAAGAGCCCTTTCTGTGAAGACACTATTTACTG 840
Db 924 ATCAATGACGCGCTGCACTCAATGAAGAGCCCTTTCTGTGAAGACACTATTTACTG 983
Qy 841 TGTCCAGCGCTATCTTAAAGAGTTGGCATGAAGCTGCACTCCAGTCAAGTGAAC 900
Db 984 TGTCCAGCGCTATCTTAAAGAGTTGGCATGAAGCTGCACTCCAGTCAAGTGAAC 1043
Qy 901 GATGCGCTCTCTTTATCTCCAGTTCTGTCATCATCAACACACACTGTTCTGACGT 960
Db 1044 GATGCGCTCTCTTTATCTCCAGTTCTGTCATCATCAACACACACTGTTCTGACGT 1103
Qy 961 TCCATCTGCGCCATCGCCCTGCTGATCTGTTCTGCTCTGAGTCTCTCTCTG 1020
Db 1104 TCCATCTGCGCCATCGCCCTGCTGATCTGTTCTGCTCTGAGTCTCTCTCTG 1163
Qy 1021 TGGTTGCGCCCTGCTGCACTGATATCAAGAGGTCCCTGACCCCTGCGAG 1080
Db 1164 TGGTTGCGCCCTGCTGCACTGATATCAAGAGGTCCCTGACCCCTGCGAG 1223
Qy 1081 GAGAGTGAAGAAA 1094
Db 1224 GAGAGTGAAGAAA 1237
RESULT 8
US-10-474-794-231
; Sequence 231, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 5540

TYPE: DNA
ORGANISM: Homo sapiens
US-10-974-794-231

Query Match 98.8%; Score 1090.8; DB 8; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCACGGGCGAGAGCCCTGGGATCGGCTTCAGTGGCTCTTTGGCCACT 60
DB 144 ATGGCCACGGGCGAGAGCCCTGGGATCGGCTTCAGTGGCTCTTTGGCCACT 203

QY 61 CTGCTGCTCATCTGCGCGGGAAGGGGAGCGCAGGAGAGTGGGGTCCAGCTGCTAC 120
DB 204 CTGCTGCTCATCTGCGCGGGAAGGGGAGCGCAGGAGAGTGGGGTCCAGCTGCTAC 263

QY 121 GGGGGAATTTGACCTGTATCTTCAATTTTGACAAATCAGAAAGTGTCTGCACTGGAAT 180
DB 264 GGGGGAATTTGACCTGTATCTTCAATTTTGACAAATCAGAAAGTGTGTGCACTGGAAT 323

QY 181 GAAATCTATTACTTTGTGGAACAGTTGGCTCACAATTCATCAGCCCACTGGAGAAATG 240
DB 324 GAAATCTATTACTTTGTGGAACAGTTGGCTCACAATTCATCAGCCCACTGGAGAAATG 383

QY 241 TCCCTTATTTGTTTCTCCACCCGAGAAACAACCTTAATGAACCTGACAGAAAGACAGAA 300
DB 384 TCCCTTATTTGTTTCTCCACCCGAGAAACAACCTTAATGAACCTGACAGAAAGACAGAA 443

QY 301 CAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 360
DB 444 CAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 503

QY 361 CATGAAGAGATTGAAAAGGCGCAGTGAAGCAATTTATGAAAACAGACAGAGGTACAGG 420
DB 504 CATGAAGAGATTGAAAAGGCGCAGTGAAGCAATTTATGAAAACAGACAGAGGTACAGG 563

QY 421 ACAGCCAGCGTCATCATTTGCTTGTGACTGATGAGAACTCATGAAAGATCTCTTTTCTAT 480
DB 564 ACAGCCAGCGTCATCATTTGCTTGTGACTGATGAGAACTCATGAAAGATCTCTTTTCTAT 623

QY 481 TCAGAGAGGAGGCTAATAGTCTCGAATCTTGTCGAATTTGTTTACTGTGTGTGTG 540
DB 624 TCAGAGAGGAGGCTAATAGTCTCGAATCTTGTCGAATTTGTTTACTGTGTGTGTG 683

QY 541 AAAAGATTTCATAGAGACAGCTGGCCCGAATGGGACAGTAAGATCATGTGTTTCCC 600
DB 684 AAAAGATTTCATAGAGACAGCTGGCCCGAATGGGACAGTAAGATCATGTGTTTCCC 743

QY 601 GTGAATGAGGCTTTTCAAGGCTTGGCAAGGATCATCCACTCAATTTTGAAGAGTCTGTC 660
DB 744 GTGAATGAGGCTTTTCAAGGCTTGGCAAGGATCATCCACTCAATTTTGAAGAGTCTGTC 803

QY 661 ATCGAAATTTAGCAGCTGAACCATCCACATATGTCAGAGAGTCAATTTCAAGTTGTC 720
DB 804 ATCGAAATTTAGCAGCTGAACCATCCACATATGTCAGAGAGTCAATTTCAAGTTGTC 863

QY 721 GTGAGAGGAAACGGCTTCCGACATGCCCGACAGTGAAGGCTCTTGCAGCTTCAAG 780
DB 864 GTGAGAGGAAACGGCTTCCGACATGCCCGACAGTGAAGGCTCTTGCAGCTTCAAG 923

QY 781 ATGAATGAGCTGGTCACTCAATGAGAACCCCTTTCTGTGAAAGTACTTATTTTAACTG 840
DB 924 ATGAATGAGCTGGTCACTCAATGAGAACCCCTTTCTGTGAAAGTACTTATTTTAACTG 983

QY 841 TGTCCAGCGCTTATCTTAAAGAAAGTTGGATGAAAGTCACTCCAGCTCAGCATGAAC 900
DB 984 TGTCCAGCGCTTATCTTAAAGAAAGTTGGATGAAAGTCACTCCAGCTCAGCATGAAC 1043

QY 901 GATGGCTCTCTTTTATCTTCAAGTTGTGTATCATCAACACACACTGTTTCAAGGCT 960
DB 1044 GATGGCTCTCTTTTATCTTCAAGTTGTGTATCATCAACACACACTGTTTCAAGGCT 1103

QY 961 TCATCTGTGCGCATGCGCTGTGATCTGTCTGTCTGCTTCAAGCCCTGTCTCTCTG 1020

DB 1104 TCATCTGTGCGCATGCGCTGTGATCTGTCTGTCTTCAAGCCCTGTCTCTCTG 1163

QY 1021 TGCTTCCGCGCTCTGCTGCTGACATGATTAATCAAGAGGTCCCTCCAGCCCTGCCGAG 1080

DB 1164 TGCTTCCGCGCTCTGCTGCTGACATGATTAATCAAGAGGTCCCTCCAGCCCTGCCGAG 1223

QY 1081 GAGAGTGAGGAAA 1094

DB 1224 GAGAGTGAGGAGA 1237

RESULT 9
US-10-979-159-176
Sequence 176, Application US/10979159
Publication No. US20050142138A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/10/979,159
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US/09/918,715
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 176
LENGTH: 5540
TYPE: DNA
ORGANISM: Homo sapiens
US-10-979-159-176

Query Match 98.8%; Score 1090.8; DB 9; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCACGGGCGAGAGCCCTGGGATCGGCTTCAGTGGCTCTTTGGCCACT 60
DB 144 ATGGCCACGGGCGAGAGCCCTGGGATCGGCTTCAGTGGCTCTTTGGCCACT 203

QY 61 CTGCTGCTCATCTGCGCGGGAAGGGGAGCGCAGGAGAGTGGGGTCCAGCTGCTAC 120
DB 204 CTGCTGCTCATCTGCGCGGGAAGGGGAGCGCAGGAGAGTGGGGTCCAGCTGCTAC 263

QY 121 GGGGGAATTTGACCTGTATCTTCAATTTTGACAAATCAGAAAGTGTCTGCACTGGAAT 180
DB 264 GGGGGAATTTGACCTGTATCTTCAATTTTGACAAATCAGAAAGTGTCTGCACTGGAAT 323

QY 181 GAAATCTATTACTTTGTGGAACAGTTGGCTCACAATTCATCAGCCCACTGGAGAAATG 240
DB 324 GAAATCTATTACTTTGTGGAACAGTTGGCTCACAATTCATCAGCCCACTGGAGAAATG 383

QY 241 TCCCTTATTTGTTTCTCCACCCGAGAAACAACCTTAATGAACCTGACAGAAAGACAGAA 300
DB 384 TCCCTTATTTGTTTCTCCACCCGAGAAACAACCTTAATGAACCTGACAGAAAGACAGAA 443

QY 301 CAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 360
DB 444 CAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 503

QY 361 CATGAAGAGATTGAAAAGGCGCAGTGAAGCAATTTATGAAAACAGACAGAGGTACAGG 420
DB 504 CATGAAGAGATTGAAAAGGCGCAGTGAAGCAATTTATGAAAACAGACAGAGGTACAGG 563

QY 421 ACAGCCAGGCTCATCATTTGCTTGTGACTGATGAGAACTCATGAAAGATCTCTTTTCTAT 480

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|||||
Db 564 ACAGCCAGGCGTCATCTGCTTCTGACTGAGAGAACTCATGAAAGATCTCTTTTCTAT 623
Qy 481 TCAGAGAGGAGGCTAAATAGTCTGAGATCTTGGGCAATGTTTACGTGTGTG 540
Db 624 TCAGAGAGGAGGCTAAATAGTCTGAGATCTTGGGCAATGTTTACGTGTGTG 683
Qy 541 AAAGATTTCAATGAGACACAGCTGCGCCGGATTTGCGAGAGTAAAGATCATGTGTTCC 600
Db 684 AAAGATTTCAATGAGACACAGCTGCGCCGGATTTGCGAGAGTAAAGATCATGTGTTCC 743
Qy 601 GTGAATGACGCTTTTCAAGCTCTGCAAGGCAATCATCTCAATTTTGAAGAATCTTCC 660
Db 744 GTGAATGACGCTTTTCAAGCTCTGCAAGGCAATCATCTCAATTTTGAAGAATCTTCC 803
Qy 661 ATCGAAATCTTACGAGCTGACATCATCATATGCGAGAGTCAATTTGAAGTTC 720
Db 804 ATCGAAATCTTACGAGCTGACATCATCATATGCGAGAGTCAATTTGAAGTTC 863
Qy 721 GTGAGAGGAAAGCGCTTCCGACATGCGCCGCAAGTGGACAGGGTCTCTGACGTTCAAG 780
Db 864 GTGAGAGGAAAGCGCTTCCGACATGCGCCGCAAGTGGACAGGGTCTCTGACGTTCAAG 923
Qy 781 ATCAATGACTCGTCACTCAATGAGAAAGCCCTTTCTGTGAGAGACCTTATTACTG 840
Db 924 ATCAATGACTCGTCACTCAATGAGAAAGCCCTTTCTGTGAGAGATCTTATTACTG 983
Qy 841 TGTCCAGGCGCTATCTTAAAGAGTGGCATGAAAGCTGCACTCCAGGTCAGCATGAC 900
Db 984 TGTCCAGGCGCTATCTTAAAGAGTGGCATGAAAGCTGCACTCCAGGTCAGCATGAC 1043
Qy 901 GATGGCTCTCTTTTATCTCAAGTCTGTATCATCATCACCACACACACTGTTCTGACG 960
Db 1044 GATGGCTCTCTTTTATCTCAAGTCTGTATCATCATCACCACACACACTGTTCTGACG 1103
Qy 961 TCCATCTTGGCCATGCGCTCTGTATCTGTTCTGTCTCTGAGCCCTGCTCTCTCTG 1020
Db 1104 TCCATCTTGGCCATGCGCTCTGTATCTGTTCTGTCTCTGAGCCCTGCTCTCTCTG 1163
Qy 1021 TGGTCTTGGCCCTCTGCTGCACTGATGATTAATCAAGAGGTCCTCCAGCCCTGCGAG 1080
Db 1164 TGGTCTTGGCCCTCTGCTGCACTGATGATTAATCAAGAGGTCCTCCAGCCCTGCGAG 1223
Qy 1081 GAGAGTGAGAGAAA 1094
Db 1224 GAGAGTGAGAGAAA 1237

RESULT 10
US-10-979-159-231
; Sequence 231, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Beir Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 231
; LENGTH: 5540
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-10-979-159-231
Query Match 98.8%; Score 1090.8; DB 9; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGCCACGGCGGAGCGGAGAGCCCTCGGCATCGGCTTCAAGTGGCTCTCTTGGCCACT 60
Db 144 ATGGCCACGGCGGAGCGGAGAGCCCTCGGCATCGGCTTCAAGTGGCTCTCTTGGCCACT 203
Qy 61 CTGGGTCTATCTTGGGCGGGGCAAGGGGAGCGCAGAGGAGATGGGGGTCCAGCCCTGATC 120
Db 204 CTGGGTCTATCTTGGGCGGGGCAAGGGGAGCGCAGAGGAGATGGGGGTCCAGCCCTGATC 263
Qy 121 GCGGATTTGACCTGTACTTCAATTTTGGACAAATGAGAAAGTGTCTGACCACTGGAAT 180
Db 264 GCGGATTTGACCTGTACTTCAATTTTGGACAAATGAGAAAGTGTCTGACCACTGGAAT 323
Qy 181 GAAATCTATTAATTTGTGGAACAGTTGCTCAAAATTCATCAGCCCAAGTTGAGAAATG 240
Db 324 GAAATCTATTAATTTGTGGAACAGTTGCTCAAAATTCATCAGCCCAAGTTGAGAAATG 383
Qy 241 TCCCTTATTTGTTTTCTCCACCAGAGAAACAACCTTAATGAACCTGACAGAAACAGAGAA 300
Db 384 TCCCTTATTTGTTTTCTCCACCAGAGAAACAACCTTAATGAACCTGACAGAAACAGAGAA 443
Qy 301 CAATCCGTCAGAGGCTTGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 360
Db 444 CAATCCGTCAGAGGCTTGAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 503
Qy 361 CATGAAGATTTGAAGAGGCGAGTAGAGCAATTATTAAGAAACAGACAGAGGTACAG 420
Db 504 CATGAAGATTTGAAGAGGCGAGTAGAGCAATTATTAAGAAACAGACAGAGGTACAG 563
Qy 421 ACAGCCAGGCTCATATGCTTTGATCTGATGAGAAATCCCATGAAGATCTCTTTTCTAT 480
Db 564 ACAGCCAGGCTCATATGCTTTGATCTGATGAGAAATCCCATGAAGATCTCTTTTCTAT 623
Qy 481 TCAGAGAGGAGGCTAAATAGGCTGAGATCTTGGTGCATTTTACTGTGTGTG 540
Db 624 TCAGAGAGGAGGCTAAATAGGCTGAGATCTTGGTGCATTTTACTGTGTGTG 683
Qy 541 AAAGATTTCAATGAGACACAGCTGCGCCGGATTTGCGAGAGTAAAGATCATGTGTTCC 600
Db 684 AAAGATTTCAATGAGACACAGCTGCGCCGGATTTGCGAGAGTAAAGATCATGTGTTCC 743
Qy 601 GTGAATGACGCTTTTCAAGCTCTGCAAGGCAATCATCTCAATTTTGAAGAATCTTCC 660
Db 744 GTGAATGACGCTTTTCAAGCTCTGCAAGGCAATCATCTCAATTTTGAAGAATCTTCC 803
Qy 661 ATCGAAATCTTACGAGCTGACATCATCATATGCGAGAGTCAATTTTGAAGTTC 720
Db 804 ATCGAAATCTTACGAGCTGACATCATCATATGCGAGAGTCAATTTTGAAGTTC 863
Qy 721 GTGAGAGGAAAGCGCTTCCGACATGCGCCGCAAGTGGACAGGGTCTCTGACGTTCAAG 780
Db 864 GTGAGAGGAAAGCGCTTCCGACATGCGCCGCAAGTGGACAGGGTCTCTGACGTTCAAG 923
Qy 781 ATCAATGACTCGTCACTCAATGAGAAAGCCCTTTCTGTGAGAGACCTTATTACTG 840
Db 924 ATCAATGACTCGTCACTCAATGAGAAAGCCCTTTCTGTGAGAGATCTTATTACTG 983
Qy 841 TGTCCAGGCGCTATCTTAAAGAGTGGCATGAAAGCTGCACTCCAGGTCAGCATGAC 900
Db 984 TGTCCAGGCGCTATCTTAAAGAGTGGCATGAAAGCTGCACTCCAGGTCAGCATGAC 1043
Qy 901 GATGGCTCTCTTTTATCTCAAGTCTGTATCATCATCACCACACACACTGTTCTGACG 960
Db 1044 GATGGCTCTCTTTTATCTCAAGTCTGTATCATCATCACCACACACACTGTTCTGACG 1103
Qy 961 TCCATCTTGGCCATGCGCTCTGTATCTGTTCTGTCTCTGAGCCCTGCTCTCTCTG 1020
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Db 1104 TCCATCCTGGCCATCGCCCTGCTGATCTGTCTCTGCTCTAGCCCTGCTCTCTCTG 1163
Qy 1021 TGGTTCTGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1164 TGGTTCTGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1223
Qy 1081 GAGAGTGAGGAAA 1094
Db 1224 GAGAGTGAGGAAA 1237

RESULT 11
US-11-047-278-5
Sequence 5, Application US/11047278
Publication No. US20050196407A1
GENERAL INFORMATION:
APPLICANT: Young, John A.T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TITLE OF INVENTION: Anthrax Toxin Receptor
FILE REFERENCE: 960296, 97745
CURRENT APPLICATION NUMBER: US/11/047, 278
CURRENT FILING DATE: 2005-01-31
PRIOR APPLICATION NUMBER: US/09/970, 076
PRIOR FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/251, 481
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 5540
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (144)..(1835)
US-11-047-278-5

Query Match 98.8%; Score 1090.8; DB 10; Length 5540;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGCCACGGCGGAGCGGAGAGCCCTGCGCATCGGCTTCCAGTGGCTCTTTGGCCACT 60
Db 144 ATGGCCACGGCGGAGCGGAGAGCCCTGCGCATCGGCTTCCAGTGGCTCTTTGGCCACT 203
Qy 61 CTGGTGTCTATCTGCGCGGCGGAGAGCGGAGAGATGGGGGTCCAGCTGCTAC 120
Db 204 CTGGTGTCTATCTGCGCGGCGGAGAGCGGAGAGATGGGGGTCCAGCTGCTAC 263
Qy 121 GCGGATTTGACCTGTATCTTATTTGACAAATCAGAAAGTGTCTGCACTGAGAT 180
Db 264 GCGGATTTGACCTGTATCTTATTTGACAAATCAGAAAGTGTCTGCACTGAGAT 323
Qy 181 GAAATCTATTAATCTTGTGGAACAGTTGGCTCAAAATTCACAGCCCAAGTTGAGATG 240
Db 324 GAAATCTATTAATCTTGTGGAACAGTTGGCTCAAAATTCACAGCCCAAGTTGAGATG 383
Qy 241 TCCCTTATTTGTTTCTCCACCCGAGGAACCTTAATGAACAGAGAGAGAGAGAGAA 300
Db 384 TCCCTTATTTGTTTCTCCACCCGAGGAACCTTAATGAACAGAGAGAGAGAGAGAA 443
Qy 301 CAATCCGTCAGAGCTAGAGAACTCCAGAAAGTTCTGCCAGAGAGAGACCTTACATG 360
Db 444 CAATCCGTCAGAGCTAGAGAACTCCAGAAAGTTCTGCCAGAGAGAGACCTTACATG 503
Qy 361 CATGAAGATTGAAAGGCGCAGTGAAGATTTATTAAGAAACAGAGAGGTTACAGG 420
Db 504 CATGAAGATTGAAAGGCGCAGTGAAGATTTATTAAGAAACAGAGAGGTTACAGG 563
Qy 421 ACAGCCAGCGTCATCTTGTGAGTGAAGAGAACTCCAGAAAGTCTTTTCTAT 480

Db 564 ACAGCCAGCGTCATCTTGTGAGTGAAGAGAACTCCAGAAAGTCTTTTCTAT 623
Qy 481 TCAGAGAGGAGGCTTAATAGTCTGAGATCTTGGCAATGTTACTGTGTGGTGG 540
Db 624 TCAGAGAGGAGGCTTAATAGTCTGAGATCTTGGCAATGTTACTGTGTGGTGG 683
Qy 541 AAAATTTCAATAGACACAGCTGCGCCGAGATTCGAGACAGTAAGATCATGTTC 600
Db 684 AAAATTTCAATAGACACAGCTGCGCCGAGATTCGAGACAGTAAGATCATGTTC 743
Qy 601 GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAGTCTG 660
Db 744 GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAGTCTG 803
Qy 661 ATCGAAATCTAGCAGCTTAACCATCAATATGAGAGAGATTTCAAGTTGTC 720
Db 804 ATCGAAATCTAGCAGCTTAACCATCAATATGAGAGAGATTTCAAGTTGTC 863
Qy 721 GTGAGAGAAAAGGCTTCCGACATGCGCCCAAGTGAAGAGGTCCTGCAAGCTTCAAG 780
Db 864 GTGAGAGAAAAGGCTTCCGACATGCGCCCAAGTGAAGAGGTCCTGCAAGCTTCAAG 923
Qy 781 ATCAATGACTCGGTCACTCAATGAGAAAGCTTTTCTGTGAGAGACCTTATTTACTG 840
Db 924 ATCAATGACTCGGTCACTCAATGAGAAAGCTTTTCTGTGAGAGATTTATTTACTG 983
Qy 841 TGTCCAGCGCTATCTTAAAGAAAGTTGGCAATGAAGCTGCACTCCAGGTCAAGTAAAC 900
Db 984 TGTCCAGCGCTATCTTAAAGAAAGTTGGCAATGAAGCTGCACTCCAGGTCAAGTAAAC 1043
Qy 901 GATGAGCTCTCTTATATCTCAAGTTCTGTCATCATCAACACACACACTGTTGACGGT 960
Db 1044 GATGAGCTCTCTTATATCTCAAGTTCTGTCATCATCAACACACACACTGTTGACGGT 1103
Qy 961 TCCATCCTGGCCATCGCCCTGCTGATCTGTTCTGCTCTCTGAGCCCTGCTCTCTG 1020
Db 1104 TCCATCCTGGCCATCGCCCTGCTGATCTGTTCTGCTCTCTGAGCCCTGCTCTCTG 1163
Qy 1021 TGGTTCTGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1164 TGGTTCTGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1223
Qy 1081 GAGAGTGAGGAAA 1094
Db 1224 GAGAGTGAGGAAA 1237

RESULT 12
US-10-038-307-17
Sequence 17, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OKAYMAK
TITLE OF INVENTION: Judith J. HEALEY
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 1674
TYPE: DNA
ORGANISM: Homo sapiens
US-10-038-307-17

Query Match 87.0%; Score 960.8; DB 6; Length 1674;
Best Local Similarity 99.8%; Pred. No. 5,2e-303;
Matches 962; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGCCACGGCGGAGCGGAGAGCCCTGCGCATCGGCTTCCAGTGGCTCTTTGGCCACT 60

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Db 13 ATGGCCACGGCGAGGAGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTGGCACT 72
Qy 61 CTGGGTCTCATCTGCGCCGGGCAAGGGGGACCGAGGAGAGATGGGGGTCCACCTGCTAC 120
Db 73 CTGGGTCTCATCTGCGCCGGGCAAGGGGGACCGAGGAGAGATGGGGGTCCACCTGCTAC 132
Qy 121 GCGGATTTGACCTGTACTTCAATTTTGGACAAATCAGAAAGTGTGCTGACCACTGGAAAT 180
Db 133 GCGGATTTGACCTGTACTTCAATTTTGGACAAATCAGAAAGTGTGCTGACCACTGGAAAT 192
Qy 181 GAAATCTATTACTTGTGTGAACAAGTGGCTCAAAATTCATCATGCCCAAGTTGAGAAATG 240
Db 193 GAAATCTATTACTTGTGTGAACAAGTGGCTCAAAATTCATCATGCCCAAGTTGAGAAATG 252
Qy 241 TCCCTTATTTGTTTCTCCACCCGAGGAAACAACCTTAAATGAATCTGACAGAAACAGAGAA 300
Db 253 TCCCTTATTTGTTTCTCCACCCGAGGAAACAACCTTAAATGAATCTGACAGAAACAGAGAA 312
Qy 301 CAATTCCTGCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG 360
Db 313 CAATTCCTGCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG 372
Qy 361 CATGAAGATTGAAAGGGCCAGTGAAGATTTATTAAGAAAACAGACAGGGTACAG 420
Db 373 CATGAAGATTGAAAGGGCCAGTGAAGATTTATTAAGAAAACAGACAGGGTACAG 432
Qy 421 ACAGCCAGGCTCATCTTTCCTTGAAGTGAAGAACTCCAGAAAGTTCTTCTTCTAT 480
Db 433 ACAGCCAGGCTCATCTTTCCTTGAAGTGAAGAACTCCAGAAAGTTCTTCTTCTAT 492
Qy 481 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTGCAATTTTACTGTGTGTGTG 540
Db 493 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTGCAATTTTACTGTGTGTGTG 552
Qy 541 AAAGATTTCAATGAGACACAGCTGGCCCGAGTTGCCGACATGAAGATCATGTGTTCCC 600
Db 553 AAAGATTTCAATGAGACACAGCTGGCCCGAGTTGCCGACATGAAGATCATGTGTTCCC 612
Qy 601 GTGAATGAGGCTTTCAGGCTCGAGAGCATCATCACTCAATTTTGAAGAAAGTCTGCG 660
Db 613 GTGAATGAGGCTTTCAGGCTCGAGAGCATCATCACTCAATTTTGAAGAAAGTCTGCG 672
Qy 661 ATCGAATTTCTAGCAGCTGAACCATCCACATATGTGACAGAGAGTCAATTTCAAGTTGTC 720
Db 673 ATCGAATTTCTAGCAGCTGAACCATCCACATATGTGACAGAGAGTCAATTTCAAGTTGTC 732
Qy 721 GTGAGAGGAAACGGCTTCCGACATGCCCGCAAGCTGGAACAGGGTCTCTGACAGCTTCAAG 780
Db 733 GTGAGAGGAAACGGCTTCCGACATGCCCGCAAGCTGGAACAGGGTCTCTGACAGCTTCAAG 792
Qy 781 ATCAATGACTCGGTCACTCACTCAATGAGAGCCCTTTCTGTGAAGAAACCTTATTTACG 840
Db 793 ATCAATGACTCGGTCACTCACTCAATGAGAGCCCTTTCTGTGAAGAAATCTTATTTACG 852
Qy 841 TGTCCAGCGCTATCTTAAAGAGTGGCATGAAGAGTCACTCCAGGTCAAGCATGAAC 900
Db 853 TGTCCAGCGCTATCTTAAAGAGTGGCATGAAGAGTCACTCCAGGTCAAGCATGAAC 912
Qy 901 GATGGCTCTCTTTATCTCCAGTCTGTATCATCAACCAACACACTGTTCTGACGGT 960
Db 913 GATGGCTCTCTTTATCTCCAGTCTGTATCATCAACCAACCAACACTGTTCTGACGGT 972
Qy 961 TCCA 964
Db 973 CCA 976
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RESULT 13
US-10-201-292-17
; Sequence 17, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
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; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-17

Query Match 87.0%; Score 960.8; DB 6; Length 1674;
Best Local Similarity 99.8%; Pred. No. 5.2e-303; Indels 0; Gaps 0;
Matches 962; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGCCACGGCGAGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTGGCACT 60
Db 13 ATGGCCACGGCGAGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTGGCACT 72
Qy 61 CTGGGTCTCATCTGCGCCGGGCAAGGGGGACCGAGGAGAGATGGGGGTCCACCTGCTAC 120
Db 73 CTGGGTCTCATCTGCGCCGGGCAAGGGGGACCGAGGAGAGATGGGGGTCCACCTGCTAC 132
Qy 121 GCGGATTTGACCTGTACTTCAATTTTGGACAAATCAGAAAGTGTGCTGACCACTGGAAAT 180
Db 133 GCGGATTTGACCTGTACTTCAATTTTGGACAAATCAGAAAGTGTGCTGACCACTGGAAAT 192
Qy 181 GAAATCTATTACTTGTGTGAACAAGTGGCTCAAAATTCATCATGCCCAAGTTGAGAAATG 240
Db 193 GAAATCTATTACTTGTGTGAACAAGTGGCTCAAAATTCATCATGCCCAAGTTGAGAAATG 252
Qy 241 TCCCTTATTTGTTTCTCCACCCGAGGAAACAACCTTAAATGAATCTGACAGAAACAGAGAA 300
Db 253 TCCCTTATTTGTTTCTCCACCCGAGGAAACAACCTTAAATGAATCTGACAGAAACAGAGAA 312
Qy 301 CAATTCCTGCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG 360
Db 313 CAATTCCTGCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG 372
Qy 361 CATGAAGATTGAAAGGGCCAGTGAAGATTTATTAAGAAAACAGACAGGGTACAG 420
Db 373 CATGAAGATTGAAAGGGCCAGTGAAGATTTATTAAGAAAACAGACAGGGTACAG 432
Qy 421 ACAGCCAGGCTCATCTTTCCTTGAAGTGAAGAACTCCAGAAAGTTCTTCTTCTAT 480
Db 433 ACAGCCAGGCTCATCTTTCCTTGAAGTGAAGAACTCCAGAAAGTTCTTCTTCTAT 492
Qy 481 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTGCAATTTTACTGTGTGTGTG 540
Db 493 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTGCAATTTTACTGTGTGTGTG 552
Qy 541 AAAGATTTCAATGAGACACAGCTGGCCCGAGTTGCCGACATGAAGATCATGTGTTCCC 600
Db 553 AAAGATTTCAATGAGACACAGCTGGCCCGAGTTGCCGACATGAAGATCATGTGTTCCC 612
Qy 601 GTGAATGAGGCTTTCAGGCTCGAGAGCATCATCACTCAATTTTGAAGAAAGTCTGCG 660
Db 613 GTGAATGAGGCTTTCAGGCTCGAGAGCATCATCACTCAATTTTGAAGAAAGTCTGCG 672
Qy 661 ATCGAATTTCTAGCAGCTGAACCATCCACATATGTGACAGAGAGTCAATTTCAAGTTGTC 720
Db 673 ATCGAATTTCTAGCAGCTGAACCATCCACATATGTGACAGAGAGTCAATTTCAAGTTGTC 732
Qy 721 GTGAGAGGAAACGGCTTCCGACATGCCCGCAAGCTGGAACAGGGTCTCTGACAGCTTCAAG 780
Db 733 GTGAGAGGAAACGGCTTCCGACATGCCCGCAAGCTGGAACAGGGTCTCTGACAGCTTCAAG 792
Qy 781 ATCAATGACTCGGTCACTCACTCAATGAGAGCCCTTTCTGTGAAGAAACCTTATTTACG 840
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Db      793 ATCAATGACTCGGTCACACTCAATGAGAACCCCTTTCTGTGGAAGTACTTATTTACTG 852
      841 TGTCCAGCGGCTTATCTTTAAAGAAAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAAAC 900
      853 TGTCCAGCGGCTTATCTTTAAAGAAAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAAAC 912
Qy      901 GATGGCCTCTCTTTTATCTTCAAGTCTGTGATCATCATCCACACACACACTGTCTTGACGGT 960
      913 GATGGCCTCTCTTTTATCTTCAAGTCTGTGATCATCATCCACACACACACTGTCTTGACGGT 972
Db      961 TCCA 964
      973 CCCA 976
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RESULT 14

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US-10-038-307-13
; Sequence 13, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-13
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Query Match 86.3%; Score 952.4; DB 6; Length 1650;

Best Local Similarity 99.4%; Pred. No. 2.9e-300;

Matches 956; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy      1 ATGGCCAGCGGCGGAGCGGAGAGCCCTGCGGATCGGCTTCCAGTGGCTCTCTTTGGCCACT 60
      1 ATGGCCAGCGGCGGAGCGGAGAGCCCTGCGGATCGGCTTCCAGTGGCTCTCTTTGGCCACT 60
Db      61 CTGGTGTCTCATCTGCGCGGCGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGTCTAC 120
      61 CTGGTGTCTCATCTGCGCGGCGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGTCTAC 120
Qy      121 GGGCGATTGACCTGTACTTCTTATTTGGACAATTCAGGAAGTGTGTGACCACTGGAAT 180
      121 GGGCGATTGACCTGTACTTCTTATTTGGACAATTCAGGAAGTGTGTGACCACTGGAAT 180
Db      121 GGGCGATTGACCTGTACTTCTTATTTGGACAATTCAGGAAGTGTGTGACCACTGGAAT 180
      121 GGGCGATTGACCTGTACTTCTTATTTGGACAATTCAGGAAGTGTGTGACCACTGGAAT 180
Qy      181 GAAATCTATTAATCTTGGGAGCAATGGCTCAAAATTCACAGCCCAAGTTGAGATG 240
      181 GAAATCTATTAATCTTGGGAGCAATGGCTCAAAATTCACAGCCCAAGTTGAGATG 240
Db      181 GAAATCTATTAATCTTGGGAGCAATGGCTCAAAATTCACAGCCCAAGTTGAGATG 240
      181 GAAATCTATTAATCTTGGGAGCAATGGCTCAAAATTCACAGCCCAAGTTGAGATG 240
Qy      241 TCTTTATTTGTTTCTCCAGCCGAGGAACAATTGAAGAACTGACAGAGAGAGAGAA 300
      241 TCTTTATTTGTTTCTCCAGCCGAGGAACAATTGAAGAACTGACAGAGAGAGAGAA 300
Db      241 TCTTTATTTGTTTCTCCAGCCGAGGAACAATTGAAGAACTGACAGAGAGAGAGAA 300
      241 TCTTTATTTGTTTCTCCAGCCGAGGAACAATTGAAGAACTGACAGAGAGAGAGAA 300
Qy      301 CAAATCCGTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACATTTACATG 360
      301 CAAATCCGTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACATTTACATG 360
Db      301 CAAATCCGTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACATTTACATG 360
      301 CAAATCCGTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACATTTACATG 360
Qy      361 CATAGAAGATTGAAGGGGCGAGTGAAGCAATTTATTTGAAGAAAGAGGGAAGG 420
      361 CATAGAAGATTGAAGGGGCGAGTGAAGCAATTTATTTGAAGAAAGAGGGAAGG 420
Db      361 CATAGAAGATTGAAGGGGCGAGTGAAGCAATTTATTTGAAGAAAGAGGGAAGG 420
      361 CATAGAAGATTGAAGGGGCGAGTGAAGCAATTTATTTGAAGAAAGAGGGAAGG 420
Qy      421 ACAGCGACGCTCATCATTTGCTTTGACTGATGAGAGAACTCAATGAAGATCTTTTCTAT 480
      421 ACAGCGACGCTCATCATTTGCTTTGACTGATGAGAGAACTCAATGAAGATCTTTTCTAT 480
Db      421 ACAGCGACGCTCATCATTTGCTTTGACTGATGAGAGAACTCAATGAAGATCTTTTCTAT 480
      421 ACAGCGACGCTCATCATTTGCTTTGACTGATGAGAGAACTCAATGAAGATCTTTTCTAT 480
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RESULT 15

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US-10-038-307-15
; Sequence 15, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-15
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Query Match 86.3%; Score 952.4; DB 6; Length 1650;

Best Local Similarity 99.4%; Pred. No. 2.9e-300;

Matches 956; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy      1 ATGGCCAGCGGCGGAGCGGAGAGCCCTGCGGATCGGCTTCCAGTGGCTCTCTTTGGCCACT 60
      1 ATGGCCAGCGGCGGAGCGGAGAGCCCTGCGGATCGGCTTCCAGTGGCTCTCTTTGGCCACT 60
Db      61 CTGGTGTCTCATCTGCGCGGCGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGTCTAC 120
      61 CTGGTGTCTCATCTGCGCGGCGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGTCTAC 120
Qy      121 GGGCGATTGACCTGTACTTCTTATTTGGACAATTCAGGAAGTGTGTGACCACTGGAAT 180
      121 GGGCGATTGACCTGTACTTCTTATTTGGACAATTCAGGAAGTGTGTGACCACTGGAAT 180
Db      121 GGGCGATTGACCTGTACTTCTTATTTGGACAATTCAGGAAGTGTGTGACCACTGGAAT 180
      121 GGGCGATTGACCTGTACTTCTTATTTGGACAATTCAGGAAGTGTGTGACCACTGGAAT 180
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OY 181 GAAATCTATTACTTTGTGGAACAGTTGGCTCAAAATTCATGAGCCCAAGTTGAGATG 240
|
|
|
Db 181 GAAATCTATTACTTTGTGGAACAGTTGGCTCAAAATTCATGAGCCCAAGTTGAGATG 240
|
|
|
OY 241 TCCCTTATTGTTTTTCTCCACCCGAGGAACAACCTTATGAAACTGACAGAGACAGAGAA 300
|
|
|
Db 241 TCCCTTATTGTTTTTCTCCACCCGAGGAACAACCTTATGAAACTGACAGAGACAGAGAA 300
|
|
|
OY 301 CAAATCCGTCAGAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG 360
|
|
|
Db 301 CAAATCCGTCAGAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG 360
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|
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OY 361 CATGAAGATTGAAAAGGCGCAGTGAAGAGATTATATGAAAACAGACAAAGGTACAGG 420
|
|
|
Db 361 CATGAAGATTGAAAAGGCGCAGTGAAGAGATTATATGAAAACAGACAAAGGTACAGG 420
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|
|
OY 421 ACAGCCAGCGTCATCTTGGCTTTGACTGATGAGAACTCCATGAGAGATCTTTTTCAT 480
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|
|
Db 421 ACAGCCAGCGTCATCTTGGCTTTGACTGATGAGAACTCCATGAGAGATCTTTTTCAT 480
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|
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OY 481 TCAGAGAGGAGGCTTAAGTCTGAGATCTTGGTCAATTGTTACTGTGTGGTGTG 540
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Db 481 TCAGAGAGGAGGCTTAAGTCTGAGATCTTGGTCAATTGTTACTGTGTGGTGTG 540
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OY 541 AAAGATTTCAATGAGACACAGCTGCGCCGGAATTCGGAACGTAAAGATCATGTGTTCCC 600
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|
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Db 541 AAAGATTTCAATGAGACACAGCTGCGCCGGAATTCGGAACGTAAAGATCATGTGTTCCC 600
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|
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OY 601 GTGAATGACGCGCTTTCAGGCTCTGCAAGGATCATCCACTCAATTTTGAAGAGTCTGC 660
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|
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|
|
OY 661 ATCGAAATTTCTGACAGCTGAACCATCCACCATATGTGCAAGAGATCATTTCAAGTGTG 720
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|
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Db 661 ATCGAAATTTCTGACAGCTGAACCATCCACCATATGTGCAAGAGATCATTTCAAGTGTG 720
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|
|
OY 721 GTGAGAGAAAACGCGCTTCCGACATGCGCCGCAACGTGACAGGCTCTGACAGCTTCAAG 780
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|
|
Db 721 GTGAGAGAAAACGCGCTTCCGACATGCGCCGCAACGTGACAGGCTCTGACAGCTTCAAG 780
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|
|
OY 781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTTCTGTGAGAGACACTTATTTACTG 840
|
|
|
Db 781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTTCTGTGAGAGACACTTATTTACTG 840
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|
|
OY 841 TGTCCAGCGGCTATCTTAAGAAAGTTGAGATGAAGCTGCACTCCAGGTCAAGCATGAAC 900
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|
|
Db 841 TGTCCAGCGGCTATCTTAAGAAAGTTGAGATGAAGCTGCACTCCAGGTCAAGCATGAAC 900
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|
|
OY 901 GATGCGCTCTCTTTATCTCAGATTGTGCATCATACACACACACTGTTCTGACGGT 960
|
|
|
Db 901 GATGCGCTCTCTTTATCTCAGATTGTGCATCATACACACACACTGTTCTGACCAA 960
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|
|
OY 961 TC 962
|
|
|
Db 961 TC 962
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Search completed: December 17, 2005, 18:47:14
Job time : 1019.43 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 17, 2005, 13:29:40 ; Search time 200.369 Seconds
(without alignments)
2700.811 Million cell updates/sec

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Perfect score:	1104
Sequence:	1 atgcccacgcgcgagcgcgag.....gtcagagaaataaataaaaa 1104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4161431 beqs, 245089505 residues

Total number of hits satisfying chosen parameters: 83228622

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing first 45 summaries

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3: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq.*
5: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq.*
6: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq.*
7: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
8: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq2.*
9: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq3.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1090.8	98.9	5540	7	US-11-186-284-198	Sequence 198, App
2	61.4	5.6	2765	6	US-10-750-185-55275	Sequence 25275, A
3	36.4	3.3	201	6	US-10-995-561-83675	Sequence 83675, A
4	35.6	3.2	2368	6	US-10-111-8264-423	Sequence 423, App
5	35.2	3.2	201	6	US-10-995-561-83660	Sequence 83660, A
6	35.2	3.2	201	6	US-10-995-561-83669	Sequence 83669, A
7	35.2	3.2	201	6	US-10-995-561-83674	Sequence 83674, A
8	35.2	3.2	201	6	US-10-995-561-83814	Sequence 83814, A
9	35.2	3.2	201	6	US-10-995-561-83925	Sequence 83925, A
10	35.2	3.2	2016	7	US-11-029-003-7	Sequence 7, App11
11	34.8	3.2	201	6	US-10-995-561-83647	Sequence 83647, A
12	34.8	3.2	201	6	US-10-995-561-83658	Sequence 83658, A
13	34.8	3.2	40000	6	US-10-995-561-13509	Sequence 13509, A
14	34.6	3.1	600	6	US-10-750-185-21593	Sequence 21593, A
15	34.6	3.1	4856	6	US-10-750-185-83111	Sequence 83111, A
16	34.4	3.1	201	6	US-10-995-561-83654	Sequence 83654, A
17	34.4	3.1	153376	7	US-11-121-086-5	Sequence 5, App11
18	34.2	3.1	918	6	US-10-750-185-62250	Sequence 62250, A
19	34	3.1	1449	6	US-10-982-234-561	Sequence 561, App
20	33.8	3.1	98716	6	US-10-995-561-13331	Sequence 13331, A
21	33.8	3.1	134999	7	US-11-117-187-192	Sequence 192, App
22	33.6	3.0	201	6	US-10-995-561-70418	Sequence 70418, A
23	33.6	3.0	1054	6	US-10-750-185-58946	Sequence 58946, A

ALIGNMENTS

C 24	33.6	3.0	28849	6	US-10-995-551-1420	A	Sequence 13420, A
C 25	32.8	3.0	15448	7	US-11-121-086-33	A	Sequence 33, Appl
C 26	32.6	3.0	1838	6	US-10-750-185-6565	A	Sequence 6065, A
C 27	32.4	2.9	1005	6	US-10-858-793-191	A	Sequence 191, Appl
C 28	32.2	2.9	1841	6	US-10-750-185-55750	A	Sequence 55750, A
C 29	32	2.9	2553	7	US-11-126-468-25	A	Sequence 25, Appl
C 30	32	2.9	3010	6	US-10-750-185-35112	A	Sequence 35112, A
C 31	32	2.9	139054	7	US-11-121-086-96	A	Sequence 96, Appl
C 32	32	2.9	155989	7	US-11-121-086-57	A	Sequence 57, Appl
C 33	32	2.9	193363	7	US-11-112-908-32	A	Sequence 32, Appl
C 34	31.8	2.9	3388	6	US-10-750-185-34560	A	Sequence 34560, A
C 35	31.8	2.9	176503	7	US-11-121-086-53	A	Sequence 53, Appl
C 36	31.6	2.9	3040	6	US-10-750-185-48628	A	Sequence 48628, A
C 37	31	2.8	655	6	US-10-750-185-29911	A	Sequence 29911, A
C 38	31	2.8	187745	7	US-11-121-086-83	A	Sequence 83, Appl
C 39	30.8	2.8	1785	6	US-10-750-185-50775	A	Sequence 50775, A
C 40	30.8	2.8	3505	6	US-11-000-463-560	A	Sequence 560, Appl
C 41	30.8	2.8	3551	7	US-11-000-463-88	A	Sequence 88, Appl
C 42	30.6	2.8	1118	6	US-10-750-185-54797	A	Sequence 54797, A
C 43	30.6	2.8	1371	7	US-11-102-240-27	A	Sequence 27, Appl
C 44	30.6	2.8	1655	6	US-10-750-185-55355	A	Sequence 55355, A
C 45	30.6	2.8	85682	7	US-11-117-187-205	A	Sequence 205, Appl

RESULT 1
US-11-186-284-198

```

? Sequence 198, Application US/11186284
? Publication No. US20050266493A1
? GENERAL INFORMATION:
? APPLICANT: Millennium Pharmaceuticals, Inc.
? APPLICANT: Berger, Allison
? APPLICANT: Guillemette, Tracy L.
? APPLICANT: Kamatkar, Shubhangi
? APPLICANT: Schlegel, Robert
? APPLICANT: Monahan, John E.
? APPLICANT: Thibodeau, Stephen N.
? APPLICANT: Burgart, Lawrence J.
? TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
? TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
? FILE REFERENCE: PPM01-029P2RNM
? CURRENT APPLICATION NUMBER: US/11/186,284
? CURRENT FILING DATE: 2005-07-21
? PRIOR APPLICATION NUMBER: US/10/301,822
? PRIOR FILING DATE: 2002-11-21
? PRIOR APPLICATION NUMBER: US 60/339,971
? PRIOR FILING DATE: 2001-12-10
? PRIOR APPLICATION NUMBER: US 60/361,978
? PRIOR FILING DATE: 2002-03-05
? PRIOR APPLICATION NUMBER: US 60/381,988
? PRIOR FILING DATE: 2002-05-20
? NUMBER OF SEQ ID NOS: 228
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 198
? LENGTH: 5540
? TYPE: DNA
? ORGANISM: Homo Sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (144)...(1838)
? US-11-186-284-198

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Query Match	98.8%	Score 1090.8	DB 7	Length 5540
Best Local Similarly	99.8%	Pred. No. 0		
Matches 1092, Conservative	0	Mismatches 2	Indels 0	Gaps 0

QY 1 ATGGCCACGGGCGAGCGGAGAGCCCTCGGCAATCGGCTTCCAGATGGGCTCTCTTTGGGCACT 60
 |||||
 DB 144 ATGGCCACGGGCGAGCGGAGAGCCCTCGGCAATCGGCTTCCAGATGGGCTCTCTTTGGGCACT 203

QY 61 CTGGTCTCATCTGCGCCGGGCAAGGGGACGACGAGGAGATGGGGTCCAGCTGCTAC 120
DB 204 CTGGTCTCATCTGCGCCGGGCAAGGGGACGACGAGGAGATGGGGTCCAGCTGCTAC 263
QY 121 GGGGGATTTGACCTGTAATTTTGGACAATTCAGAAAGTGTCTGCACTCTGGAT 180
DB 264 GGGGGATTTGACCTGTAATTTTGGACAATTCAGAAAGTGTCTGCACTCTGGAT 323
QY 181 GAAATCTATTACTTTGAGAACAGTTGGCTCAAAATTCAGCCACAGTTGAGAAATG 240
DB 324 GAAATCTATTACTTTGAGAACAGTTGGCTCAAAATTCAGCCACAGTTGAGAAATG 383
QY 241 TCCTTATTGTTTCTCCACCCGAGGAACAATTAATGAACTGACAGAAACAGAGAA 300
DB 384 TCCTTATTGTTTCTCCACCCGAGGAACAATTAATGAACTGACAGAAACAGAGAA 443
QY 301 CAAATCCGTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCAGAGAGAGACATTACATG 360
DB 444 CAAATCCGTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCAGAGAGAGACATTACATG 503
QY 361 CATGAAGATTTGAAAGGCGAGTGAAGAGATTTATTATGAAACAGACAAAGGTAACAG 420
DB 504 CATGAAGATTTGAAAGGCGAGTGAAGAGATTTATTATGAAACAGACAAAGGTAACAG 563
QY 421 ACAGCAGCGTCACTATGCTTGTGATGAGAACTCCATGAAAGATCTTTTCTAT 480
DB 564 ACAGCAGCGTCACTATGCTTGTGATGAGAACTCCATGAAAGATCTTTTCTAT 623
QY 481 TCAGAAAGGAGGCTTAATAGTCTCGAGATCTTGGTGCAATTTTAACTGTGTGTGTG 540
DB 624 TCAGAAAGGAGGCTTAATAGTCTCGAGATCTTGGTGCAATTTTAACTGTGTGTGTG 683
QY 541 AAAGATTTTCAATAGACACAGCTGCGCCGGATGGCGAGACGTAAAGATCATGTGTCC 600
DB 684 AAAGATTTTCAATAGACACAGCTGCGCCGGATGGCGAGACGTAAAGATCATGTGTCC 743
QY 601 GTGAATGACGCGCTTTCAGGCTTCGACAAAGCATCATCAATTTTGAAGAAGTCTGC 660
DB 744 GTGAATGACGCGCTTTCAGGCTTCGACAAAGCATCATCAATTTTGAAGAAGTCTGC 803
QY 661 ATGAAATTTTACAGCTGAAACATCCATATGTGACAGAGAGTCAATTTCAAGTTGTC 720
DB 804 ATGAAATTTTACAGCTGAAACATCCATATGTGACAGAGAGTCAATTTCAAGTTGTC 863
QY 721 GTGAGAGAAAGCGCTTCCGACATGCGCCGCAAGGTGAGCAAGGTCCTGACAGCTTCAAG 780
DB 864 GTGAGAGAAAGCGCTTCCGACATGCGCCGCAAGGTGAGCAAGGTCCTGACAGCTTCAAG 923
QY 781 ATCAATGACTCGTCACTCAATGAGAAAGCCCTTTTGTGTGAGAGACATTATTTACTG 840
DB 924 ATCAATGACTCGTCACTCAATGAGAAAGCCCTTTTGTGTGAGAGACATTATTTACTG 983
QY 841 TGTCCAGCGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAAC 900
DB 984 TGTCCAGCGCTTATCTTAAAGAAAGTTGGCATGAAAGCTGCACTCCAGGTCAAGATGAAC 1043
QY 901 GATGAGCTCTCTTTTATCTCAGTTCGTATCATACACACACACATGTTTGAAGGT 960
DB 1044 GATGAGCTCTCTTTTATCTCAGTTCGTATCATACACACACACATGTTTGAAGGT 1103
QY 961 TCCATCTGAGCCATGCGCCCTGATATCTGTTCTGTCTGAGCCCTGAGCTCTCTGAG 1020
DB 1104 TCCATCTGAGCCATGCGCCCTGATATCTGTTCTGTCTGAGCCCTGAGCTCTCTGAG 1163
QY 1021 TGGTTCTGAGCCCTCTGCTGCACTGTGATATCAAGAGGTCTCTGACCCCTGCGCAG 1080
DB 1164 TGGTTCTGAGCCCTCTGCTGCACTGTGATATCAAGAGGTCTCTGACCCCTGCGCAG 1223
QY 1081 GAGAGTGAGGAAAA 1094
DB 1224 GAGAGTGAGGAAAA 1237

RESULT 2

US-10-185-25275/c
; Sequence 25275, Application US/10750185
; Publication No. US2005026063A1
; GENERAL INFORMATION:
; APPLICANT: MVI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25275
; LENGTH: 2765
; TYPE: DNA
; ORGANISM: Bovine 19866881163262
US-10-750-185-25275

Query Match 5.6%; Score 61.4; DB 6; Length 2765;
Best Local Similarity 77.9%; Pred. No. 1.9e-09;

Matches 74; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 630 CATCATCCACTCAATTTTGAAGAGTCTGATCGAAATTTAGACGCTGAACATCCAC 689
DB 211 CCTCTCCTCTGATATTGAGAAATCTGCATCGAAATTTAGACGCTGAACATCCAC 152
QY 690 CATATGTGACAGAGAGTCAATTTCAAGTGTCTGA 724
DB 151 CATATGTGACAGAGAGTCAATTTGAAGTGTGA 117

RESULT 3

US-10-995-561-83675
; Sequence 83675, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83675
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-83675

Query Match 3.3%; Score 36.4; DB 6; Length 201;
Best Local Similarity 62.5%; Pred. No. 0.059;
Matches 55; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

QY 928 GTCAATCATACACACACACACTGTTCTGACGGTTCATCTGAGCCATGCGCCGCTGATC 987
DB 69 GTCAATCATCCACGACGTAAGTCCCGGACACTACCAACAGACATGCGCTGCTCCGC 128
QY 988 CTGTTCTGCTCTCTAGACCTGAGCTCTCC 1015
DB 129 CTGACACAGCCGCTGCTCTCACTGACC 156

RESULT 4

```

US-10-131-826A-423/c
Sequence 423, Application US/10131826A
Publication No. US20050245730A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeGeorge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zhenh
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 423
LENGTH: 2368
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-826A-423

Query Match 3.2%; Score 35.6; DB 6; Length 2368;
Beet Local Similarity 50.6%; Pred. No. 0.54;
Matches 86; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 884 TCCAGGTGAGCATGAAACGATGGCCCTCTTTTATCTCCAGTCTGTCAATCACCACCA 943
DB 1002 TCCACACGACGACGCCAAGTTGCTCTCTCTTTTCTCTGCTTCAATCCATGCGCA 943
QY 944 CACACTGTCTTACGAGTTTCATCTCTGCGCATCGCCCTGTGATTCCTGTCTCTCTAG 1003
DB 942 AGATCTTCTTCTCTTCTTTCATCATCTACAAAGCGTCTTTGTTTCTTCTTCAATTGA 883
QY 1004 CCTGAGCTCTCTCTGTGAGTTCTGAGCCCTCTGCTGCACGTGTATATC 1053
DB 882 TCATCTTTTCTCTCTCCGCGCATCTGCAACTGTGAGCTGTATGAGCCTC 833

RESULT 5
US-10-995-561-83660

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; Sequence 83660, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83660
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-83660

Query Match          3.2%; Score 35.2; DB 6; Length 201;
Best Local Similarity 62.5%; Pred. No. 0.15;
Matches 55; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 928 GTCATCATCACCAACACACTGTGTCGCGTTCATCTCGGCATCGCCCTGCTGATC 987
      |||||
DB 44 GTCATCATCCCCAGACAGTAGTCGCCGGGACACCAACACGATCGCGCTGCTGCG 103
      |||||

QY 988 CTGTTCTGCTCTTACGCGCTTGCTCTGC 1015
      |||||
DB 104 CTGCACCAAGCCCGGTGCTCTTCACTGACC 131
      |||||

RESULT 6
US-10-995-561-83669
; Sequence 83669, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83669
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-83669

Query Match          3.2%; Score 35.2; DB 6; Length 201;
Best Local Similarity 62.5%; Pred. No. 0.15;
Matches 55; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 928 GTCATCATCACCAACACACTGTGTCGCGTTCATCTCGGCATCGCCCTGCTGATC 987
      |||||
DB 29 GTCATCATCCCCAGACAGTAGTCGCCGGGACACCAACACGATCGCGCTGCTGCG 88
      |||||

QY 988 CTGTTCTGCTCTTACGCGCTTGCTCTGC 1015
      |||||
DB 89 CTGCACCAAGCCCGGTGCTCTTCACTGACC 116
      |||||

RESULT 7
US-10-995-561-83674
; Sequence 83674, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF

```

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/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FASTSEQ for windows Version 4.0
/ SEQ ID NO 83674
/ LENGTH: 201
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-83674

Query Match
Best Local Similarity 62.5%; Pred. No. 0.15;
Matches 55; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 928 GTCATCATCACCAACACAGCTGTTCTGACGGTTCATCTGGCCATCGCCCTGCTGATC 987
DB 79 GTCATCATCTCCAGACGATCGMCCGGGACCAACCAACGACATCGCGCTGCTCCGC 138

QY 988 CTGTTCTGCTCTCTAGCCCTGGCTCTCC 1015
DB 139 CTGCACCAAGCCCGTGTCTCTCACTGACC 166

RESULT 8
US-10-995-561-83814
/ Sequence 83814, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 83814
/ LENGTH: 201
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-83814

Query Match
Best Local Similarity 3.2%; Score 35.2; DB 6; Length 201;
Matches 55; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 928 GTCATCATCACCAACACAGCTGTTCTGACGGTTCATCTGGCCATCGCCCTGCTGATC 987
DB 43 GTCATCATCTCCAGACGATCGMCCGGGACCAACCAACGACATCGCGCTGCTCCGC 102

QY 988 CTGTTCTGCTCTCTAGCCCTGGCTCTCC 1015
DB 103 CTGCACCAAGCCCGTGTCTCTCACTGACC 130

RESULT 9
US-10-995-561-83925
/ Sequence 83925, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FASTSEQ for windows Version 4.0
/ SEQ ID NO 83925
/ LENGTH: 201
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/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-83925

Query Match
Best Local Similarity 62.5%; Pred. No. 0.15;
Matches 55; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 928 GTCATCATCACCAACACAGCTGTTCTGACGGTTCATCTGGCCATCGCCCTGCTGATC 987
DB 112 GTCATCATCTCCAGACGATCGTCCGGGACCAACCAACGACATCGCGCTGCTCCGC 171

QY 988 CTGTTCTGCTCTCTAGCCCTGGCTCTCC 1015
DB 172 CTGCACCAAGCCCGTGTCTCTCACTGACC 199

RESULT 10
US-11-029-003-7
/ Sequence 7, Application US/11029003
/ Publication No. US20050260194A1
/ GENERAL INFORMATION:
/ APPLICANT: PETERS, ROBERT T.
/ APPLICANT: MEZO, ADAM R.
/ APPLICANT: RIVERA, DANIEL S.
/ APPLICANT: BITONTI, ALAN J.
/ APPLICANT: STATTEL, JAMES
/ TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
/ FILE REFERENCE: 08945.0007-01000
/ CURRENT APPLICATION NUMBER: US/11/029,003
/ CURRENT FILING DATE: 2005-01-05
/ PRIOR APPLICATION NUMBER: 60/539,207
/ PRIOR FILING DATE: 2004-01-26
/ PRIOR APPLICATION NUMBER: 60/487,964
/ PRIOR FILING DATE: 2003-07-17
/ PRIOR APPLICATION NUMBER: 60/469,600
/ PRIOR FILING DATE: 2003-05-06
/ NUMBER OF SEQ ID NOS: 91
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 7
/ LENGTH: 2016
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-029-003-7

Query Match
Best Local Similarity 3.2%; Score 35.2; DB 7; Length 2016;
Matches 55; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 928 GTCATCATCACCAACACAGCTGTTCTGACGGTTCATCTGGCCATCGCCCTGCTGATC 987
DB 796 GTCATCATCTCCAGACGATCGTCCGGGACCAACCAACGACATCGCGCTGCTCCGC 855

QY 988 CTGTTCTGCTCTCTAGCCCTGGCTCTCC 1015
DB 856 CTGCACCAAGCCCGTGTCTCTCACTGACC 883

RESULT 11
US-10-995-561-83647
/ Sequence 83647, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
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; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83647
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-83647

Query Match
Best Local Similarity 61.4%; Pred. No. 0.2;
Matches 54; Conservative 1; Mismatches 33; Indels 0; Gaps 0;

QY 928 GTGATCATCACCAACACACTGTTCTGAGGTTTCATCTGGCGCATCGCCCTGCTGATC 987
Db 52 GTGATCATCCCCAGACGATGCTCCCGGACCAACCAACACGATCGTGTCTCCG 111
QY 988 CTGTCCTGCTCCTAGCCCTGCTCTCC 1015
Db 112 CTGCACCAAGCCCGTGTCTCATCTGACC 139

RESULT 12
US-10-995-561-83658
; Sequence 83658, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83658
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-83658

Query Match
Best Local Similarity 61.4%; Pred. No. 0.2;
Matches 54; Conservative 1; Mismatches 33; Indels 0; Gaps 0;

QY 928 GTGATCATCACCAACACACTGTTCTGAGGTTTCATCTGGCGCATCGCCCTGCTGATC 987
Db 53 GTGATCATCCCCAGACGATGCTCCCGGACCAACCAACGATCGTGTCTCCG 112
QY 988 CTGTCCTGCTCCTAGCCCTGCTCTCC 1015
Db 113 CTGCACCAAGCCCGTGTCTCATCTGACC 140

RESULT 13
US-10-995-561-13509
; Sequence 13509, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13509
; LENGTH: 40000
; TYPE: DNA
; ORGANISM: Homo sapiens
FEATURE:
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; NAME/KEY: misc feature
; LOCATION: (1)...(40000)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-995-561-13509

Query Match
Best Local Similarity 59.1%; Pred. No. 6.4;
Matches 52; Conservative 4; Mismatches 32; Indels 0; Gaps 0;

QY 928 GTGATCATCACCAACACACTGTTCTGAGGTTTCATCTGGCGCATCGCCCTGCTGATC 987
Db 33430 GTGATCATCCCCAGACGATGCTCCCGGACCAACCAACGATCGTGTCTCCG 33489
QY 988 CTGTCCTGCTCCTAGCCCTGCTCTCC 1015
Db 33490 CTGCACCAAGCCCGTGTCTCATCTGACC 33517

RESULT 14
US-10-750-185-21593
; Sequence 21593, Application US/10750185
; Publication No. US200502603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21593
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-21593

Query Match
Best Local Similarity 48.6%; Pred. No. 0.47;
Matches 85; Conservative 3; Mismatches 87; Indels 0; Gaps 0;

QY 195 TGTGAAACAGTTGGCTCACAAATTTCATCAGCCACAGTTGAGAAATGCTTATTGTTT 254
Db 398 TATGTTCAATTTTCTCAGGATCTTTCATTTGAAATTACAGTGTGAGGGAAACGTA 457
QY 255 CTCACCCGAGAAACCTTAATGAAACTGACAGAAAGACAAATCCGTCAGG 314
Db 458 YAGTRAGAGGCGCAACACAAAGAAAGAAAGACCACTAATATAGCGAGTAGT 517
QY 315 CTTAGAAAGAACTCCAGAAAGTTCTGCCAGGAGAGACCTTACATGATGAAGA 369
Db 518 CTGAAGGACAGCTAGCAACTCTGAAAGGGAGAGACTRACCTTGAAGGTGAGA 572

RESULT 15
US-10-750-185-43111
; Sequence 43111, Application US/10750185
; Publication No. US200502603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
```

/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 43111
/ LENGTH: 4856
/ TYPE: DNA
/ ORGANISM: Bovine 1986680415951
US-10-750-185-43111

Query Match 3.1%; Score 34.6; DB 6; Length 4856;
Best Local Similarity 50.3%; Pred. No. 1.9;
Matches 85; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 886 CAGGTCAGCATGAAAGATGGCCTCTCTTTATCTCCAGTTCTGTCTATCATACACACACA 945
DB 3707 CTGTACACATGCTGTGGCCGCTTCAAGATGTGTCTACTTCTCATCATCTCAAC 3766
QY 946 CACTGTTTGAGGGTTCCATCCGTGGCAATGCCCTGTGATCTGTCTGTCTCTAGGC 1005
DB 3767 CACATGGTCTCCGTTCATGATCACCCCTGAGCTGCCCATCTTCATCTCTGATCC 3826
QY 1006 CTGGCTCTCCTGTGTGATGTTCTGGCCCTCTGTGCACTGTGATATCA 1054
DB 3827 ATGCTGTCCATCCCTGGCCCAAGGCACTTCTGATGATGGCATCA 3875

Search completed: December 17, 2005, 18:54:55
Job time : 203.369 secs

Db 23 ValIeuSerGlyProGluYglYleuLeuAxcGAlaInGluInProSerCySaAxcGAla 42

Qy 127 TTGACCTGCTACTTCATTTTGGACAAATCAAGAAAGTGTCTGCACCACTGGAATGAAATC 186

Db 43 PheApeLeuTyPheValIeuAspLysSerGlySerValAlaAsnAnrPrIleGluIle 62

Qy 187 TATPACTTGTGGAACAGTTGGCTCTCAAAATTCATCAGCCCAAGTTGGAATGTCTTT 246

Db 63 TyrAnpPheValGInGInLeuAlaGluAaPheValSerProGluMetArgLeuSerPhe 82

Qy 247 ATTTGTTTCTCCACCCGAGAAACAACCTTAATGAAACTGACAGAGAACAATC 306

Db 83 IleValPheSerSerGlnAlaThrIleIleLeuProLeuThrGlyAspArgGlyLysIle 102

Qy 307 CGTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGAAACACTTTCATGCTGAA 366

Db 103 SerLysGlyLeuGlnAspLeuAspLysArgValSerProValGlyGluThrTyrlleHsGlu 122

Qy 367 GGATTTGAAAGGCGCCAGTGAAGATTTATTAAGAAACAGACAAAGGTTACAGACAGCC 426

Db 123 GlyLeuLysLeuAlaAsnGluInIle-----GlnLysAlaGlyLeuLysThrSer 140

Qy 427 AGCGTCATCATTTGCTTGACTGATGAGAACTCCATGAAGATCTTTTCTATTCAGAG 486

Db 141 SerIleIleIleIleAlaLeuThrAspGlyLysLeuAspGlyLeuValProSerTyrlaGlu 160

Qy 487 AGGAGGCTAATAAGCTCTCGAAGATCTTGGTGCATTTGTTACTGTGTGGTGAAGAT 546

Db 161 LysGlnAlaLysAlaSerArgSerLeuGlyAlaSerValTyrcySaValGlyValLeuAsp 180

Qy 547 TTCATATGACACACAGCTGCGCCGAGTTGGGGAACAGTAAGATCATGTTCCCGGAAAT 606

Db 181 PheGluGlnAlaGlnLeuGluThrGlyLeuAlaAspSerLysGluGlnAlaPheProValLys 200

Qy 607 GACGCTTTCAAGGCTCTGCAGGCAATCATCTCATTTTGAAGAGTCTCCATCGAA 666

Db 201 GLyGlyPheGlnAlaLeuLysGlyIleIleAsnSerIleLeuAlaGlnSerCySthrGlu 220

Qy 667 ATTCTAGACGTGAACCATCCACCATATGTGCAGAGAGTCAATTTCAAGTTGTCTGAGA 726

Db 221 IleLeuGlnLeuGlnProSerSerValCySaValGlyGluInPheGlnIleValLeuSer 240

Qy 727 GGAACCGCTTCCGACATGCCGCCAACGTGCAAGGCTCTCTGACGCTTCAAGTCAAT 786

Db 241 GlyArgGlyPheMetLeuGlySerArgAsnGlySerValLeuCySthrTyrlThrValAsn 260

Qy 787 GACTCGGTACACTCATGAGAAGACCCCTTTCTGTGGAAGACATTATTAATCTGTGCCA 846

Db 261 GluThrTyrlThrThrSerValLysProValSerValGlnLeuAsnSerMetLeuCyPro 280

Qy 847 GCGCTATCTTAAGAAGCTGGCATGAAAGCTGCACTCCAGGTCAAGATGAACGATGCC 906

Db 281 AlaProIleLeuAsnLysAlaGlyGluThrLeuAspAlaSerValSerPheAsnGlyIle 300

Qy 907 CTCTCTTTTATCTCCAGTCTGTGCATCATCAACAACAACAGTCTGACGGTTCATC 966

Db 301 LysSerValIleSerGlySerLeuIleValThrAlaThrGluInPheSerArgGlyIleAla 320

Qy 967 CTGGCAGCTGCGCTGTGATCCGTTCTGCTCTCTAGCCCTGGCTCTCTGGTGGTTC 1026

Db 321 AlaIleIleValIleLeuValIleLeuValIleLeuLeuLeuGlyIleGlyLeuMetTrpTrpPhe 340

Qy 1027 TGGCCCTCTGCTGCACGTGTATTCATCAAGAGAGTCCCTCCACCCCTGCG----- 1077

Db 341 TrpProLeuCyGlybLysValValIleLysAspProProProProProAlaProAlaPro 360

Qy 1078 ---GAGGAGAGTGAAGAA 1092

Db 361 LysGlnGluGlnGluIn 366

RESULT 2

US-08-286-889-46

i Sequence 46, Application US/08286889

```

; Patent No.5470953
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Mich
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSSE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,889
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: P38,659
; REFERENCE/DOCKET NUMBER: 27866/32168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3866
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-889-46

Alignment Scores:
Pred. No.:      2.9e+09      Length:      1155
Score:          166.00      Matches:     66
Percent Similarity: 46.15%   Conservative: 42
Best Local Similarity: 28.21% Mismatches:    96
Query Match:      8.29%      Indels:      30
DB:               1         Gaps:        12

US-09-970-076-1_COPY_104_1207 (1-1104) x US-08-286-889-46 (1-1155)
QY      109 CGAGCGTCTACGCGC--GGATTGACCTGTACTTCATTTTGAGCAAAATCGAGAAGTG 165
       ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      144 ProglucySPProgl[GL]nGlumeraSpIlealaphelleuIIeaSplyserglySerile 163
       ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      166 ---CTGCACCACTGGAATGAATCTATTACTTTGTTCGGAACAAGTGCGCTCACAAATTCATC 222
       ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
Db      164 AsgInserAspPheThrGlnMetLysAspPheValLysAlaLeuMetGlyGlnLeuAla 193
       ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      223 AGCCACAGTTGAGATGATGCCCTTATTGTGTTTCTCCACCAGAGAACACTTAATGAAA 282
       ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      184 SerThrSerThrSerPheSerLeuMetGlnIyrSerAsnIleLeuLySthrHrIspeThr 203
       ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      283 CTGACGAGACAGACA-----GAACAATCCGTCAAGGCGCTTAGAAGACTC 327
       ||||| ||| ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
Db      204 PheThrGlnPheLysSerSerLeuSerProGlnSerLeuValAspAlaIleValGlnLeu 223
       ||||| ||| ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
QY      328 CAGAAAGTTCTGCCAGAGAGACACTTACATGCATGAAGATTGAAAAGGCCCATGAG 387
       ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      224 Gln-----GlyLeuThrYrrHraIaseGlyIleGlnIynsValVallys 238
       ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      388 CAGATTATTATGAABAACGACAAAGGTTACAGAGACGCC---AGCGTCATCATTTGCTTTG 444
       :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 239 GluLeuPheHisSerLysAsnGlyAlaArgLysSerAlaLysLysIleLeuIleValIle 258
 QY 445 ACTGATGAGAACTCCATGAGATCTCTTTTATTATTCAGAG-----AGGAGAGCTAAT 498
 Db 259 ThrAspGlyGlnLysPheArgAspProLeuGluTyrArgHisValIleProGluAlaGlu 278
 QY 499 AGGTCGCGAGATCTTGTCGAATGTTTACTGTGGTGGTGAAGAAT---TTCAATGAG 555
 Db 279 LysAla-----GlyIleIleArgTyrAlaIleGlyValGlyAspAlaPheArgGlu 295
 QY 556 ---ACACAGCTGGCCCGAAT-----GCGACAGTAAGATCATGTGTT 597
 Db 296 ProThrAlaLeuGlnGluLeuAsnThrIleGlySerAlaProSerGlnAspHisValPhe 315
 QY 598 CCCGTGAATGACGCTTTACAGCTCTGCAAGGATCATCATCAATTTTGAAGAAGTCC 657
 Db 316 LysValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnIleGlnGluLys--- 333
 QY 658 TGCATGGAATTCTACAGCTGCAACATCCACCATATGTGCAGAGAGTCAATTCAGATT 717
 Db 334 -----IlePheAlaIleGlnGluGlyThrGluSerArgSerSerSerPheGlnHis 350
 QY 718 GTCGTGAGAGAAACGCTTCCGACATGCCCGCAGCTGAG 759
 Db 351 GluMetSerGlnGluGlyPheSerSerAlaLeuSerMetAsp 364
 RESULT 3
 US-08-485-618-46
 ; Sequence 46, Application US/08485618
 ; Patent No. 5728533
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallatin, W. Michael
 ; APPLICANT: Van der Vlieten, Monica
 ; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
 ; NUMBER OF SEQUENCES: 103
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 South Wacker Drive, 6300 Sear Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/485,618
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/173,497
 ; FILING DATE: 23-DEC-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/286,889
 ; FILING DATE: 5-AUG-1994
 ; APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/362,652
 ; FILING DATE: 21-DEC-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Williams Jr., Joseph A.
 ; REGISTRATION NUMBER: 38,659
 ; REFERENCE/DOCKET NUMBER: 27866/32797
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-474-6300
 ; TELEFAX: 312-474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 46:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1155 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear

; MOLECULE TYPE: protein
 US-08-485-618-46
 Alignment Scores:
 Pred. No.: 2.9e-09
 Score: 166.00
 Percent Similarity: 46.15%
 Best Local Similarity: 28.21%
 Query Match: 8.29%
 DB: 1
 Gaps: 12
 US-09-970-076-1_copy_104_1207 (1-1104) x US-08-485-618-46 (1-1155)
 QY 109 CCAGCTGCTACGCG---GATTTGACCTGATCTTCAATTTTGACAAATGAGAGCTGG 165
 Db 144 ProGluCysProGlyGlnLeuMetAspIleAlaPheLeuIleAspGlySerGlySerIle 163
 QY 166 ---CTGCACCACTGGAATGAAATCTATTATCTTTGCAACAGTGGCTCACAATTCATC 222
 Db 164 AspGlnSerAspPheThrGlnMetLysAspPheValIleAlaLeuMetGlyGlnLeuAla 183
 QY 223 AGCCCACTGAGAAATGCTTTATTTCTTCTCCACCCGAGAACAACTTAATGAA 282
 Db 184 SerThrSerThrSerPheSerLeuMetGlnTyrSerAsnIleLeuLysThrHisPheThr 203
 QY 283 CTGCAGAGACAGCA-----GAACAATCCGTCAAGCCTAGAAAGACTC 327
 Db 204 PheThrGluPheLysSerSerLeuSerProGlnSerLeuValAspAlaIleValGlnLeu 223
 QY 328 CAGAAAGTTCTGCACAGAGAGACACTTACATGATGAAAGATTGAAAGGCGCACTGAG 387
 Db 224 Gln-----GlyLeuThrTyrThrAlaSerGlyIleGlnLysValValLys 238
 QY 388 CAGATTATTTGAAACACAGACAGGTCACAGACGCC---AGCCTCATATTGCTTGG 444
 Db 239 GluLeuPheHisSerLysAsnGlyAlaArgLysSerAlaLysLysIleLeuIleValIle 258
 QY 445 ACTGATGAGAACTCCATGAGATCTCTTTTATTATTCAGAG-----AGGAGAGCTAAT 498
 Db 259 ThrAspGlyGlnLysPheArgAspProLeuGluTyrArgHisValIleProGluAlaGlu 278
 QY 499 AGGTCGCGAGATCTTGTCGAATGTTTACTGTGGTGGTGAAGAAT---TTCAATGAG 555
 Db 279 LysAla-----GlyIleIleArgTyrAlaIleGlyValGlyAspAlaPheArgGlu 295
 QY 556 ---ACACAGCTGGCCCGAAT-----GCGACAGTAAGATCATGTGTT 597
 Db 296 ProThrAlaLeuGlnGluLeuAsnThrIleGlySerAlaProSerGlnAspHisValPhe 315
 QY 598 CCCGTGAATGACGCTTTACAGCTCTGCAAGGATCATCATCAATTTTGAAGAAGTCC 657
 Db 316 LysValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnIleGlnGluLys--- 333
 QY 658 TGCATGGAATTCTACAGCTGCAACATCCACCATATGTGCAGAGAGTCAATTCAGATT 717
 Db 334 -----IlePheAlaIleGlnGluGlyThrGluSerArgSerSerSerPheGlnHis 350
 QY 718 GTCGTGAGAGAAACGCTTCCGACATGCCCGCAGCTGAG 759
 Db 351 GluMetSerGlnGluGlyPheSerSerAlaLeuSerMetAsp 364
 RESULT 4
 US-08-362-652-46
 ; Sequence 46, Application US/08362652
 ; Patent No. 5766850
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallatin, W. Michael
 ; APPLICANT: Van der Vlieten, Monica
 ; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
 ; NUMBER OF SEQUENCES: 93
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 South Wacker Drive, 6300 Sear Tower

Percent similarity: 46.15% Conservative: 42
 Best Local Similarity: 28.21% Mismatches: 96
 Query Match: 8.29% Indels: 30
 DB: 1 Gaps: 12

US-09-970-076-1_COPY_104_1207 (1-1104) x US-08-605-672-46 (1-1155)

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QY 109 CCGAGCTGCTAGGCGC---GGATTGACCTGCTACTTCTTTGGACAAATCAGAAAGTGTG 165
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DB 144 ProGluCySerProGluYngInGluMetAspIleAlaPheLeuIleAspGlySerGlySerIle 163
QY 166 ---CTGCACACCTGGAATGAAATCTATTACTTTGTGACAGATTGGCTCTCAAAATTCATC 222
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 164 AspGlnSerAspPheThrGlnMetIleAspPheValIleAlaLeuMetGlyGlnLeuAla 183
QY 223 AGCCACAGTTGAGAAATGCTCTTTATTTCTTCACCCGAGGACAACTTAATGAAA 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 184 SerThrSerThrSerPheSerLeuMetGlnTySerAsnIleLeuIleuIleuIleuIleuIle 203
QY 283 CTGACGAGACAGACA-----GAACAAATCCGTCAAGGCTTCAAGAAATC 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 204 PheThrGlnPheIleuSerSerLeuSerProGlnSerLeuValAspAlaIleValGlnLeu 223
QY 328 CAGAAAGTTGTCGACAGAGAGACACTTACATGATGAGATTGAAAGGCGCAGTGAG 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 224 Gln-----GlyLeuThrTyThrAlaSerGlyIleGlnIleValIleValIle 238
QY 388 CAGATTATATGAAAAACAGACAGGATGACAGACAGC---AGCGTCATCATTTGCTTGG 444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 239 GluLeuPheIleSerIleuAsnGlyAlaArgIleSerIleuIleuIleuIleuIleuIle 258
QY 445 ACTGATGAGAACTCCATGAAATCTCTTTTCTTATTCAGAG-----AGGAGGCTAAT 498
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 259 ThrAspGlyGlnIleuPheArgAspProLeuGlnIleuIleuIleuIleuIleuIleuIle 278
QY 499 AGGCTCGAGATCTTGTCGAAATGTTTACTGTGTGTGTTGTTGTTGTTGTTGTTGTTGTT 555
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 279 LysAla-----GlyIleIleArgTyAlaIleGlyValIleGlyAlaPheAlaPheArgGlu 295
QY 556 ---ACACAGCTGCGCCGCGATT-----GCGACAGTAAAGATCATGTGTGT 597
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 296 ProThrAlaLeuGlnIleuLeuAsnThrIleGlySerIleAlaProSerGlnAspIleValIle 315
QY 598 CCCGTGATGACGCGCTTTCAGGCTTTCAGGACGATCCATCCATCAATTTGAAAGATCC 657
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 316 LysValIleGlyAsn---PheValIleLeuArgSerIleGlnArgGlnIleGlnIleuIle 333
QY 658 TGCATCGAAATTTCTAGACAGTGAACATCCACCATATGTGACAGAGATCATTTCAAGTT 717
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 334 -----IlePheAlaIleGlyGlyIleGlyIleuSerIleuArgSerSerSerPheGlnHis 350
QY 718 GTCGTGAGAGAAACGCTTCCGACATGCCCGCAGCATGTGAC 759
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 351 GluMetSerGlnIleuGlyPheSerSerAlaLeuSerMetAsp 364

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-46
Alignment Scores:
Pred. No.: 2.9e-09 Length: 1155
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.29% Indels: 30
DB: 1 Gaps: 12
US-09-970-076-1_COPY_104_1207 (1-1104) x US-08-482-293A-46 (1-1155)
QY 109 CCGAGCTGCTAGGCGC---GGATTGACCTGCTACTTCTTTGGACAAATCAGAAAGTGTG 165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 144 ProGluCySerProGluYngInGluMetAspIleAlaPheLeuIleAspGlySerGlySerIle 163
QY 166 ---CTGCACACCTGGAATGAAATCTATTACTTTGTGACAGATTGGCTCTCAAAATTCATC 222
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 164 AspGlnSerAspPheThrGlnMetIleAspPheValIleAlaLeuMetGlyGlnLeuAla 183
QY 223 AGCCACAGTTGAGAAATGCTCTTTATTTCTTCACCCGAGGACAACTTAATGAAA 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 184 SerThrSerThrSerPheSerLeuMetGlnTySerAsnIleLeuIleuIleuIleuIleuIle 203
QY 283 CTGACGAGACAGACA-----GAACAAATCCGTCAAGGCTTCAAGAAATC 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 204 PheThrGlnPheIleuSerSerLeuSerProGlnSerLeuValAspAlaIleValGlnLeu 223
QY 328 CAGAAAGTTGTCGACAGAGAGACACTTACATGATGAGATTGAAAGGCGCAGTGAG 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 224 Gln-----GlyLeuThrTyThrAlaSerGlyIleGlnIleValIleValIle 238
QY 388 CAGATTATATGAAAAACAGACAGGATGACAGACAGC---AGCGTCATCATTTGCTTGG 444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 239 GluLeuPheIleSerIleuAsnGlyAlaArgIleSerIleuIleuIleuIleuIleuIle 258
QY 445 ACTGATGAGAACTCCATGAAATCTCTTTTCTTATTCAGAG-----AGGAGGCTAAT 498
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 259 ThrAspGlyGlnIleuPheArgAspProLeuGlnIleuIleuIleuIleuIleuIleuIle 278
QY 499 AGGCTCGAGATCTTGTCGAAATGTTTACTGTGTGTGTTGTTGTTGTTGTTGTTGTTGTT 555
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 279 LysAla-----GlyIleIleArgTyAlaIleGlyValIleGlyAlaPheAlaPheArgGlu 295

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```

; SEQ ID NO 46
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-193-043-46

Alignment Scores:
Pred. No.: 2.9e-09 Length: 1155
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.29% Indels: 30
DB: 2 Gaps: 12

US-09-970-076-1_COPY_104_1207 (1-1104) x US-09-193-043-46 (1-1155)
QY 109 CCAGCTGCTACGGC---GGATTGACCTGTACTTCTTGGACAATTCAGGAAGTGTG 165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 144 Proglucybrolylglnglumetabpillealpheuleuleapglserglyserille 163
QY 166 ---CTGCACCACTGGAATGAATCTATTACTTTGGACAGTTGGCTCAAAATTCATC 222
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 164 AepglserapherthrglmctlyabpPhevallyalauleumetglylnleuala 183
QY 223 AGCCACAGTTGGAATGTCCTTATTGTTTCTCCACCGAGAAACAACCTTAATGAA 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 SerthserthserPheSerleuMetGlnTySerasnilleuLystrHispethr 203
QY 283 CTGACAGAACAGACA-----GAACAAATCCGTCAAGGCTTGAAGAACTC 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 204 PheThrgluphelyserSerleuserProglInservuValaspaIleValGlnLeu 223
QY 328 CAGAAAGTTCTGCAGAGAGACACTTACATGATGAAAGATTGAAAGGCCAGTGAG 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 224 Gln-----GlyLeuthrTyThrAlaserglylleglnlyVallyls 238
QY 388 CAAATTTATTGAAAAACAGACAGGTACAGACAGCC---AGCGTCATCATTCCTTGG 444
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 239 GluleuphehiserlybaenglylaArglyserlalyblyserlileuIleValille 258
QY 445 ACTGATGAGAACTCCATGAAGATCTTTTTCATTCAGAG-----AGGAGGCTAAT 498
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 259 ThrAspIyglInlyspheArgasProleuglutytrghIsvalIleProgluIlaGlu 278
QY 499 AGGCTCGAGACTTGGTGCAATTTTACTGTGTGGTGAAGAT---TTCATGAG 555
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 279 Lyvala-----GlyIlelleArgTyAlaIleGlyValGlyAspaIlaPheArgGlu 295
QY 556 ---ACACAGCTGGCCCGGATT-----GCGGACATGAAGATCATGTGTT 597
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 296 ProThralaLeuglnIleuAenThrIleGlySerIlaProserGlnaPheIasvalPhe 315
QY 598 CCGGTGAATACGGCTTTCAGGCTCTGCAAGGCTCATCCATCATTTGAAAGAACTCC 657
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 316 LyvalaIglYasn---PheValaIalaLeuArgserIleGlnArgGlnIleGlnGluys 333
QY 658 TGCAATGAAATTTAGACAGCTGAACCATCATATATGTGCAGAGAGATTCATTCAAGTT 717
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 334 -----IlePhealalleGlnGlyThrgluserArgserSerSerPheGlnHis 350
QY 718 GTCTGTAGAGAAAAGGCTTCCAGCATGCCCCGCAACGTGAC 759
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 351 GlumetserGlnIglnglyPheSerSerAlaLeuserMetasp 364

RESULT 9
US-09-688-307A-46
; Sequence 46; Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
```

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; CURRENT APPLICATION NUMBER: US/09/688,307A
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-688-307A-46

Alignment Scores:
Pred. No.: 2.9e-09 Length: 1155
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.29% Indels: 30
DB: 2 Gaps: 12

US-09-970-076-1_COPY_104_1207 (1-1104) x US-09-688-307A-46 (1-1155)
QY 109 CCAGCTGCTACGGC---GGATTGACCTGTACTTCTTGGACAATTCAGGAAGTGTG 165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 144 Proglucybrolylglnglumetabpillealpheuleuleapglserglyserille 163
QY 166 ---CTGCACCACTGGAATGAATCTATTACTTTGGACAGTTGGCTCAAAATTCATC 222
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 164 AepglserapherthrglmctlyabpPhevallyalauleumetglylnleuala 183
QY 223 AGCCACAGTTGGAATGTCCTTATTGTTTCTCCACCGAGAAACAACCTTAATGAA 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 SerthserthserPheSerleuMetGlnTySerasnilleuLystrHispethr 203
QY 283 CTGACAGAACAGACA-----GAACAAATCCGTCAAGGCTTGAAGAACTC 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 204 PheThrgluphelyserSerleuserProglInservuValaspaIleValGlnLeu 223
QY 328 CAGAAAGTTCTGCAGAGAGACACTTACATGATGAAAGATTGAAAGGCCAGTGAG 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 224 Gln-----GlyLeuthrTyThrAlaserglylleglnlyVallyls 238
QY 388 CAAATTTATTGAAAAACAGACAGGTACAGACAGCC---AGCGTCATCATTCCTTGG 444
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 239 GluleuphehiserlybaenglylaArglyserlalyblyserlileuIleValille 258
QY 445 ACTGATGAGAACTCCATGAAGATCTTTTTCATTCAGAG-----AGGAGGCTAAT 498
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 259 ThrAspIyglInlyspheArgasProleuglutytrghIsvalIleProgluIlaGlu 278
QY 499 AGGCTCGAGACTTGGTGCAATTTTACTGTGTGGTGAAGAT---TTCATGAG 555
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 279 Lyvala-----GlyIlelleArgTyAlaIleGlyValGlyAspaIlaPheArgGlu 295
QY 556 ---ACACAGCTGGCCCGGATT-----GCGGACATGAAGATCATGTGTT 597
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 296 ProThralaLeuglnIleuAenThrIleGlySerIlaProserGlnaPheIasvalPhe 315
QY 598 CCGGTGAATACGGCTTTCAGGCTCTGCAAGGCTCATCCATCATTTGAAAGAACTCC 657
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 316 LyvalaIglYasn---PheValaIalaLeuArgserIleGlnArgGlnIleGlnGluys 333
QY 658 TGCAATGAAATTTAGACAGCTGAACCATCATATATGTGCAGAGAGATTCATTCAAGTT 717
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Db 334 -----1lePhehla1leGluglyThrGluSerArgSerSerSerPheGlnHis 350
QY 718 GTCGTGAGAGAAACGGCTTCCGACATGCCCGAAGCTGAC 759
Db 351 GluMetSerGlnGluGlyPheSerSerAlaLeuSerMetAsp 364

RESULT 10
US-09-350-259-46
/ Sequence 46, Application US/09350259
/ Patent No. 6620915
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 6620915el Human 2
/ FILE REFERENCE: 27866/35004
/ CURRENT APPLICATION NUMBER: US/09/350,259
/ EARLIER FILING DATE: 1999-07-08
/ EARLIER APPLICATION NUMBER: 09/193,043
/ EARLIER FILING DATE: 1998-11-16
/ EARLIER APPLICATION NUMBER: 08/173,497
/ EARLIER FILING DATE: 1993-12-23
/ EARLIER APPLICATION NUMBER: 08/286,889
/ EARLIER FILING DATE: 1994-08-05
/ EARLIER APPLICATION NUMBER: 08/362,652
/ EARLIER FILING DATE: 1994-12-21
/ EARLIER APPLICATION NUMBER: 08/943,363
/ EARLIER FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 46
/ LENGTH: 1155
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-350-259-46

Alignment Scores:
Pred. No.: 2.9e-09 Length: 1155
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.29% Indels: 30
DB: 2 Gaps: 12

US-09-970-076-1_COPY_104_1207 (1-1104) x US-09-350-259-46 (1-1155)

QY 109 CCAGCCTGCTACGGC---GGATTGACCTGTACTTCTTATTTGGACAATACGAGAAGTGTG 165
Db 144 ProGluCySerProGlyGlnGluMetAspIleAlaPheLeuIleAspGlySerGlySerIle 163
QY 166 ---CTGCACACACGGAATGAATCTATTCTTTGTGGAACAGTTGGCTCACAAATTCATC 222
Db 164 AspGlnSerAspPheThrGlnMetLysAspPheValLysAlaLeuMetGlyGlnLeuAla 183
QY 223 AGCCACAGTTGAGATGTCCTTATTTATTTTCTCCACCCGAGAAACAACCTTAATGAA 282
Db 184 SerThrSerThrSerPheSerLeuMetGlnTyrSerAsnIleLeuIleThrHisPheThr 203
QY 283 CTGCACGAAGACAGA-----GAACAATCCGCTCAAGGCTTAGAAGAACTC 327
Db 204 PheThrGluPheLysSerSerLeuSerProGlnSerLeuValAspAlaIleValGlnLeu 223
QY 328 CAGAAAGTTCTGCAGAGAGACACTTACATGCATGAGAGATTGAAAGGCGCAGTGAG 387
Db 224 Gln-----GlyLeuThrTyrThrAlaSerGlyIleGlnLysValValLys 238
QY 388 CAGATTATATGAAAAACAGACAAGGAGTACAGAGACAGCC---AGCTCATCATTTGCTTG 444
Db 239 GluLeuPheHisSerLysAsnGlyAlaArgLysSerAlaLysLysIleLeuIleValIle 258
QY 445 ACTGATGAGAGACTCCATGAAATCTCTTTTCTATTTCAGAG-----AGGAGGCTAAT 498
Db 259 ThrAspGlyGlnLysPheArgAspProLeuGluTyrArgHisValIleProGluAlaGlu 278

QY 499 AGGTCTCAGATCTTGTGCAATTGTTACTGTGTGTGTAAGAT---TTCAATGAG 555
Db 279 LysAla-----GlyIleIleArgTyrAlaIleGlyValGlyAspAlaPheArgGlu 295
QY 556 ---ACACAGCTGCGCCCGATT-----GCCGACAGTAAAGATCATGTGTT 597
Db 296 ProThrAlaLeuGlnGluLeuAsnThrIleGlySerAlaProSerGlnAspHisValPhe 315
QY 598 CCCGTGAATGACGGCTTCCAGCTTCGCAAGGACATCATCATCAATTGTAAGAGTCC 657
Db 316 LysValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnIleGlnGlyLys--- 333
QY 658 TCATCAAGAAATCTTAGCAGCTGACATCCACCATATGTGACAGAGAGTCAATTCAGTT 717
Db 334 -----1lePhehla1leGluglyThrGluSerArgSerSerSerPheGlnHis 350

QY 718 GTCGTGAGAGAAACGGCTTCCGACATGCCCGAAGCTGAC 759
Db 351 GluMetSerGlnGluGlyPheSerSerAlaLeuSerMetAsp 364

RESULT 11
US-08-485-618-53
/ Sequence 53, Application US/08485618
/ Patent No. 5728533
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentln Releasee #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/485,618
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32797
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 53:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1161 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-485-618-53

Alignment Scores:
Pred. No.: 2.91e-09 Length: 1161

Score:	166.00	Matches:	66
Percent Similarity:	46.1%	Conservative:	422
Best Local Similarity:	28.2%	Mismatches:	96
Query Match:	8.2%	Indels:	30
DB:	1	Gaps:	12

US-09-970-076-1_COPY_104_1207 (1-1104) X US-08-485-618-53 (1-1161)

QY	109	CCAGCTGCTAGGAC--GGATTGACCTGACTTCAATTTGGACAAATGAGAAAGTGTG	165
DB	144	ProgluCyapProgluIngluMetAapIleAlaPheIleuIleAapGlySerIle	163
QY	166	---CTGCACACCGAAGTAAATCTATTACTTGTGGAAAGTGGCTCAATTCATC	222
DB	164	AapGlnSerAapPheThrGlnMetLysAapPheValLysAlaLeuMetGlyLnuLeuAla	183
QY	223	AGCCCACTTGGAGATGTCCTTATATGTTTTCACCCGAGAGAACACCTTAATGAAA	282
DB	164	SerThrSerThrSerPheSerIleuMetGlnTySerAsnIleLeuTyThrIlePheThr	203
QY	283	CTGCAGAAACACA-----GAACAAATCCGTACAGGCCCTAGAGAAATC	327
DB	204	PheThrGlnPheLysSerSerIleuSerProGlnSerIleuValAapAlaIleValGlnIleu	223
QY	328	CAGAAAGTTCTCCAGAGAGAGACCTTAATCATCATGAAAGATTGAAAGGCCAGTAG	387
DB	224	Gln-----GlyLeuThrTyThrAlaSerIlyIleGlnLysValLys	238
QY	388	CAGATTATTATGAAAAACAGACAAGGGTACAGAGACC---AGCCATCATTCGTTTG	444
DB	239	GluLeuPheHisSerLysAengIylAlaGlyLysSerAlaLysLysIleuIleValIle	255
QY	445	ACTGATGAGAACTCCATGAGATCTCTTTTCTATTACAG-----AGGAGGCTAAT	498
DB	259	ThrAapGlyGlnLysPheAapPheProLeuGlnTyThrGlnValIleProGlnAlaGln	278
QY	499	AGGTCTGAGANTTGTGTGCATTTGTTACTGTGTGTGTGTAAGAT--TTCATGAG	555
DB	279	LysAla-----GlyIleIleAargTyAlaIleGlyAlaGlyAapAlaPheAargLnu	295
QY	556	---ACACACTGGCCCCGATT-----CGGACACTAAGATCATGTGCTTT	597
DB	296	ProThrAlaLeuGlnIleuLeuAenThrIleGlySerAlaProSerGlnAapHsAlaPhe	315
QY	598	CCCGTAATGACGGCTTTCAGGCTCTGACAGCATCATCCATCAATTTTGAAGATGCC	657
DB	316	LysValGlyAen---PheValAlaLeuAargSerIleGlnAargGlnIleGlnGlnLys---	333
QY	658	TGCATCGAAATTTAGACCTGACCTGAACCATCACCATATGTGCAGAGAGCATTTCAATT	717
DB	334	-----IlePheAlaIleGlnGlyThrGlnLysAargSerSerSerPheGlnHis	350
QY	718	GTCTGTCAGAGAAACGGCTTCCACATGCCCGCAACCTGCAC	759
DB	351	GluMetSerGlnGlnGlyPheSerSerAlaLeuSerMetAap	364

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RESULT 12
US-08-362-652-53
; Sequence 53, Application US/08362652
; Patent No. 5766850
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5766850e1 Human 2 Integrin Alpha Subunit
;
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Seear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
;
; COMPUTER READABLE FORM:

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MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/362,652
  FILING DATE:
  CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/173,497
    FILING DATE: 23-DEC-1993
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/286,889
    FILING DATE: 5-AUG-1994
  ATTORNEY/AGENT INFORMATION:
    NAME: Williams Jr., Joseph A.
    REGISTRATION NUMBER: 38,659
  REFERENCE/DOCKET NUMBER: 27866/32391
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 312-474-6300
    TELEFAX: 312-474-0448
    TELEX: 25-3856
  INFORMATION FOR SEQ ID NO: 53:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 1161 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
    MOLECULE TYPE: protein
  US-08-362-652-53

Alignment Scores:
Pred. No.: 2,916-09      Length: 1161
Score: 166.00      Matches: 66
Percent Similarity: 46.15%      Conservative: 42
Best Local Similarity: 28.21%      Mismatches: 96
Query Match: 8.29%      Indels: 30
DB: 1      Gaps: 12

US-09-970-076-1_COPY_104_1207 (1-1104) x US-08-362-652-53 (1-1161)
QY 109 CCAAGCTGCTACGGC---GGATTGACCTGTACTTGTGACAAATCAGAAAGCTG 165
DB 144 ProGluCyvProGluGlnGluMetAspIleAlaPheLeuIleAspGlySerGlySerIle 163
QY 166 ---CTGCACCACTGGAATGATCATCTATTACTTTGTGGAACAGTGGCTCAAAATTCATC 222
DB 164 AsgGlnSerAspPheThrGlnMetGlyAspPheValIlyAlaLeuMetGlyGlnLeuAla 163
QY 223 AGCCACAGTTGAGATGTCCTTTATGTTTCTCCACCCGAGGAACACTTAATGAAA 202
DB 184 SerThrSerThrSerPheSerLeuMetGlnIlySerAsnIleuLysThrHisPheThr 203
QY 283 CTGACAGAAAGACAGA-----GAACAAATCCGTCATAAGCCCTAGAAAGAACTC 327
DB 204 PheThrGlnPheLysSerSerLeuSerProGlnSerLeuValAspAlaIleValGlnLeu 223
QY 328 CAGAAAGTTCTCAGAGGAGACACTTACATGCATGAAAGATTGAAGGCGCAGTGAG 387
DB 224 Gln-----GlyLeuThrIlyThrAlaSerGlyIleGlnIlySerValIlyLys 238
QY 388 CAGATTTATATGAAAAACAGACAAAGGTTACAGGACAGCC---AGCGTCATCATGCTTG 444
DB 239 GlnLeuPheHisSerLysAsnGlyAlaGlyLysSerAlaIlyLysIleLeuIleValIle 258
QY 445 ACTGATGGAACATCTCATGAAGATCTCTTTTCTATTACAGAG-----AGGAGGCTTAAT 498
DB 259 ThrAspGlyGlnIlyLysPheArgAspProLeuGlnIlyArgHisValIleProGlnAlaGln 278
QY 499 AGGTCGCGAGACTTGTCATATGTTGTTCTGTCGGTGGTGAAGAT---TTCATATGAG 555
DB 279 LysAlaA-----GlyIleIleAlaGlyIlyAlaIleGlyIlyAlaIlyAspAlaPheAspGln 295
556 ---ACACAGCTGCGCCGAGAT-----GCGGACAGTAAGATCATGTGCTTT 597

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DB 296 ProthAlaLeuGlnIleuValenThrIleGlySerAlaProSerGlnAspHisValPhe 315
QY 598 CCCGTAATGAGCGGCTTCAGGCTGCAAGCATCATCATTTTGAAGAGTCC 657
DB 316 LysValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnIleGlnGluys--- 333
QY 658 TGCATCGAAATTCAGCTGAGTGAACCATCCATATGTGCAGAGAGTCAATTCAGATT 717
DB 334 -----IlePheAlaIleGlnGluGlyThrGluSerArgSerSerSerSerPheGlnHis 350
QY 718 GTCGTGAGAGAAAGCGCTTCGACATGCCCGCAAGTGGAC 759
DB 351 GluMetSerGlnGluGlyPheSerSerAlaLeuSerMetAsp 364
RESULT 13
US-08-605-672-53
Sequence 53, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESSES:
ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-53
Alignment Scores:
Pred. No.: 2.91e-09 Length: 1161
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Beet Local Similarity: 28.21% Mismatches: 96
Query Match: 8.29% Indels: 30
DB: 1 Gaps: 12

US-09-970-076-1_COPY_104_1207 (1-1104) x US-08-605-672-53 (1-1161)
QY 109 CCAGCCTGTAAGCG---GGAATTGACCTGTATCTTATTTGACAAATCAGGAAGTGG 165
DB 144 ProGluCyArgProGlyGlnGluMetAspIleAlaPheLeuIleAspGlySerGlySerIle 163
QY 166 ---CTGCACCACTGGAATGAAATCTATTACTTTGTGGAAACAGTTGGCTTCACAAATTCATC 222
DB 164 AsgGlnSerAspPheThrGlnMetGlyMetLysAspPheValIleAlaLeuMetGlyGlnLeuAla 183
QY 223 AGCCCAAGTGAAGATGCTTATTTGTTTCTCCACCCGAGAAACAACCTTAATGAA 282
DB 184 SerThrSerThrSerPheSerLeuMetGlnIlyrSerAsnIleLeuLysThrIlePheThr 203
QY 283 CTGCACAGAGACAGA-----GAACAATTCCTCAAGCGCTTGAAGAACTC 327
DB 204 PheThrGlnPheLysSerSerLeuSerProGlnSerLeuValAspAlaIleValGlnLeu 223
QY 328 CAGAAAGTTCTGCCAGAGAGACACTTACATGATGAAGATTGAAAGGCCAGTGA 387
DB 224 Gln-----GlyLeuThrTyThrAlaSerGlyIleGlnIleValIlys 238
QY 388 CAGATTATATGAAACACAGACAGGTCACAGACAGC---AGCCTCATCTTGTCTTG 444
DB 239 GluLeuPheHisSerLysAsnGlyAlaArgLysSerAlaLysAlaLysIleLeuIleVal 258
QY 445 ACTGATGAGAACTCCATGAAAGATCTCTTTTCTATTTCAGAG-----AGGAGAGCTAAT 498
DB 259 ThrAspGlyGlnLysPheArgAspProLeuGluTyArgHisValIleProGluAlaGlu 278
QY 499 AGGCTCGAGATCTTGGTGCATTTGTTACTGTCTGTTGGTGAAGAT---TTCAATGAG 555
DB 279 LysAla-----GlyIleIleArgTyAlaIleGlyValGlyAspAlaPheArgGln 295
QY 556 ---ACACAGCTGGCCCGGATT-----GGCGACAGTGAAGATCATGTGTT 597
DB 296 ProthAlaLeuGlnIleuValenThrIleGlySerAlaProSerGlnAspHisValPhe 315
QY 598 CCCGTAATGAGCGGCTTCAGGCTGCAAGCATCATCATTTTGAAGAGTCC 657
DB 316 LysValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnIleGlnGluys--- 333
QY 658 TGCATCGAAATTCAGCTGAGTGAACCATCCATATGTGCAGAGAGTCAATTCAGATT 717
DB 334 -----IlePheAlaIleGlnGluGlyThrGluSerArgSerSerSerPheGlnHis 350
QY 718 GTCGTGAGAGAAAGCGCTTCGACATGCCCGCAAGTGGAC 759
DB 351 GluMetSerGlnGluGlyPheSerSerAlaLeuSerMetAsp 364
RESULT 14
US-08-482-293A-53
Sequence 53, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESSES:
ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A

FILING DATE: 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA: US 08/173,497
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA: US 08/362,652
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-53

Alignment Scores:

Pred. No.: 2,91e-09 Length: 1161
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.29% Indels: 30
DB: Gaps: 12

US-09-970-076-1_COPY_104_1207 (1-1104) x US-08-482-293A-53 (1-1161)

109 CCGAGCTGCTAAGCGC--GGATTGACCTGCTACTTATTTGGACAAATCAGGAAGTGTG 165
144 ProGluCySerProGluGlnGluMetAspIleAlaPheLeuIleAspGlySerGlySerIle 163
166 ---CTGACACCATGGAATGGAATCTATTCTTGTGGAAGTGGCTGCAAAATTCATC 222
164 AspGlnSerAspPheThrGlnMetLysAspPheValLysAlaLeuMetGlyGlnLeuAla 163
223 AGCCACAGTTGGAATGCTCTTATTTGCTCCACCCGAGAACCAACTTAATGAA 282
184 SerThrSerThrSerPheSerLeuMetGlnTyrSerAsnIleLeuLysThrHisPheThr 203
283 CTGACAGACAGACAGA-----GAAACAAATCCGTCAGAGCCCTAGAAAGAACTC 327
204 PheThrGlnPheLysSerSerLeuSerProGlnSerLeuValAspAlaIleValGlnLeu 223
328 CAGAAGTTTGGCAGAGAGACACTTACATGATGATGAAGATTGGAAGGCCAGTGTG 387
224 Gln-----GlyLeuThrThrAlaSerGlyIleGlnLysValValLys 228
388 CAGATTATTATGAAAAACAGACAGGCTGACAGACACC--AGCGTCATCATTTGCTTTG 444
239 GluLeuPheHisSerLysAsnGlyAlaArgLysSerLysLysIleLeuIleValIle 258
445 ACTGATGAGAACTCCATGAAATCTCTTTTCTATTCAAG-----AGGAGGCTTAAT 498
259 ThrAspGlyGlnLysPheArgAspProLeuGlnLysArgHisValIleProGlnLysLys 278
499 AGGCTTCGAGATCTTGTCATGATTTTACTGCTGTGTTGGAAGAT---TTCATAGAG 555
279 LysAla-----GlyIleIleArgTyrAlaIleGlyValGlyAspAlaPheArgGln 295
556 ---ACACAGCTGGCCCGGATT-----GCGGACAGTAAGATCATGTGTT 597
296 ProThrAlaLeuGlnGlnLysLeuAsnThrIleGlySerLysAlaProSerGlnAspHisValPhe 315

598 CCGTGAATGACGAGCTTTCAGGCTCTGACAGCATCATCAATTTTGAAGAATGCC 657
316 LysValGlyAsn---PheValAlaLeuArgSerIleGlnArgGlnIleGlnGly---- 333
658 TGCATGAAATTTCTAGACAGCTGAAACCATCCACCATATGTGCAGAGAGTCATTTCAAGTT 717
334 -----IlePheAlaIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 350
718 GTGCTGAGAGAAACGCTTCCGACATGCGCCGAGAGCTGAC 759
351 GluMetSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 364

RESULT 15

US-08-943-363-53
Sequence 53, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OR INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borzun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-53

Alignment Scores:
Pred. No.: 2,91e-09 Length: 1161
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.29% Indels: 30
DB: Gaps: 12

US-09-970-076-1_COPY_104_1207 (1-1104) x US-08-943-363-53 (1-1161)

109 CCGAGCTGCTAAGCGC--GGATTGACCTGCTACTTATTTGGACAAATCAGGAAGTGTG 165

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 14, 2005, 11:59:14 ; Search time 165.732 Seconds
(without alignments)
5566.636 Million cell updates/sec

Title: US-09-970-076-1_COPY_104_1207

Perfect score: 2003

Sequence: 1 atggcaccgagcgagcgagcgag.....gtgcgagaaataataataaa 1104

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications AA Main -OEMT=faasta -SUFFIX=rapbm -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human0.cdi -LIST=45 -DOCCALIGN=200 -THR SCORE=ppct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEARSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09970076 @CGN_1_1 604 @runat 14122005 110511 26579
-NCPU=6 -ICPU=3 -NO MMAP -LARGESOURCY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_AA_Main:*

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4: /cgn2_6/prodata/1/pubppaa/us10_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppaa/us10B_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubppaa/us11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1914	95.6	368	6	US-11-047-278-2
2	1894	94.6	564	3	US-09-918-715-187
3	1894	94.6	564	3	US-09-918-715-187
4	1894	94.6	564	3	US-09-918-715-187
5	1894	94.6	564	4	US-10-301-822-199
6	1894	94.6	564	4	US-10-301-822-199
7	1894	94.6	564	4	US-10-408-765A-1823
8	1894	94.6	564	4	US-10-474-794-187
9	1894	94.6	564	4	US-10-474-794-187
10	1894	94.6	564	5	US-10-979-159-187
11	1889	94.3	403	3	US-09-833-245-621
12	1870	93.4	403	3	US-09-833-245-621

13	1793	89.5	562	3	US-09-918-715-194	Sequence 194, App
14	1793	89.5	562	3	US-09-918-715-194	Sequence 301, App
15	1793	89.5	562	4	US-10-474-794-194	Sequence 194, App
16	1793	89.5	562	4	US-10-474-794-194	Sequence 301, App
17	1793	89.5	562	5	US-10-979-159-187	Sequence 301, App
18	1793	89.5	562	5	US-10-979-159-187	Sequence 18, App
19	1670	83.4	551	4	US-10-038-307-18	Sequence 18, App
20	1670	83.4	551	4	US-10-038-307-18	Sequence 20, App
21	1654.5	82.6	564	4	US-10-038-307-20	Sequence 20, App
22	1654.5	82.6	564	4	US-10-201-292-20	Sequence 20, App
23	1649	82.3	333	3	US-09-796-753-12	Sequence 12, App
24	1649	82.3	333	4	US-10-038-307-2	Sequence 2, App
25	1649	82.3	333	4	US-10-201-292-2	Sequence 2, App
26	1649	82.3	333	6	US-11-047-278-8	Sequence 8, App
27	1649	82.3	345	4	US-10-038-307-24	Sequence 24, App
28	1649	82.3	345	4	US-10-201-292-24	Sequence 24, App
29	1636	81.7	328	4	US-10-038-307-26	Sequence 26, App
30	1636	81.7	328	4	US-10-201-292-26	Sequence 26, App
31	1636	81.7	543	4	US-10-038-307-14	Sequence 14, App
32	1636	81.7	543	4	US-10-201-292-14	Sequence 14, App
33	1634.5	81.6	342	4	US-10-038-307-22	Sequence 22, App
34	1634.5	81.6	342	4	US-10-201-292-22	Sequence 22, App
35	1633	81.5	543	4	US-10-038-307-16	Sequence 16, App
36	1633	81.5	543	4	US-10-201-292-16	Sequence 16, App
37	1626	81.2	543	4	US-10-038-307-10	Sequence 10, App
38	1626	81.2	529	4	US-10-201-292-10	Sequence 10, App
39	1555	77.6	534	4	US-10-038-307-12	Sequence 12, App
40	1495	74.6	534	4	US-10-201-292-36	Sequence 36, App
41	1495	74.6	534	4	US-10-038-307-12	Sequence 12, App
42	1434.5	71.6	504	4	US-10-201-292-34	Sequence 34, App
43	1307	65.3	479	4	US-10-201-292-32	Sequence 32, App
44	1193	59.6	460	4	US-10-201-292-28	Sequence 28, App
45	1183	59.1	460	4	US-10-201-292-30	Sequence 30, App

ALIGNMENTS

RESULT 1
US-11-047-278-2
; Sequence 2, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, Kenneth A.
; APPLICANT: Bradley, John A.T.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296, 97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-047-278-2

Alignment Scores:

Pred. No.: 2,766-182

Score: 1914.00 Length: 368

Percent Similarity: 100.00% Matches: 368

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 95.56% Indels: 0

DB: 6 Gaps: 0

US-09-970-076-1_COPY_104_1207 (1-1104) x US-11-047-278-2 (1-368)

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Db	21	LeuValleuilecyaalaglyglnolylglnarglnabpdlgylproalacyletyr	40
Oy	121	GCGGAGTTTGACCTGTACTTCATTTTGGACAAATCAGGAAGTGTGTCCACCACTGAAT	180
Db	41	GlyglyPheabpLeutyrrPheilleuabpYsserGylservalleuiahiletyrbyn	60
Oy	181	GAATCTTATCTTTGGACAGTGGCTCAAAATTCATCAGGSCCACTTGAAGATG	240
Db	61	GluiletyrYrrPheValGlnGlnleuadlahlvlyrPheilleSerproGlnleuarghet	80
Oy	241	TCCTTTATGTTTCTCCACCCGAGAAACAACCTTAAAGAACTGACAGAAACAGAGA	300
Db	81	SerPheillevalPheSerThrargglythrThrleuMetvlyleuThrGlnabpArgln	100
Oy	301	CAAACTCGTCAAGGCTTAGAAGAACTCCAGAAAGTTGTCCAGAGAGAGACTTACATG	360
Db	101	GlnllearglnGlnlyleuGlnGlnleuGlnlyleuGlnlyValleupProGlyGlyAspThrtyMet	120
Oy	361	CATGAAGATTGAAAGGCGCCAGTGAAGCATTTATTGAAACAGACAGGGTACACGG	420
Db	121	HlsglnGlyPhegluarglnaserGlnGlnleetyrYrrGlnabpArglnlytyrarg	140
Oy	421	ACAGCAGGTCATCATTTGACTTTGACTGTGATGGAGAACTCCATGAAGATCTCTTTTCTAT	480
Db	141	ThrllaserValleillelaleuThrabpdlgylleuabhlsglnabpLeuPhePheTyx	160
Oy	481	TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGGTGCATTTGTTACTGTGTGTGTG	540
Db	161	SerGlnargGlnlalaabpSerargabpLeuGlyalallevaltyrCysValGlyal	180
Oy	541	AAAGTTTTCATGAACACAGCTGGCCCGGATGTGGACAGTGAAGATCATGTGTTTCCC	600
Db	181	LysabpPheabpGlnThrGlnleuadlArgllealabpSerlyrAspHilevalPhePro	200
Oy	601	GTGAATGACGGCTTTCAGGCTCTGCAAGGACATCATCCACTCAATTTTGAAGAGCTCGC	660
Db	201	ValabpabpGlyPheGlnHlaleuGlnGlylellehileSerlleuulvaysserCys	220
Oy	661	ATCGAAATTTAGACACTGAACCATCCACCATATGTGCAAGAGACTCATTTCAAGTGTG	720
Db	221	llegulilleuadlahlaglnproSerthrlliecyvalaglyGlnserPheGlnValal	240
Oy	721	GTGAAGAAACGCGCTTCGACATGCCCGGCAACGTGACAGGGTCTCTGCACTTCAAG	780
Db	241	ValArgGlyAsnGlyPheArgHlhalArgabnValabpArgValleuCysSerPheIys	260
Oy	781	ATCATATGACTGGTGACACTCAATATAGAAAGCCCTTTCTGTGGAGACACTTATTACTG	840
Db	261	lIleabpabpSerValthrIleuabnGlnulvyrProPheSerValGlnabpThrlytleuIeu	280
Oy	841	TGTCAGAGCGCTATTTAAAGAAATGGCATGAAGAGCTGCACCTCCAGTCAAGATCAAC	900
Db	281	CysproalaproilleuulysGlnvalGlyMetvlyValalaleuGlnValSerMetvsn	300
Oy	901	GATGGCTCTCTTTTATCTCCAGTTCTGTCAATCATCACCAACCAACTGTTTGTACGGT	960
Db	301	AerGlyLeuSerPheilleSerSerValillellethrlnThrHlHlCysSerabpIy	320
Oy	961	TCCATCTCGGCATAGGCGCTGTGATCTGTTCCTCGGCTCCAGGCTGTCTCTCTCG	1020
Db	321	SerilleleuadlallealaleuIeuilleuPheleuIeuIeuadlaleuadlaleuIeuIyr	340
Oy	1021	TGGTCTTGAGCCCTCTGCTGCACCTGTGATTTATCAAGAGAGTCCCTCCACCCCTCGAG	1080
Db	341	TrpPheIrrProleuCysCysThrValillellelysglnValproproProalagln	360
Oy	1081	GAGAGTGAAGAAATTAATAATAA	1104

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Db      361 GluSerGluGluAenLysIleLys 368

RESULT 2
US-09-918-715-187
; Sequence 187, Application US/09918715
; Publication No. US20030017157A1
;
GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOMETRIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-187

Alignment Scores:
Pred. No.:      3,24e-180      Length:      564
Score:          1894.00      Matches:      364
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      94.56%      Indels:      0
DB:                3          Gaps:          0

US-09-970-076-1_COBY_104_1207 (1-1104) x US-09-918-715-187 (1-564)

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QY      61 CTGGTGTCTCATCTCGCGCGGCGAGGGGAGCCAGGAGAGATGGGGGTCCAGCTGTAC 120
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QY      121 GGGCGATTGACCCGTACTCTTCAATTTGGACAATGACGAAAGTGCTGACCACTGGAAAT 180
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QY      181 GAAATCTATTACTTGTGTGAAACAGTTGGCTCAAAATTCATCATGCCACAGTTGAGAAATG 240
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QY      241 TCCTTTATTGTTTCTCCACCCGAGAAACACCTTATGAAACTGACAGAAACAGAGAA 300
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QY      361 CATGAAGGATTGAAAGGCGCAGTAGCAGCAGATTATATGAAAACAGAAAGGATACAGG 420
Db      121 HisGlnGlyPheGlnArgAlaSerGlnGlnIleTyrTyrGlnLysAspArgGlnGlyTyrArg 140

QY      421 ACAGCAGACGTCATCATTTGCTTGACTGATGAGAAATCCATGAAGAATCTCTTTTCTAT 480
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QY      481 TCAGAGAGGAGGCTAATTAAGTCTCGAAGATCTTGGTGCAATTTGTTACTGTGTGGTGG 540
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QY 541 AAGATTTCAATGACACACAGCTGGCCCGGATTCGGACAGTAAGATCATGNTTCCC 600
DB 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
QY 601 GTCAATGACGGCTTTGAGCTCTGCAAGGATCATCACTCAATTTTGAAGAGTCTCG 660
DB 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuYslySerCys 220
QY 661 ATGAAATTTAGACAGCTGAACCATCCCATATGTGACAGAGAGTCAATTTCAAGTTGTC 720
DB 221 IleGluIleLeuAlaIaGluProSerThrIleCysValGlyGluSerPheGlnValVal 240
QY 721 GTGAGAGAAACGGCTTCGACATGCCCCGACAGTGACAGGCTCTCTGACCTTCAAG 780
DB 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
QY 781 ATCAATGACTGGGACACTCAATGAGAGACCTTTTCTGTGAAGACATTAATTAATG 840
DB 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu 280
QY 841 TGTCACGGCTTAATCTTAAAGAGTTGGCATGAAGCTGCACCTCCAGTCAAGATGAAC 900
DB 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaIaLeuGlnValIleSerMetAsn 300
QY 901 GATGGCTCTCTTTATCTCACTGTCTGATCATCAACACACACTGTTTGAAGGT 960
DB 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
QY 961 TCATCTGGGCAATCGCCCTGCTGATCTGTCTGCTCTGAGCCCTGCTCTCTG 1020
DB 321 SerIleLeuAlaIleAlaLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTyr 340
QY 1021 TGGTTTGCCCTCTGCTGCTGCTGATGATTAACAAGAGTCCCTCCAGCCCTGCGAG 1080
DB 341 TrpPheThrProLeuCysCysThrValIleIleLysGluValProProProAlaGlu 360
QY 1081 GAGAGTAGGAA 1092
DB 361 GluSerGluGlu 364

RESULT 3

US-09-918-715-232
Sequence 232, Application US/09918715
Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918.715
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 232
LENGTH: 564
TYPE: PRT
ORGANISM: Homo sapiens
US-09-918-715-232

Alignment Scores:
Pred. No.: 3,24e-180 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.56% Indels: 0

DB: 3 Gaps: 0
US-09-970-076-1_copy_104_1207 (1-1104) x US-09-918-715-232 (1-564)
QY 1 ATGGCCACGGCGAGCGAGAGACCCCTGGCATCGGCTTCCAGTGGCTCTTTGGCCACT 60
DB 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnThrPheSerLeuAlaThr 20
QY 61 CTGGGCTCATCTGCGCCCGGAGAGGCCAGGAGAGAGGGGGTCTCAGCTTCC 120
DB 21 LeuValLeuIleCysAlaGlyGlnGlyLysArgGluAspGlyGlyProAlaCysTyr 40
QY 121 GGGGATTTGACCTGATCTCAATTTTGAACAATCAGAAGTGCTGACCACTGGAAT 180
DB 41 GlyGlyPheAspLeuThrPheIleLeuAspLysSerCysValLeuHisStrPan 60
QY 181 GAAATCTATTAATCTTTGTGGAACAGTTGGCTCACAATTCATACGCCCACTTGAGATG 240
DB 61 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
QY 241 TCTTTAATGTTTCTCCACCGGAGAGACACCTTAATGAACCTGACAGAGACAGAGA 300
DB 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
QY 301 CAAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTCTCCAGAGAGACATTAATG 360
DB 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
QY 361 CATGAGAGATTGAAAGGCGCATGAGACAGATTATTAATGAACAAGAGGTACAG 420
DB 121 HisGluGlyPheGluArgLysSerGluGlnIleTyrGluAsnArgGlnGlyTyrArg 140
QY 421 ACGACGAGGTCAATCAATGCTTTGATGATGAGAACTCCAGTAATGCTTTTCTAT 480
DB 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGluAspLeuPheTyr 160
QY 481 TCAGAGAGGAGGCTAATGAGTCTCGAGATCTTGTCGCAATGTTTACTGTGTGGTGTG 540
DB 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
QY 541 AAGATTTCAATGACACACAGCTGGCCCGGATTCGGACAGTAAGATCATGNTTCCC 600
DB 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
QY 601 GTCAATGACGGCTTTGAGCTCTGCAAGGATCATCACTCAATTTTGAAGAGTCTCG 660
DB 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuYslySerCys 220
QY 661 ATGAAATTTAGACAGCTGAACCATCCCATATGTGACAGAGAGTCAATTTCAAGTTGTC 720
DB 221 IleGluIleLeuAlaIaGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
QY 721 GTGAGAGAAACGGCTTCGACATGCCCCGACAGTGACAGGCTCTCTGACCTTCAAG 780
DB 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
QY 781 ATCAATGACTGGGACACTCAATGAGAGACCTTTTCTGTGAAGACATTAATTAATG 840
DB 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu 280
QY 841 TGTCACGGCTTAATCTTAAAGAGTTGGCATGAAGCTGCACCTCCAGTCAAGATGAAC 900
DB 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaIaLeuGlnValIleSerMetAsn 300
QY 901 GATGGCTCTCTTTATCTCACTGTCTGATCATCAACACACACTGTTTGAAGGT 960
DB 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
QY 961 TCATCTGGGCAATCGCCCTGCTGATCTGTCTGCTCTGAGCCCTGCTCTCTG 1020
DB 321 SerIleLeuAlaIleAlaLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTyr 340
QY 1021 TGGTTTGCCCTCTGCTGCTGATGATTAACAAGAGTCCCTCCAGCCCTGCGAG 1080

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|||||
Db      341 TrpPheTrpProLeuCyScyThrValIleIleLeuGluValProProProProIaGlu 360
QY      1081 GAGAGTGAGGAA 1092
Db      361 GluSerGluGlu 364

RESULT 4
US-10-301-822-199
; Sequence 199, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamackar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-301-822-199

Alignment Scores:
Pred. No.: 3,24e-180 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.56% Indels: 0
DB: 4 Gaps: 0

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-301-822-199 (1-564)
QY      1 ATGGCCACGGCGGAGGAGAGCCCTCGGCATGGGCTTCAGTGGCTCTTTGGCCACT 60
Db      1 MetAlaThrAlaIleuArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
QY      61 CTGGTCTCATCTCGCGCGGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
Db      21 LeuValLeuLeuLeuCyAlaGlyGlnGlyAlaArgGluAspGlyGlyProIaCySerY 40
QY      121 GCGGATTTGACCTGTACTTCAATTTGGACAATTCAGGAAGTGTCTGCCACCTGGAAT 180
Db      41 GlyGlyPheAspLeuTrpPheIleLeuAspLysSerGlySerValLeuHisIleTPAan 60
QY      181 GAATCATATCACTTTGGGAACAGTTGGCTCAAAATTCATCGCCCAAGTTGAGAATG 240
Db      61 GluIleTrpTrpPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
QY      241 TCTTTATTTGTTTCTCCACCAGGAACAACCTTAATGAATGACAGAAAGACAGAGAA 300
Db      81 SerPheIleValPheSerThrArgGlyThrThreuleuMetLysLeuThrGluAspArgGlu 100
QY      301 CAATCCGTACAGGCTTAGAAGAACTTCAGAAAGTTCTGCCAGAGAGACACTTAACAG 360
Db      101 GlnIleArgGlnGlnGluGlnGluLeuGlnValLeuProGlyGlyAspThrTrpMet 120
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QY      361 CATGAAGATTTGAAGGCGCAGTGAAGATTTATGAAACAGACAAAGGTAACAG 420
Db      121 HisGluGlyPheGluArgAlaSerGluGlnIleTrpTrpGluAsnArgGlnGlyArg 140
QY      421 ACAGCCAGGCTCATATTGCTTGACTGATGGAAATTCACGAAGATCTTTTCTAT 480
Db      141 ThrIaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTrp 160
QY      481 TCAGAGAGGAGGAGCTAAATAGCTGTGAGATCTGTGGCAATGTTACTGTGTGGTG 540
Db      161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTrpCyValGlyVal 180
QY      541 AAAGATTTCAATGACACACAGCTGCGCGGATGGCGGACAGTAAGATCATGTGTTCC 600
Db      181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
QY      601 GTGAATGACGGCTTCAGGCTCTGCAAGGCATCATCCACTCAATTTTGAAGAATCTGC 660
Db      201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCyS 220
QY      661 ATCGAAATTTGACAGCTGAACCATCCACCATATGTGACAGAGATCAATTAAGTGC 720
Db      221 IleGluIleLeuAlaIleGluProSerThrIleCyAlaGlyGluSerPheGlnVal 240
QY      721 GTGAGAGGAAACGGCTTCGACATGCGCGCAACGTGACAGGGTCTCTGACGTTCAAG 780
Db      241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCySerPheLys 260
QY      781 ATCAATGACTCGGTCACTCAATAGAAAGCCCTTTCTGTGGAAGACCTATTACTG 840
Db      261 IleAsnAspSerValThrLeuAsnGlnLysProPheSerValGluAspThrTrpLeuLeu 280
QY      841 TGTCCAGGCGCTATCTTAAAGATGGCAAGAGGCACTCCAGGTCGACATGAC 900
Db      281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnAlaSerMetAsn 300
QY      901 GATGCGCTCTCTTTATCTCCAGTCTGTGCATCATCACCCACACACACTGTTCTGACGT 960
Db      301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThreLysSerAspGly 320
QY      961 TCCATCTCGGCATGCGCCTGCTGATCTGTCTCTGCTCTGAGCCCTCTCTCTG 1020
Db      321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340
QY      1021 TGGTCTGGCGCCCTGTGCGACCTGTGATTCAGGAAGGTCCTCCACCCCTGCGCGAG 1080
Db      341 TrpPheTrpProLeuCyScyThrValIleIleLysGluValProProProProIaGlu 360

QY      1081 GAGAGTGAGGAA 1092
Db      361 GluSerGluGlu 364

RESULT 5
US-10-408-765A-1823
; Sequence 1823, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boia D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088,465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1823
```



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; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1823

Alignment Scores:
Prod. No.: 3 24e-180 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.56% Indels: 0
DB: 4 Gaps: 0

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-408-765A-1823 (1-564)

QY 1 ATGGCCAGCGCGAGCGAGAGCCCTCGGATCGGCTTCAGTGGCTCTTTGGCCACT 60
DB 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20

QY 61 CTGGTGTCTATCTGCGCGGCGAGGCGAGCGAGGAGATGGGGTCCAGCTGTCTAC 120
DB 21 LeuValLeuIleCybAlaGlyGlnGlyAlaArgGluAparGlyGlyProAlaCybTr 40

QY 121 GGGGATTGACCTGTACTTCATTTTGAACAATCAGGAAGTGCTGACCACTGGAAT 180
DB 41 GlyGlyPheAspLeuTrpPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60

QY 181 GAATCTATTACTTTGTGAAACAGTTGGCTCACAATTCATCAGCCCACTTGAGATG 240
DB 61 GluIleTrpTrpPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80

QY 241 TCTCTTATTTGTTTCTCCACCCGAGGAACAACCTTATGAAACTGACAGAAACAGAA 300
DB 81 SerPheIleValPheSerThrArgGlyThrThreuleMetLysLeuTrpGluAparGlyGlu 100

QY 301 CAATCCGTCAGGCGCTAGAAAGAACTCCAGAAATTCGCGAGGAGAGACACTTACATG 360
DB 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnValLeuProGlyGlyAparThrTyMet 120

QY 361 CATGAGAGATTGTAAGAGCGCCAGTGAAGATTTATTATGAAAACAGACAGGTCACAG 420
DB 121 HisGluGlyPheGluArgAlaSerGluGlnIleTrpTrpGluAparGlnGlyTyArg 140

QY 421 ACAGCCAGCTCATCATTTGCTTGTGATGAGAAACTCCATGAAGATCTTTTCTAT 480
DB 141 ThrIleSerValIleIleAlaLeuThrAparGlyGluLeuHisGluAparPhePheTr 160

QY 481 TCAGAGAGGAGGCTAATAGGCTCGAATCTTGTCGCAATGTTTCTGTTGGTGGTGTG 540
DB 161 SerGluArgGluAlaAspArgSerArgAparLeuGlyAlaIleValTyrcyValGlyVal 180

QY 541 AAAGATTTCATGAGACACAGCTGCGCCGGAATTCGGAACAGTAAGATCATGTGTTCC 600
DB 181 LysAspPheAspGlnGluTrpGlnLeuAlaArgIleAlaAparSerLysAparHisValPhePro 200

QY 601 GTGAATACGGCTTCAGGCTCTCGAAGGCAATCATCCACTGAATTTTGAAGAATCTTCC 660
DB 201 ValAsnAparGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCyb 220

QY 661 ATCGAATTTCTAGAGAGTGAACATCCATCCATATGTGAGAGAGATCATTTCAAGTTGTC 720
DB 221 IleGluIleLeuAlaAlaGluProSerThrIleCybAlaGlyGlyUserPheGlnValVal 240

QY 721 GTGAGAGAAACGGCTTCGACATGCCCGCAACGTGAACAGGTCCTCTGACGCTTCAG 780
DB 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAparGValLeuCybSerPheLys 260

QY 781 ATCAATGACTGGGTACACTGAATGAGAAAGCTTTTGTGGAAGACATTAATTTACTG 840
DB 261 IleAsnAparSerValThrLeuAsnGlyLysProPheSerValGluAparThrTyLeuLeu 280

QY 841 TGTCAGGCGCTATCTTTAAAGAGTTGGCATGAAGTGCATCCAGGTCAAGATGAAC 900
DB 841 TGTCAGGCGCTATCTTTAAAGAGTTGGCATGAAGTGCATCCAGGTCAAGATGAAC 900
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DB 281 CybProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
QY 901 GATGGCTCTCTTTTATCTCCAGTTCTGTGCATCATCACCACCACTGTTCTGACGGT 960
DB 301 AapGlyLeuSerPheIleSerSerSerValIleIleThrThrThrHisCybSerAparGly 320

QY 961 TCCATCTGGCCATCGCCCTGTGATCTGTCTGTCTGTCTGACCCCTGCGCTCTCTG 1020
DB 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340

QY 1021 TGGTGTGCGCCCTCTGTCTGTGACCTGTGATTAACAGAGAGTCCCTGACCCCTGCGAG 1080
DB 341 TrpPheTrpProLeuCybCybThrValIleIleIleLysGluValProProProAlaGlu 360

QY 1081 GAGAGTGAAGAA 1092
DB 361 GluSerGluGlu 364

RESULT 6
US-10-474-794-187
; Sequence 187, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107,00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-187

Alignment Scores:
Prod. No.: 3 24e-180 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.56% Indels: 0
DB: 4 Gaps: 0

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-474-794-187 (1-564)

QY 1 ATGGCCAGCGCGAGCGAGAGCCCTCGGATCGGCTTCAGTGGCTCTTTGGCCACT 60
DB 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20

QY 61 CTGGTGTCTATCTGCGCGGCGAGGCGAGCGAGGAGATGGGGTCCAGCTGTCTAC 120
DB 21 LeuValLeuIleCybAlaGlyGlnGlyAlaArgGluAparGlyGlyProAlaCybTr 40

QY 121 GGGGATTGACCTGTACTTCATTTTGAACAATCAGGAAGTGCTGACCACTGGAAT 180
DB 41 GlyGlyPheAspLeuTrpPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60

QY 181 GAATCTATTACTTTGTGAAACAGTTGGCTCACAATTCATCAGCCCACTTGAGATG 240
DB 61 GluIleTrpTrpPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80

QY 241 TCTCTTATTTGTTTCTCCACCCGAGGAACAACCTTATGAAACTGACAGAAACAGAA 300
DB 81 SerPheIleValPheSerThrArgGlyThrThreuleMetLysLeuTrpGluAparGlyGlu 100
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Oy		301	AAATCGGTCAAGGCTGTGAAGAATCCAGAAAGTTCTMGCCAGAGGAGACACTTACAATG	360
Db		101	Ginlleatglnnglyleuglignleuendimulyvalleuproglyglyasprhntrytnc	120
Oy		361	CATAAAGATTGTGAAGGGCCAGTGAGAGATTTATATGA AAA CAG AAGGGTAGCAG	420
Db		121	Hieglunghpneghluarglasberclundinletyrtyrgrluamnarngldnlytryrhrg	140
Oy		421	ACAGCCAGCTCATTCATTCGTTTGA CTGATGAGAACTCCATGAAGATCTCTTTTCTAT	480
Db		141	ThrlaserValillellealleuleuthzrhpoglygtuleuhnlsgluasprleupheheryx	160
Oy		481	TCCAGAGGGGAGGGCTAATAGSTCTCGAATCTGTGGTAATGGTTTACTGTGGTGGTGC	540
Db		161	Serqluatrgluualaaenarxserxtgaspneuglyalallevaltycyvalaglyval	180
Oy		541	AAAGATTTCATGAGACACACAGCTGGCCGAGATTCGCGGACAGTAAAGATCATGTGTTCC	600
Db		181	Lysaprpheahengluthrghleuhalargllealeahabserlyshaphilevalphero	200
Oy		601	GTGAATGACGGCTTTCAGGCTCTCGMAAGCATATCCACTCAATTTTGAAGAAGTCTGC	660
Db		201	Valaenaherglyphegnlalaleuandnglylerleliehsertleleuulylserycs	220
Oy		661	ATCCAAATTCATGACAGCTGGAACCATCCACTATGTGTGACAGAGATCATTTCAAGTGTG	720
Db		221	Ileguilieleuhalablagnuproserthrlllecysalaglgyluserphegnlaval	240
Oy		721	GTGAGAGAAA CGGCTTCGCA CATGCCGCAACGTGGA CAGGGTCTCTGCAGCTTCAAG	780
Db		241	Valargglyahenglyphearghlialaarhamnalabphargvalleucyserphelys	260
Oy		781	ATCAAATGACTCGGTCACTCAATGAGAAGCCCTTTGTGTGAAGA CACTTATTTACTG	840
Db		261	Ileaenaheservaithrleuansdnlulyspropheservailgluaspthrtrytleuenu	280
Oy		841	TGTCCAGGCGCTATTTTAAAAAGATTGGCATGAAAGCTGCATCTCACAGTCA GATAC	900
Db		281	Cysproalaaproilieleuulysgluvalajimetylvsaalaleuqlnvalsetwercan	300
Oy		901	GATGGCCCTCTCTTATATCTCCAGTGTGTGCATCAATCACCAACACACACTGTTGTGACGT	960
Db		301	Aepglylseuserpheilleserserservallleietmrnthrhiascyseerhapoly	320
Oy		961	TCCATCTCTGAGCCATGCCCCGTGTGATCCGTTCCTGCTCTAGACCCTGGCTCTCCTCGG	1020
Db		321	Serlleleuhalialellealleuenuilleupheueuenualeuhalaleuenuitp	340
Oy		1021	TGTTTTGTGGCCCCCTCTGCTGC ACTGTGATTTATCAAGAGAGTCCCTCCACCCCCTGGAG	1080
Db		341	TrpnetprrprouecycysethrValilleilysgluvalProProproalaaglu	360
Oy		1081	GAGAGTGAGGAA 1092	
Db		361	Gluserglnulu 364	
RESULT 7				
US-10-474-794-232				
Sequence 232, Application US/10474794				
Publication No. US20040213793A1				
GENERAL INFORMATION:				
APPLICANT: Carson-Walter, Eleanor				
APPLICANT: St. Croix, Brad				
APPLICANT: Vogelstein, Bert				
APPLICANT: Kinsler, Kenneth				
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS				
FILE REFERENCE: 1107.00179				
CURRENT APPLICATION NUMBER: US/10/474,794				
CURRENT FILING DATE: 2003-10-14				
PRIOR APPLICATION NUMBER: 60/282,850				
PRIOR FILING DATE: 2001-04-11				
PRIOR APPLICATION NUMBER: 60/308,829				
PRIOR FILING DATE: 2001-08-01				

NUMBER OF SEQ ID NOS: 359									
SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 232									
; LENGTH: 564									
; TYPE: PR1									
; ORGANISM: Homo sapiens									
US-10-474-794-232									
Alignment Scores:									
Pred. No.: 3,24e-180 Length: 564									
Score: 1894.00 Matches: 364									
Percent Similarity: 100.00% Conservative: 0									
Best Local Similarity: 100.00% Mismatches: 0									
Query Match: 94.56% Indels: 0									
DB: 4 Gaps: 0									
US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-474-794-232 (1-564)									
QY	1	ATGGCCACGGGGAGCGGAGAGCCCTCGGCAATCGGCTCCAGTGGCTCTTGGCACT	60						
DB	1	Metatntralaagluatrgalalaenuliyilegiphegintprleusenleualatr	20						
QY	61	CTGNGCTCATCTCGCGCGGCAAGGGGAGAGCAGCAGAGATGAGGGATCCAGCTTGC	120						
DB	21	leuValleuilecybalaigylglnlylaryargluabeglydylprolaacystry	40						
QY	121	GGCGGATTTGACCTGTACTTCATTTTGGACAACAATCAGGAAGTGCTGCACCACTGGAAT	180						
DB	41	GllyglPheapleuryrPheilleuabpyserglserValleuishi8trpaen	60						
QY	181	GAATCTATTACTTTGTGGAAACGTGGCTCACAAATTCATCAGGCCACAGTTGGAATG	240						
DB	61	GlunlelyrtyrPhevaGluglneulaahlsylsPheilleserProglneuargwet	80						
QY	241	TCCTTTATGTTTCTCCACCAGGAGCAACCTTAATGAAACTGACAGAGAAGAGAA	300						
DB	81	SertheilevalPheaserThrarglylthrThreleumelyleuthrciunaparglu	100						
QY	301	CAAAATCCGTCAGGCTGAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG	360						
DB	101	Glnlearglngllyleuglgluenglnlysvallleuproglygllyasphrtyrmec	120						
QY	361	CATGAAGATTGAAAGGGCCAGTGCAGCATTTTATGAAACAGACAAAGGTTCAGG	420						
DB	121	HlsglunglyPhegluarglaserlunlilelyrtyrGluabnarglngllytyraag	140						
QY	421	ACAGCAGCGTCATCATGCTTTGACTGATGGAGAACTCCATGAAAGATCTCTTTCTAT	480						
DB	141	Thrlaservalllelialaenuthrapslyglulnehlsglunbepneupheptyr	160						
QY	481	TCAGAGAGGAGGCTAATAGGTCTTCGAGATCTTGGTGCAAATGTTACTGTGTGGTGTG	540						
DB	161	SergluaraglunlaaenargrserargapleugllylalleValtyrcyvalglVal	180						
QY	541	AAAGATTCAATGAGACACAGCTGGCCCGGATGGCGACAGTAAAGATCATGTGTTCCC	600						
DB	181	LysaspPheanngluthrGlnleulaartrilealaasberlyasphlsvalPhepro	200						
QY	601	GTCGATGACGGCTTCAGGCTCTCGCAAGGACATCCACTCAATTTTGAAGAACTCTGC	660						
DB	201	ValasnbpglPheglinalaenulnolylellehasserilleuulysbercyb	220						
QY	661	ATCGAAATTCAGACAGTGAACCATCCACATATGTGCAGAGAGATCATTTCAAGTTGTC	720						
DB	221	lleguileleuulaialgluproserthrilecybalaigylgluserhegnlVal	240						
QY	721	GTCGAGGAGAAACGGCTTCCGACATGCCCGCAACGTGACAGGGGTCTCTGCAGCTTCAAG	780						
DB	241	ValaraglYannglyPhearghlsialargranValaapargValleucysserPheyls	260						
QY	781	ATCATATGCTGGTGCACCTCAATGAGAAAGCCCTTTCTGTGGAGAGACCTTATTACTG	840						
DB	261	lleanapbservallThreleuasnululysProPheaserValglunspthryrleu	280						

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QY      841 TGTCCAGCGCTATCTTAAAGAAGTTGGATGAAAGCTGACTCCAGGTCACATGAAC 900
DB      281 CysProlaIaProIleuLysGluValGlyMetClyAlaIleuGlnValSerMetAen 300
QY      901 GATGGCCTCTCTTTTATCTCAGATTCTGTCATCATCACACACACTTTCTGACGCT 960
DB      301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAaspGly 320
QY      961 TCCATCTGGCCATCGCCCTGCTGATCTGTCTCTGCTCTAGCCCTGCTCTCTG 1020
DB      321 SerIleuAlaIleAlaIleuLeuIleLeuPheLeuLeuAlaIleuAlaLeuLtrp 340
QY      1021 TGGTTCTGGCCCTCTGCTGCTGATGATGATATCAAGAGAGTCCCTCCACCCCTGCCGAG 1080
DB      341 TrpPheTrpProLeuCysCysThrValIleIleIleGluValProProProAlaGlu 360
QY      1081 GAGAGTGAGGAA 1092
DB      361 GluSerGluGlu 364

RESULT 8
US-10-979-159-187
; Sequence 187, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: PaedSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-979-159-187

Alignment Scores:
Pred. No.: 3,246-180 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.56% Indels: 0
DB: 5 Gaps: 0

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-979-159-187 (1-564)
QY      1 ATGGCCAGCGGCGAGGAGAGCCCTGCGGCTTCAGGCTCTTTGGCCACT 60
DB      1 MetAlaThrAlaGluValArgAlaLeuGlyIleGlyPheGlnTrpLeuSerIleuAlaThr 20
QY      61 CTGGTGTCTCATCTCGCCGCGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGTAC 120
DB      21 LeuValLeuIleCysAlaGlyGlnGlyValArgArgGluAaspGlyValProAlaCysTrp 40
QY      121 GCGGGAATTTGACCTGTACTTATTTTGAACAATCAAGAAATGTGCTGCACACTGGAAT 180
DB      41 GlyIlePheAepLeuIlePheIleLeuAaspLysSerGlySerValIleuHisIleTrpAasn 60
QY      181 GAAATCTATTCTTTGAGAACAGTGGCTCAAAATTCACAGCCCAAGTTGAGATG 240
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DB      61 GluIleTrpPheValGluGlnIleuAlaHisLysPheIleSerProGlnIleuArgMet 80
QY      241 TCCCTTATGTTTTTCCACCAGGAGACAACTTATGAAATGACAGAGACAGAGAA 300
DB      81 SerPheIleValPheSerThrArgGlyThrThrLeuMetClyLeuThrGluAaspGlu 100
QY      301 CAATCCGTCAGGCGCTAGAGAACTCCAGAAAGTTCTGCGCAGAGAGACACTTACATG 360
DB      101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAaspThrTrpMet 120
QY      361 CATGAAGATTTGAAGAGGCGCAGTGCAGATTTATTTAAGAAACAGACAGAGGTACAG 420
DB      121 HisGlnGlyPheGlnArgAlaSerGlnGlnIleTrpGlyGluAasnArgGlnGlyTrpArg 140
QY      421 ACAGCCAGGCTCATCTTGGCTTGTGATGATGAGAACTCCATGAAATGCTCTTTCTAT 480
DB      141 ThrAlaSerValIleIleAlaLeuThrAaspGlyGlnIleuHisGlnIleuPhePheTrp 160
QY      481 TCAGAGAGGAGGCTATAGTCTCGAGATCTTGATGCAATGTTTACTGTGTGTGTG 540
DB      161 SerGluArgGluAlaAasnArgSerArgAaspLeuGlyAlaIleValTrpCysValGlyVal 180
QY      541 AAGATTTCAATGAGACACAGCTGCGCCGAGATTGCGACAGTAAAGATCATGTTTCCC 600
DB      181 LysAaspPheAasnGlnThrGlnIleuAlaArgIleAlaAaspSerLysAaspHisValPhePro 200
QY      601 GTGAATGACGCGCTTTTCAAGCTCTGCAAGGATATCATCATATTTTGAAGAAGTCTCG 660
DB      201 ValAasnAaspLysPheGlnAlaLeuGlnGlyIleIleHisSerIleuLysSerCys 220
QY      661 ATGAAATTTACACAGCTGAACCATCCACATATGTCAGAGAGTCAATTTCAAGTTGTC 720
DB      221 IleGlnIleuAlaIleAlaGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
QY      721 GTGAGAGGAAACGCTTCCGACATGCGCCGACAGCTGAGACAGGTTCTCTGACCTTCAAG 780
DB      241 ValArgGlyAasnGlyPheArgHisAlaArgAasnValAaspArgValIleuCysSerPheLys 260
QY      781 ATCAATGATCTCGGTTCACATCATGAGAACCTTTTGTGGAAGCACTTATTTATCTG 840
DB      261 IleAasnAaspSerValThrIleuAasnGluLysPheSerValGluAaspThrTrpLysLeu 280
QY      841 TGTCCAGCGCTATCTTAAAGAAGTTGGATGAAAGCTGCACTCCAGCTCACATGAAC 900
DB      281 CysProlaIaProIleuLysGluValGlyMetClyAlaIleuGlnValSerMetAen 300
QY      901 GATGGCCTCTCTTTATCTCAGATTCTGTCATCATCACACACACTTTCTGACGCT 960
DB      301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAaspGly 320
QY      961 TCCATCTGGCCATCGCCCTGCTGATCTGTCTCTGCTCTAGCCCTGCTCTCTG 1020
DB      321 SerIleuAlaIleAlaIleuLeuIleLeuPheLeuLeuAlaIleuAlaLeuLtrp 340
QY      1021 TGGTTCTGGCCCTCTGCTGCTGATGATGATATCAAGAGAGTCCCTCCACCCCTGCCGAG 1080
DB      341 TrpPheTrpProLeuCysCysThrValIleIleIleGluValProProProAlaGlu 360
QY      1081 GAGAGTGAGGAA 1092
DB      361 GluSerGluGlu 364

RESULT 9
US-10-979-159-232
; Sequence 232, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
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/ CURRENT FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US/09/918,715
/ PRIOR FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: 60/222,599
/ PRIOR FILING DATE: 2000-08-02
/ PRIOR APPLICATION NUMBER: 60/224,360
/ PRIOR FILING DATE: 2000-08-11
/ PRIOR APPLICATION NUMBER: 60/282,850
/ PRIOR FILING DATE: 2000-04-11
/ NUMBER OF SEQ ID NOS: 358
/ SOFTWARE: FASTSEQ for windows Version 3.0
/ SEQ ID NO 232
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-979-159-232

Alignment Scores:
Pred. No.: 3,24e-180 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.56% Indels: 0
DB: 5 Gaps: 0

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-979-159-232 (1-564)

QY 1 ATGGCCAGCGGAGGAGAGAGCCCTCGGATCGGCTTCAGGCGCTCTTTGGCCACT 60
DB 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
QY 61 CTGGCTCATCTGCGCCGCGGCAAGGGGAGCGAGGAGGATGGGGTCCAGCCTCTAC 120
DB 21 LeuValLeuIleCysAlaGlyGlnGlyArgArgGluAspGlyGlyProAlaCysTyr 40
QY 121 GCGGATTTGACCTGTGATCTTCAATTTGGACAATTCAGGAAGTGTGCTGCACCTGGAA 180
DB 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValIleuHisIstPasn 60
QY 181 GAAATCTATTACTTGTGGAGACGTTGGCTCAACAATTCATCGCCACGAGTTGAGAATG 240
DB 61 GlnIleTyrTrpPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
QY 241 TCCTTATTGTTTCTCCACCCGAGAACACCTTAATGAACCTGACAGAACAGAGAA 300
DB 81 SerPheIleValPheSerThrArgGlyThrThleuMetLysLeuThrGluAspArgGlu 100
QY 301 CAAATCGGTCAAGCCTCAGAAATCTCAGAAAGTTCTGCGAGAGAGACCTTAATG 360
DB 101 GlnIleArgGlnGlyLeuGlnGlnLeuGlnValLeuProGlyGlyAspThrTyrMet 120
QY 361 CATGAGGATTTGAAGGGCGCAGTGGAGCATTTATTGAAGAACAGACAGGCTACAG 420
DB 121 HisGlnGlyPheGlnArgAlaSerGlnGlnIleTyrTrpLysLeuArgGlnGlyTyrArg 140
QY 421 ACAGCAGCCTCATCTGCTTGAATGATGAGAACTCCATGAAGATCTTTTCTAT 480
DB 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGlnLeuPhePheTyr 160
QY 481 TCAGAGAGGAGCCTTAATGAGTCTCGAATCTTGGTGCATTTGTTACTGTGTGGTGG 540
DB 161 SerGlnArgGlnAlaAsnArgSerArgAspLeuGlyValIleValTyrCysValGlyVal 180
QY 541 AAGATTTTCAATGACACAGCTGGCCGAGATTGGCAGCATGAAGATCATGTGTTTCC 600
DB 181 LysAspPheAsnGlnTrpGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
QY 601 GTGAATGACGCGCTTTCAGGCTTCGAAAGCATCATCCATCTTGAAGAAGTCTCTG 660
DB 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
QY 661 ATCGAAATTTAGCAGCTGAACCATCCATATGTGCAGAGAGTCAATTCAAGTTGTC 720
DB 661 ATCGAAATTTAGCAGCTGAACCATCCATATGTGCAGAGAGTCAATTCAAGTTGTC 720
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DB 221 IlegIuIleLeuAlaIleGluProSerThrIleCysAlaGlyLysSerPheGlnValVal 240
QY 721 GTGAGAGGAAAGCGCTTCGACATGCGCCGACAGTGAACAGGGGCTCTGACGTTCAAG 780
DB 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
QY 781 ATCAATGACTCGGTACACTCAATGAGAACCCCTTTCTGTGGAAGACATTATTACTG 840
DB 261 IleAsnAspSerValThrLeuAsnGlnLysProPheSerValGluAspThrTyrLeuLeu 280
QY 841 TGTCCAGCGCCCTATCTTAAAGAACTTGGACATGAAGCTGCATCCAGTCAAGTGAAC 900
DB 281 CysProAlaProIleLeuLysGlnValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
QY 901 GATGCGCTCTCTTATCTTCAGTTCTGTGATCATCACCCACACACATGTTCTGACGCT 960
DB 301 AspGlyLeuSerPheIleSerSerValIleIleThrThrHisCysSerAspGly 320
QY 961 TCCATCTGGCCATGCGCTGCTGATCTGTCTGCTTCAGCCCTGAGCTCTCTCTGG 1020
DB 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340
QY 1021 TGGTTCGCGCCCTCTGCTGCTGACCTGTGATTAACAGAGGTCCCTCCACCCCTGCCAG 1080
DB 341 TrpPheTrpProLeuCysCysThrValIleIleLysGlnValProProProAlaGln 360
QY 1081 GAGGTGAGGAA 1092
DB 361 GluSerGlnGln 364
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RESULT 10

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US-11-047-278-6
/ Sequence 6, Application US/11047278
/ Publication No. US20050196407A1
GENERAL INFORMATION:
/ APPLICANT: Young, John A.T.
/ APPLICANT: Bradley, Kenneth A.
/ APPLICANT: Collier, Robert J.
/ APPLICANT: Mogridge, Jeremy S.
/ TITLE OF INVENTION: Anthrax Toxin Receptor
/ FILE REFERENCE: 960296, 97745
/ CURRENT APPLICATION NUMBER: US/11/047,278
/ PRIOR FILING DATE: 2005-01-31
/ PRIOR APPLICATION NUMBER: US/09/970,076
/ PRIOR FILING DATE: 2001-10-03
/ PRIOR APPLICATION NUMBER: 60/251,481
/ PRIOR FILING DATE: 2000-12-05
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-047-278-6
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Alignment Scores:
Pred. No.: 3,24e-180 Length: 564
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.56% Indels: 0
DB: 6 Gaps: 0
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US-09-970-076-1_COPY_104_1207 (1-1104) x US-11-047-278-6 (1-564)

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QY 1 ATGGCCAGCGGAGGAGAGAGCCCTCGGATCGGCTTCAGTGGCTCTTTGGCCACT 60
DB 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
QY 61 CTGGCTCATCTGCGCCGCGGCAAGGGGAGCGAGGAGGATGGGGTCCAGCCTCTAC 120
DB 21 LeuValLeuIleCysAlaGlyGlnGlyArgArgGluAspGlyGlyProAlaCysTyr 40
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QY 121 GGGGATTTGACCTGACTTCAATTTGGACAATTCAGAGAGTGGTGCACCACTGGAAT 180
DB 41 GYGLYPheAspLeuYrPheIleuAspLysSerGlySerValIleuHisStrpAsn 60
QY 181 GAATATCTATTACTTTGGAAAGTTGGCTCACAAATTCACGCCACAGTTGAGAAATG 240
DB 61 GluIleTyTrPheValGluGlnIleuAlaHisLysPheIleSerProGlnIleuArgMet 80
QY 241 TCCCTTAATGTTTTTCTCCACCCGAGAACTTAATGAATCTGACAGAAACAGAGA 300
DB 81 SerPheIleValPheSerThrArgGlyThrThreuMetLysLeuThrGluAspArgGlu 100
QY 301 CAATCCGTCAGAGCCCTAGAAAGATCCAGAAAGTTGTCAGAGAGACACTTCATG 360
DB 101 GlnIleArgGlnGlnLysGlnGlnLysValIleuProGlyGlyAspThrTyMet 120
QY 361 CATGAAGGATTTGAAAGGCGCAGTGAAGCAGATTTATTATGAAAAACAGACAGGTAAG 420
DB 121 HisGlnGlyPheGlnuArgAlaSerGlnGlnIleTyTrPheGluAsnArgGlnGlyTyArg 140
QY 421 ACAGCCAGCGCTCATCTGCTTGTGACTGATGAGAACTCCATGAAGATCTCTTTTCTAT 480
DB 141 ThrAlaSerValIleIleIleAlaLeuThrAspGlyGlnLeuHisGlnuAspLeuPhePheTy 160
QY 481 TCAGAGAGGAGGCTAATAGGCTCGAGATCTTGTCGCAATGTTTACCTGTTGGTGTG 540
DB 161 SerGlnuArgGlnuAlaAsnArgSerArgAspLeuGlyAlaIleValTyCysValGlyVal 180
QY 541 AAAGATTTCAATGAGACACAGCTGCGCCGAGATTCGAGACAGTAAGATCATGTGTTTCCC 600
DB 181 LysAspPheAsnGlnuThrGlnIleuAlaArgIleAlaAspSerLysAspHisValPhePro 200
QY 601 GTGAATGACGGCTTTCAGGCTCTGCAAGGCAATCATCACTCAATTTTGAAGAGTCTGC 660
DB 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleuLysLysSerCys 220
QY 661 ATGGAATTTAGAGAGTGAACCATTCACATATGTCAGAGAGTCAATTTCAAGTGTG 720
DB 221 IleGlnIleuAlaIleuAlaGlnuProSerThrIleCysAlaGlyGlnuSerPheGlnuVal 240
QY 721 GTGAGAGAAACGGCTTCCGACATGCCCGCAACGTGAGACAGGCTCTCTGACGTTTCAG 780
DB 241 ValArgGlyAsnGlnPheAlaArgHisValAspArgValIleuCysSerPheLys 260
QY 781 ATCAATGACTCGGTCACACTCAATGAGAAAGCTTTTCTGTGAAGA CACTTATTATCTG 840
DB 261 IleAsnAspSerValThrLeuAsnGlnuLysPheSerValGlnuAspThrTyLeuLeu 280
QY 841 TGTCCAGCGCTATCTTAAAAAGAGTTGGCATGAACCTGCATCCACAGCTCAGCATGAAC 900
DB 281 CysProAlaProIleLeuLysGlnuValGlyMetLysAlaAlaLeuGlnuValSerMetAsn 300
QY 901 GATGAGCTCTCTTATCTCAGTTCAGTTCATCATCACACACACACTGTTCTGACGCT 960
DB 301 AspGlyLeuSerPheIleSerSerValIleIleThrThrHisCysSerAspGly 320
QY 961 TCCATCTGGGCACTGCGCTGCTGATCTGTTCTGCTCTGAGCTGCTCTCTGCTG 1020
DB 321 SerIleuAlaIleAlaLeuLeuIleuPheLeuLeuAlaLeuAlaLeuLeuTrp 340
QY 1021 TGGTTCTGGGCGCTCTGCTGCTGATTCATTAAGAGGTCCTCCACCCCTGCGCGAG 1080
DB 341 TrpPheTrpProLeuCysCysThrValIleIleLysGlnuValProProProAlaGln 360
QY 1081 GAGAGTGAGAA 1092
DB 361 GluSerGlnuGln 364

RESULT 11
US-09-833-245-621
; Sequence 621, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Alkylman Fusion Proteins
; FILE REFERENCE: PFS46PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 621
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-621

Alignment Scores:

Pred. No.:	9,11e-180	Length:	403
Score:	1889.00	Matches:	363
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	94.31%	Indels:	0
DB:	3	Gaps:	0

US-09-970-076-1_COPY_104_1207 (1-1104) x US-09-833-245-621 (1-403)

QY 1 ATGCCACGCGGAGGCGAGAGCGCTCGGATCGGCTTCAGTGCCTCTTTGGCCACT 60
DB 1 MetAlaThrAlaGlnuArgAlaLeuGlyIleGlyPheGlnuTrpLeuSerIleuAlaThr 20
QY 61 CTGGTCTCATCTGCGCCGCGGCAAGGGGACGAGAGGAGATGGGGCTCCAGCTTCTAC 120
DB 21 LeuValLeuIleCysAlaGlyGlnGlnGlyArgArgGlnuAspGlyGlyProAlaCysTy 40
QY 121 GGGGATTTGACCTGACTTCAATTTGGACAATTCAGAGAGTGGTGCACCACTGGAAT 180
DB 41 GYGLYPheAspLeuYrPheIleuAspLysSerGlySerValIleuHisStrpAsn 60
QY 181 GAATATCTATTACTTTGGAAAGTTGGCTCACAAATTCACGCCACAGTTGAGAAATG 240
DB 61 GluIleTyTrPheValGluGlnIleuAlaHisLysPheIleSerProGlnIleuArgMet 80
QY 241 TCCCTTAATGTTTTTCTCCACCCGAGAACTTAATGAATCTGACAGAAACAGAGA 300
DB 81 SerPheIleValPheSerThrArgGlyThrThreuMetLysLeuThrGluAspArgGlu 100
QY 301 CAATCCGTCAGAGCCCTAGAAAGATCCAGAAAGTTGTCAGAGAGACACTTCATG 360
DB 101 GlnIleArgGlnGlnLysGlnGlnLysValIleuProGlyGlyAspThrTyMet 120
QY 361 CATGAAGGATTTGAAAGGCGCAGTGAAGCAGATTTATTATGAAAAACAGACAGGTAAG 420
DB 121 HisGlnGlyPheGlnuArgAlaSerGlnGlnIleTyTrPheGluAsnArgGlnGlyTyArg 140
QY 421 ACAGCCAGCGCTCATCTGCTTGTGACTGATGAGAACTCCATGAAGATCTCTTTTCTAT 480
DB 141 ThrAlaSerValIleIleIleAlaLeuThrAspGlyGlnuMetLysLeuThrGluAspArgGlu 160
QY 481 TCAGAGAGGAGGCTAATAGGCTCGAGATCTTGTCGCAATGTTTACCTGTTGGTGTG 540
DB 161 SerGlnuArgGlnuAlaAsnArgSerArgAspLeuGlyAlaIleValTyCysValGlyVal 180
QY 541 AAAGATTTCAATGAGACACAGCTGCGCCGAGATTCGAGACAGTAAGATCATGTGTTTCCC 600
DB 181 LysAspPheAsnGlnuThrGlnIleuAlaArgIleAlaAspSerLysAspHisValPhePro 200
QY 601 GTGAATGACGGCTTTCAGGCTCTGCAAGGCAATCATCACTCAATTTTGAAGAGTCTGC 660
DB 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleuLysLysSerCys 220

QY 661 ATCGAAATCTACAGCTGAACCATTCACCATATGTGCAGAGAGTTCATTTCAGTTGTC 720
Db 221 IIEGLUIIELEUAIAlaIaGIuPProSerThrIleCYAlaGIYGIuSerPheGlnValVal 240
QY 721 GTGAGAGAAACGGCTTCCGACATGCGCCGCAACGTGGACAGGGTCTCTGACGTTCAAG 780
Db 241 ValArgGIYAsnGIYPhaArgHISAlaArgAsnValAspArgValLeuCYsSerPheLys 260
QY 781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGGAAGACATTATTACTG 840
Db 261 IIEAsnAspSerValThrLeuAsnGIuLysPProPheSerValGIuAspThrIYrLeuLeu 280
QY 841 TGTCCAGCCCTATCTTAAAGAAAGTTGGATGAAGCTGACCTCAGGTCAAGTGAAC 900
Db 281 CysProAlaProIleLeuLysGIuValGIYMeLysAlaIleuGlnValSerMetAsn 300
QY 901 GATGGCTCTCTTTATCTTCAGATTCTGCATATACCCACACACTGTTTGAACGT 960
Db 301 AspGIYLeuSerPheIleSerSerValIleIleThrThrThrIscYsSerAspGIY 320
QY 961 TCCATCTGGACATGCGCCCTGTGATCTGTTCTGCTGCTGACCCCTGCTCTGCG 1020
Db 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340
QY 1021 TGGTTCTGCGCCCTGTGCTGCTGACATGTGATTATCAGAGAGTCCCTCCACCCCTGCGAG 1080
Db 341 TrpPheTrpProLeuCYsCysThrValIleIleIleLysGIuValPProPProAlaGIu 360
QY 1081 GAGAGTGAG 1089
Db 361 GIuSerGIu 363

RESULT 12

US-09-833-245-620
Sequence 620, Application US/09833245
Publication No. US2004010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PPS46PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 620
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (175)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (320)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (331)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (368)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-620

Alignment Scores:

Pred. No.: 7,29e-178 Length: 403
Score: 1870.00 Matches: 360
Percent Similarity: 99.17% Conservative: 0

Beet Local Similarity: 99.17% Mismatches: 3
Query Match: 93.36% Indels: 0
DB: 3 Gaps: 0
US-09-970-076-1_copy_104_1207 (1-1104) x US-09-833-245-620 (1-403)

QY 1 ATGGCCAGCGCGGAGCGGAGAGCCCTCGCATCGCTTCAGTGCCTCTTTGGCCACT 60
Db 1 MetAlaThrAlaGIuArgAlaLeuGIYIleGIYPheGlnTrPLeuSerLeuAlaThr 20
QY 61 CTGGTCTCATCTGGCCCGGCGGAAGGGGACCCAGGAGGAGGGGGTCCACCTGCTAC 120
Db 21 LeuValIleuIleCYAlaGIYInGIYArgArgGIuAspGIYGIYProAlaCysIYr 40
QY 121 GCGGATTTGACCTTACTTCTTATTTGCAAAATCAGAAAGTGTCTGACCACTGGAAT 180
Db 41 GIYGIYPheAspLeuTrIYrPheIleLeuAspLysSerGIYSerValLeuHISHisTrpAsn 60
QY 181 GAAATCTATTACTTTGTGGAACAGTTGGCTCAAAATTCATCAGCCCACTTGAGATG 240
Db 61 GIuIleYrYrPheValGIuGlnLeuAlaHISLysPheIleSerProGlnLeuArgMet 80
QY 241 TCCCTTATGTTTCTTCCACCCGAGAGCAACCTTAATGAAATCAGACGAGAGAG 300
Db 81 SerPheIleValPheSerThrArgGIYThrTrIleuMetLysLeuThrGIuAspArgGIu 100
QY 301 CAATCCGTCAGAGCCTAGAGAACTCCAGAAAGTTGTGCGAGAGAGACACTTACATG 360
Db 101 GlnIleArgGlnGIYLeuGlnGIuLeuGlnLysValIleuProGIYGIYAspThrIYrMet 120
QY 361 CATGAAGATTGAAAGGCGCAGTAGACAGATTATATGAAACAGACAGAGGTACAG 420
Db 121 HISGIuGIYPhaGIuArgAlaSerGIuGlnIleYrYrGIuAsnArgGlnGIYArg 140
QY 421 AAGCCAGGCTCATATGCTTGTGAATGAGAACTCCAGAAAGATCTCTTTTCTAT 480
Db 141 ThrAlaSerValIleIleAlaLeuThrAspGIYGIuLeuHISGIuAspLeuPhePheYr 160
QY 481 TCAGAGAGGAGGCTAATGATGCTCGAGATCTTGATGTCATTTACTGTGTGGTGTG 540
Db 161 SerGIuArgGIuAlaAsnArgSerArgAspLeuGIYAlaIle***YrCysValGIYVal 180
QY 541 AAAGATTTCAATGAGACACAGCTGCGCCGATGCGGACAGTGAAGATCATGTGTTCCC 600
Db 181 LysAspPheAsnGIuThrGIuLeuAlaArgIleAlaAspSerLysAspIleValPhePro 200
QY 601 GTGAATGACGGCTTTCAGGCTCTGCAAGGACATCACTCAATTTTGAAGAGCTCTGC 660
Db 201 ValAsnAspGIYPhaGlnAlaLeuGlnGIYIleIleHISerIleLeuLysLysSerCys 220
QY 661 ATCGAAATCTAGACGTGAACCATTCACCATATGTGCAGAGAGTTCATTTCAGTTGTC 720
Db 221 IIEGLUIIELEUAIAlaIaGIuPProSerThrIleCYAlaGIYGIuSerPheGlnValVal 240
QY 721 GTGAGAGAAACGGCTTCCGACATGCGCCGCAACGTGGACAGGGTCTCTGACGTTCAAG 780
Db 241 ValArgGIYAsnGIYPhaArgHISAlaArgAsnValAspArgValLeuCYsSerPheLys 260
QY 781 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGGAAGACATTATTACTG 840
Db 261 IIEAsnAspSerValThrLeuAsnGIuLysPProPheSerValGIuAspThrIYrLeuLeu 280
QY 841 TGTCCAGCCCTATCTTAAAGAAAGTTGGATGAAGCTGACCTCAGGTCAAGTGAAC 900
Db 281 CysProAlaProIleLeuLysGIuValGIYMeLysAlaIleuGlnValSerMetAsn 300
QY 901 GATGGCTCTCTTTATCTTCAGATTCTGCATATACCCACACACTGTTTGAACGT 960
Db 301 AspGIYLeuSerPheIleSerSerValIleIleThrThrThrIscYsSerAsp*** 320
QY 961 TCCATCTGGACATGCGCCCTGTGATCTGTTCTGCTGCTGACCCCTGCTCTGCG 1020
Db 321 SerIleLeuAlaIleAlaLeuLeuIleLeu***LeuLeuLeuAlaLeuAlaLeuLeuTrp 340

Percent Similarity: 97.75% Conservative: 6
Best Local Similarity: 96.07% Mismatches: 8
Query Match: 89.52% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-1_COPY_104_1207 (1-1104) x US-09-918-715-301 (1-562)

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25 CTCGGATCGGCTTCAGATGCTCTCTTTGGCCACTGTGGTCTCATCTGCGCGGCGAA 84
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db LeuGlnValaGlyLeuKArgGlyLeuCyValAlaAlaLeuValLeuValCysAlaGlyHis 26

85 GGGGGAGCGAGGAGGATGGGGGCTCAAGCTCTACGGCGGATTTGAACCTGATTCATT 144
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db G1yG1yArgArgG1yLeuArgG1yProAlaCysTyG1yG1yPheAspLeuTyrrPheIle 46

145 TTGGCAAAATTCAGGAAGTGCTGCGACCACTGGAAAGAAATCATTAATCTTTGGGAACG 204
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db LeuAspLysSerIySerValLeuHisHisIrrPAspGlnIleTyrrPheValG1yGln 66

205 TTGGCTCACAATTCATCAGCCCAAGTTGAGATGCTCTTATGTTTCTCCACCGA 264
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db LeuAlaHisArgPheIleSerProGlnLeuArgMetSerPheIleValPheSerThrArg 86

265 GGAACAACCTTAAATGAACTGACAGAGACAGAAACAAATCCGTCAAGGCTTAGAAGA 324
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db G1yThrThrLeuMetLysLeuThrG1yAspArgG1yGlnIleArgG1yGlnG1yLeuG1yGln 106

325 CTCGCAAAAGTTTGGCAGAGAGAGACACTTACATCAGAAAGATTTGAAAGGGCGAGT 384
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db LeuGlnLysValLeuProG1yG1yAspThrTyrrMetHisIleGlnIyPheG1yLeuArgAlaSer 126

385 GAGCAGATTATATGAAAAACAGACAGGAGTACAGGACCGCTCATTCATTCCTTGG 444
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db G1yGlnIleIleTyrrG1yLeuAsnSerGlnG1yTyrrArgThrAlaSerValIleIleAlaLeu 146

445 ACTGATGAGAACTCCATGAAAGATCTCTTTTCTTATTCAGAGAGGAGCTTAATAGGCTCT 504
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db ThrAspG1yG1yLeuHisIleG1yAspLeuPhePheTySerG1yArgG1yLeuAlaAsnArgSer 166

505 CGAGATCTTGGTGATCTTGTTCATCTGTTGGTGAGTGAAGATTTCAATGAGACAGCGTG 564
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db ArgAspLeuG1yAlaIleValIyrrCyValG1yValLysAspPheAsnGlnThrGlnLeu 186

565 GCCCGATTCGCGACAGTAAAGATCATGTGTTCCCGTGAATGACGGCTTTCAGGCTCTG 624
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db AlaArgIleAlaAspSerLysAspHisValPheProValAsnAspG1yPheGlnAlaLeu 206

625 CAAGCATCATCCATCAATTTTGAAGAACTCTGCATGCAAAATTCAGACGCTGAACCA 684
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db G1yGlnIyIleIleHisSerIleLeuLysLysSerCyAlleGlnIleLeuAlaIleGlnPro 226

685 TCCACATATGTCAGAGAGTGATTTCAAGTGTGTGAGAGAAACGGCTTCCGACAT 744
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db SerThrIleCyValaG1yG1yLeuSerPheGlnValValValArgG1yAsnG1yPheAspHis 246

745 GCCCGACAGCTGAGACAGGCTCTCTGCAGCTTCAAGATCATGATCCGCTCACTCAAT 804
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db AlaArgAsnValAspArgValLeuCySerPheLysIleHisAspSerValIleThrLeuAsn 266

805 GAGAACCCCTTTCTGTGAAAGCACTTATTACTGTGTCAGCGCTATCTTAAAGAA 864
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db G1yLysProPheAlaValG1yAspThrTyrrLeuLeuCySerProAlaIleLeuLysGln 286

865 GTTGGATGAAGATCGATCCAGCTGAGATGAAGATGAGCGCTCTTTTATTCACAGT 924
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db ValG1yMetLysAlaAlaLeuGlnValSerMetAsnAspG1yLeuSerPheIleSerSer 306

925 TCTGTATCATCAACCAACACACTGTTTGAAGGTTTCACTCTGGCCATCGCCCTGTG 984
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db SerValIleIleThrThrThrHisCysSerAspG1ySerIleLeuAlaIleAlaLeuLeu 326

985 ATCTGTCTCTGCTCTAGCCCTGAGCTCTCTGTGAGTTCGGCCCTCTGCTGCACT 1044
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
```

```
Db 327 ValLeuPheLeuLeuLeuAlaLeuAlaLeuLeuTyrrPheThrProLeuCySerThr 346
Qy 1045 GTGATTATCAAGAGATCCCTCCACCCCTGCGGAGAGATGAGAA 1092
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 347 ValIleIleLysGlnValProProProProProValG1yGlnSerG1yGln 362
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RESULT 15

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US-10-474-794-194
; Sequence 194, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carlson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194
; LENGTH: 562
; TYPE: PRF
; ORGANISM: Mus musculus
US-10-474-794-194
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Alignment Scores:

Pred. No.:	4,24e-170	Length:	562
Score:	1793.00	Matches:	342
Percent Similarity:	97.75%	Conservative:	6
Best Local Similarity:	96.07%	Mismatches:	8
Query Match:	89.52%	Indels:	0
DB:	4	Gaps:	0

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-474-794-194 (1-562)

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25 CTCGGATCGGCTTCAGATGCTCTCTTTGGCCACTGTGGTCTCATCTGCGCGGCGAA 84
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db LeuGlnValaGlyLeuKArgGlyLeuCyValAlaAlaLeuValLeuValCysAlaGlyHis 26

85 GGGGGAGCGAGGAGGATGGGGGCTCAAGCTCTACGGCGGATTTGAACCTGATTCATT 144
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db G1yG1yArgArgG1yLeuArgG1yProAlaCysTyrrG1yG1yPheAspLeuTyrrPheIle 46

145 TTGGCAAAATTCAGGAAGTGCTGCGACCACTGGAAAGAAATCATTAATCTTTGGGAACG 204
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db LeuAspLysSerG1ySerValLeuHisHisIrrPAspGlnIleTyrrPheValG1yGln 66

205 TTGGCTCACAATTCATCAGCCCAAGTTGAGAAATGCTTATTAATGTTTCTTCACCGCA 264
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db LeuAlaHisArgPheIleSerProGlnLeuArgMetSerPheIleValPheSerThrArg 86

265 GGAACAACCTTATGAATGAACTGACAGAGACAGAAACAAATCCGTCAAGGCTTAGAAGA 324
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db G1yThrThrLeuMetLysLeuThrG1yAspArgG1yGlnIleArgG1yGlnG1yLeuG1yGln 106

325 CTCGCAAAAGTTTGGCAGAGAGAGACACTTACATGATGAAGATTTGAAAGGGCGAGT 384
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db LeuGlnLysValLeuProG1yG1yAspThrTyrrMetHisIleGlnIyPheG1yLeuArgAlaSer 126

385 GAGCAGATTATATGAAAAACAGACAGGAGTACAGGACCGCAAGGCTCATTCATTCCTTGG 444
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db G1yGlnIleIleTyrrG1yLeuAsnSerGlnG1yTyrrArgThrAlaSerValIleIleAlaLeu 146

445 ACTGATGAGAACTCCATGAAAGATCTCTTTCTTATTCAGAGAGGAGCTAATAGGCTCT 504
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db ThrAspG1yG1yLeuHisIleG1yAspLeuPhePheTySerG1yArgG1yLeuAlaAsnArgSer 166
```



```
QY 505 CGAGATCTGTGTCATTTGTTTACTGTGTGTGTGAAGATTTCATGAGACAGACTG 564
    |||||
Db 167 ArgAspLeuGlyAlaIleValIyrCyValGlyValIysAspPheAsnGluThrGlnLeu 186
    |||||
QY 565 GCCCGGATTGCGGACAGTAAAGATCATGTGTTTCCCGTGAATGACGGCTTTCAGGCTCTG 624
    |||||
Db 187 AlaArgIleIleIleAspSerIyAspPheIleValPheProValAsnAspGlyPheGlnAlaLeu 206
    |||||
QY 625 CAAGGCATCATCCATCAATTGGAAGAAGTCCGTGCATCGAATTCGAAGTCTGAACCA 684
    |||||
Db 207 GlnGlyIleIleIleIleSerIleLeuIyIySerCyIleGlnIleLeuAlaIleGluPro 226
    |||||
QY 685 TCACCATATGTGACGAGAGATCATTTCAAGTTGTGTGAGAGAAACGGCTTCCGACAT 744
    |||||
Db 227 SerThrIleCyAlaGlyIySerPheGlnValValArgGlyAsnGlyPheArgHis 246
    |||||
QY 745 GCCCGCAACGTGACAGAGGTCTCTGCAGCTTCAAGATCAATGACTCGATCAGCTCAAT 804
    |||||
Db 247 AlaArgAsnValAspArgValIleuCySerPheIySerIleAsnAspSerValThrLeuAsn 266
    |||||
QY 805 GAGAAAGCCCTTTCTGTGTGAAGACATTATTACTGTGTCCAGCGCTATCTTAAAGAA 864
    |||||
Db 267 GluIySerProPheAlaValGluAspThrTyrlleuIySerProIleLeuIyGlu 286
    |||||
QY 865 GTTGGCATGAAGCTGACTCCAGGTGACATGAAGATGGCTCTTTATCTCCAGT 924
    |||||
Db 287 ValGlyMetIyAspAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIleSerSer 306
    |||||
QY 925 TCTGTCAATCAACACCAACACACTGTTCTGACCGGTTCCATCTGACCATCGCCCTGCTG 984
    |||||
Db 307 SerValIleIleIleThrThrThrHisCySerAspGlySerIleLeuAlaIleAlaLeuLeu 326
    |||||
QY 985 ATCTGTCTCTGCTCTAGCCCTGGCTCTCTCTGTGTGTCTGTGCCCCCTCTGTGCTGACT 1044
    |||||
Db 327 ValIleuPheLeuLeuAlaLeuAlaLeuAlaLeuIleuTrpPheTrpProLeuCySerThr 346
    |||||
QY 1045 GTGATTATCAAGAGAGTCCCTCCACCCCTGCGCAGAGAGAGTGAAGAA 1092
    |||||
Db 347 ValIleIleIyGlnValProProProValGlnGluSerGluGln 362
    |||||
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Search completed: December 14, 2005, 12:55:03
Job time : 176.732 secs

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QY 448 GATGGAACCTCATGAAGATCTTTTCTATTACAG-----AGGAGGCTAAADAG 501
    |||||
DB 258 AapGlyGluYserPheGlyAspProLeuGlyTyrGluAspValIleProGluIleAspArg 277
    |||||
QY 502 TCTCGAGATCTTGTCGAATTTGTTTACTGTGTGTGTGTAAGATTTCAATGAGACAG 561
    |||||
DB 278 Glu-----GlyValIleArgTyrValIleGlyValGlyAspAlaPheArgSerGlu 294
    |||||
QY 562 CTGGCCCGG-----ATTGCGGACAGT-----AAGATCATGTGTTTCCC 600
    |||||
DB 295 LysSerArgGlnGlnLeuLeuAsnThrIleAlaSerLysProProArgAspHisValPheGln 314
    |||||
QY 601 GTGAATGACGGCTTTCAGCTTCGCAAGGATCATCATTCATTTTGAAGAAGTCTGCG 660
    |||||
DB 315 ValAsnAsn---PheGluAlaLeuLysThrIleGlnAsnGlnLeuArgGlu----- 331
    |||||
QY 661 ATCGAATTTCTACAGATGTAACCATCATGTCAGAGAGATCATTTCAAGTTGTC 720
    |||||
DB 332 -----IlePheAlaIleGlnGlyThrGlnThrGlySerSerSerPheGlnHisGlu 349
    |||||
QY 721 GTGAGAGAAACGGCTTCCGACATGCC 747
    |||||
DB 350 MetSerGlnGlnGlyPheSerAlaAla 358
    |||||
RESULT 3
US-11-186-284-26
; Sequence 26, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangl
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: BURGART, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MEMO1-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 3063
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-26
Alignment Scores:
Pred. No.: 2,94e-05 Length: 3063
Score: 134.50 Matches: 81
Percent Similarity: 43.10% Conservative: 44
Best Local Similarity: 27.93% Mismatches: 123
Query Match: 6.71% Indels: 42
DB: 7 Gaps: 17
US-09-970-076-1_COPY_104_1207 (1-1104) x US-11-186-284-26 (1-3063)
QY 130 GACCTGACTTCATTTTGACCAATCGAGAGTGTG---CTGACACATCGAATGAATC 186
    |||||
DB 440 AspIleValPheLeuValAspGlySerTyrSerIleGlyIleAlaAsnPheValIleVal 459
    |||||
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```
QY 187 TATTACTTTGGAAACATGGCTCAAAATTC---ATCAGCCCA---CAGTTGAAATG 240
    |||||
DB 460 ArgAlaPheLeuGlnValIleuValIleValIleValIleValIleValIleValIleVal 479
    |||||
QY 241 TCTTTTATTTGTTTCTTCACCC-----CGAGAACAACTTAAATGAATGACAGAA 291
    |||||
DB 480 SerLeuValIleGlnTyrSerArgAspProHisThrGlnPheThrLeuLysPheThrLys 499
    |||||
QY 292 GACAGGAACAAATCCGTCAAGGCTTGAAGAACTCCAGAAAGTTGTGCA-----GG 345
    |||||
DB 500 ValGluAspIleIle-----GluAlaIleAsnThrPheProTyrArgGly 514
    |||||
QY 346 GGAGACACTTACATGATGATGAAGATTTGAAGGCGCAGTGAAGATTTATTAATGAAC 405
    |||||
DB 515 GlySerThrAsnThrGlyLysAlaMetThrTyrValArgGlnLysIlePheValProSer 534
    |||||
QY 406 AGACAGGGTACAGACA-----GCCACGTCATCATTTGCTTGACTGATGAGAACTC 459
    |||||
DB 535 Lys---GlySerArgSerAsnValProLysValMetIleLeuIleThrAspGlyLys--- 552
    |||||
QY 460 CATGAAGATCTCTTTTCTATTACAGAGAGGAGGCTAATAGCTCTGAGATCTTGTCGA 519
    |||||
DB 553 SerSerAspAlaPhe-----ArgAspProAlaIleLysLeuArgAsnSerAspVal 569
    |||||
QY 520 ATGTTTACTGTGTGTGTAAGATTTCAATGACACAGCTGCGCCGATTTGCGGAC 579
    |||||
DB 570 GluIlePheAlaValGlyValIleAspAlaValArgSerGlnLeuGlnAlaIleAlaSer 589
    |||||
QY 580 -----AGTAAGCATCATGTGTTCCGTAATGACGGCTTTCAGGCTTGCAGAGCATC 633
    |||||
DB 590 ProProAlaGlnThrHisValPheThrValGluAsp---PheAspAlaPheGlnArgIle 608
    |||||
QY 634 ATCCACTCAATTTTGAAGAGTCCGTCATCGAAATCTGACAGCTTCAACATCCACCAT 693
    |||||
DB 609 SerPheGlnLeuThrIleSerIleCysLeuArgIle-----GluGlnGluLeuAla 625
    |||||
QY 694 TGTGACAGAGATCATTTCAAGTTGTCGTGAGAGAAACGGCTCCGACATGCCCGCAC 753
    |||||
DB 626 AlaIleLysLysValAlaTyrValProProLysAspLeuSerPheSerGluValThrSer 645
    |||||
QY 754 GTGACAGAGGCTCTGACAGCTTCAAGATCATGACTCGTCACTCAATGAGAACCC 813
    |||||
DB 646 Tyr-----GlyPheLysThrAsnTrpSer---ProAlaGlyGluAsnVal 659
    |||||
QY 814 TTTTCTGTGGAAGACATTTTACTGTGTGTCAGCCGCTTAATAAGAAAGTTGGCATG 873
    |||||
DB 660 PheSerTyrHisIleThrTyr-----LysGluAlaIleGly 671
    |||||
QY 874 AAGCTGACCTCGAGGTCAGATGATGATGATGCTCTTTTATCTCCAGTTCTGCATC 933
    |||||
DB 672 AspAspGluValThrVal---ValGluPro-AlaSerSerThrSerValIleuSerSe 690
    |||||
QY 934 ATCACCAACACACATGTTCTGACGGTT 961
    |||||
DB 690 IleuLysProGluThrLeuTyrIleuVal 699
    |||||
RESULT 4
US-11-057-047-2
; Sequence 2, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holzer, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Raube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilkeson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057,047
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
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/ PRIOR APPLICATION NUMBER: 60/636,239
/ PRIOR FILING DATE: 2004-12-14
/ PRIOR APPLICATION NUMBER: US04/015040
/ PRIOR FILING DATE: 2004-05-13
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 2
/ LENGTH: 739
/ TYPE: PR
/ ORGANISM: Homo sapiens
US-11-057-047-2

Alignment Scores:
Pred. No.: 0.00208 Length: 739
Score: 113.50 Matches: 66
Percent Similarity: 38.28% Conservative: 63
Best Local Similarity: 19.58% Mismatches: 109
Query Match: 5.67% Indels: 99
DB: Gaps: 17

US-09-970-076-1_COPY_104_1207 (1-1104) x US-11-057-047-2 (1-739)

QY 82 CAAAGGCGACGCGAGGAGTGGG---GGTCCAGCC----- 114
   |||
   |||
   |||
Db 218 GIUGLYVALAEPALAGLUNBPGLYHISGLYPROGLYGLUGLGLNLYSARGLYSILEVAL 237
   |||
   |||
   |||
QY 115 -----TGTACGGCGGATTTGACCTGTAATCTTATTTGACAAATCAGGAAGTG--- 165
   |||
   |||
   |||
Db 238 LEUAPPROSERGLYSETHETANILETYRLEUVALLEUAPGLYSETHETILEGLY 257
   |||
   |||
   |||
QY 166 -----CTGCACCACTGGAATGAAATCTATTACTTTGTGACAGTGGCTCAC 213
   |||
   |||
   |||
Db 258 ALASERASNPHERTHRGLYALALYSYSCYLEUVALASNLEULLEGLULYSVALALASER 277
   |||
   |||
   |||
QY 214 AATTATCATGCCACAGTTGAGAAATGCTTATTGTTTCTCCACCCGAGGAACACC 273
   |||
   |||
   |||
Db 278 TYRGLYVALYLEPRO-----ARGTYRGLYLEUVALTHRYLATHRYRPROLYSILE 295
   |||
   |||
   |||
QY 274 TTAATGAACTGACAGAA-----GACAGAAACAATCCGTCAAGGCTAGAA 321
   |||
   |||
   |||
Db 296 TPVALLYVALSERGLULALAPSERSETHANALASPTRYVALTHRYSGINLEUAN 315
   |||
   |||
   |||
QY 322 GAATC-----CAGAAAGTTCTGCCAGAGGACGACCTATGACATGAGAA 369
   |||
   |||
   |||
Db 316 GIULIASNTYRGLUNBPHISLYLEULYSERGLYTHASNHR----- 330
   |||
   |||
   |||
QY 370 TTGAAAGGCGCGATGACAGATTATTTATAAACA----- 408
   |||
   |||
   |||
Db 331 ---LYELYSALALEUQINLALVALTYRSETHETMETSETRPROASBPVALPROPRO 349
   |||
   |||
   |||
QY 409 CAAGGTAC---AGGACAGCGACGTCATGCTTATGCTTGAAGTGA----- 453
   |||
   |||
   |||
Db 350 GIUGLYTRPASNARGTHARGHISVALILEILEUWETHTRASPGLYSETHETISANMET 369
   |||
   |||
   |||
QY 454 -----GAATCCATGACAGATCTCTTTTCTATTCAGAG 486
   |||
   |||
   |||
Db 370 GLYGLYASBPROLLERTHVALILEASPGIULILEARGSPLEUENURYRILEGLYLSAP 389
   |||
   |||
   |||
QY 487 AGGAGCGCTAATAGTCTCGAGATCTTGTGCAATTGTTACTGTGTGT-----GTG 540
   |||
   |||
   |||
Db 390 ARGLYASNPROARGLUNBPGTYRLEUASBPVALTYRVALPHEGLYVALGLYPROLEUVAL 409
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   |||
   |||
QY 541 AAGGATTTCAATGACACACAGCTGGCCGATTTGCCGACGTAAAGTCACTGTGTTCC 600
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   |||
Db 410 AENGLIVALASNTLEASNALALEUALASERLYLYSPASNSGILUGLNIHISVALIPHELYS 429
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   |||
QY 601 GTGATGACGGCTTTTACGCTTGCAGAGCATCATCATCAATTTTGAAGAAGTCTCG 660
   |||
   |||
   |||
Db 430 VALLYASBP---METGLUNLENLEULASBPVALPHECYRGLNMETILEASPGIUSER--- 447
   |||
   |||
   |||
QY 661 ATCGAAATTTAGACAGCTGAACCATTCACCATATGTGCGAGAGATTCATTTCAAGTTTC 720
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   |||
Db 448 -----GINSETRLEUSERLEUCY----- 453
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QY 721 GTGAGAGAAACGGCTTCGACATGCCGCAACGTGACAGGGCTCTTGACAGTTCAAG 780
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   |||
Db 454 -----GLYMETVALTRPGLNHBARGLYSGLYTHRAP----- 464
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   |||
   |||
QY 781 ATCAATGACTCGGTCAACTCAATGAGAAAGCCCTTTCTGTGGAAGACATTATTACTG 840
   |||
   |||
   |||
Db 465 -----TYRHSISYSGINPROTRPGINLALALYSILESERVAL----- 476
   |||
   |||
   |||
QY 841 TGTCCAGGCGCTATCTTAAAGAAAGTTGSCATGAAGCTGACATCCAGGTACGATGAC 900
   |||
   |||
   |||
Db 477 -----ILEARGPROSERLYSGLYHSIGLUSERCYMETELY----- 488
   |||
   |||
   |||
QY 901 GATGCGCTCTCTTTATCTCCAGTTCTGTATCATCATCACACCACTGT 951
   |||
   |||
   |||
Db 489 -----ALAVVALSERGLUNRYRHEVALLEUTHRALALAHIECY 502
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   |||
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RESULT 5
US-11-057-047-1
/ Sequence 1, Application US/11057047
/ Publication No. US20050260198A1
/ GENERAL INFORMATION:
/ APPLICANT: HOLLERS, Vernon
/ APPLICANT: THURMAN, Joshua
/ APPLICANT: TAUBE, Christian
/ APPLICANT: GELFAND, Erwin
/ APPLICANT: GILKESON, Gary
/ TITLE OF INVENTION: Inhibition of Factor B. The Alternative Complement Pathway and
/ FILE REFERENCE: 2848-66
/ CURRENT APPLICATION NUMBER: US/11/057,047
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,594
/ PRIOR FILING DATE: 2004-02-10
/ PRIOR APPLICATION NUMBER: 60/636,239
/ PRIOR FILING DATE: 2004-12-14
/ PRIOR APPLICATION NUMBER: US04/015040
/ PRIOR FILING DATE: 2004-05-13
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1
/ LENGTH: 764
/ TYPE: PR
/ ORGANISM: Homo sapiens
US-11-057-047-1

Alignment Scores:
Pred. No.: 0.0021 Length: 764
Score: 113.50 Matches: 66
Percent Similarity: 38.28% Conservative: 63
Best Local Similarity: 19.58% Mismatches: 109
Query Match: 5.67% Indels: 99
DB: Gaps: 17

US-09-970-076-1_COPY_104_1207 (1-1104) x US-11-057-047-1 (1-764)

QY 82 CAAAGGCGACGCGAGGAGTGGG---GGTCCAGCC----- 114
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   |||
Db 243 GIUGLYVALAEPALAGLUNBPGLYHISGLYPROGLYGLUGLGLNLYSARGLYSILEVAL 262
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   |||
   |||
QY 115 -----TGTACGGCGGATTTGACCTGTAATCTTATTTGACAAATCAGGAAGTG--- 165
   |||
   |||
   |||
Db 263 LEUAPPROSERGLYSETHETANILETYRLEUVALLEUAPGLYSETHETILEGLY 282
   |||
   |||
   |||
QY 166 -----CTGCACCACTGGAATGAAATCTATTACTTTGTGGAACAGTTGGCTCAC 213
   |||
   |||
   |||
Db 283 ALASERASNPHERTHRGLYALALYSYSCYLEUVALASNLEULLEGLULYSVALALASER 302
   |||
   |||
   |||
QY 214 AATTATCATGCCACAGTTGAGAAATGCTTATTGTTTCTCCACCCGAGGAACACC 273
   |||
   |||
   |||
Db 303 TYRGLYVALYLEPRO-----ARGTYRGLYLEUVALTHRYLATHRYRPROLYSILE 320
   |||
   |||
   |||
QY 274 TTAATGAACTGACAGAA-----GACAGAGAAACAATCCGTCAAGGCTAGAA 321
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Db      536 -----IlaGrProserlySGLYHslGlsSerCywmcgly----- 546
OY      901 GATGGCCCTCTCTTTATCTCCAGTTTCATCATATACCAACCACACTGT 951
Db      548 -----AlavAlvalSerGIurYPheValLeuThrAlaAlaHisCys 561

RESULT 7
US-10-131-826A-294
; Sequence 294, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P333ORIC128
; CURRENT APPLICATION NUMBER: US/10/131, 826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 294
; LENGTH: 915
; TYPE: prt
; ORGANISM: Homo Sapien
US-10-131-826A-294

Alignment Scores:
Pred. No.:          0.00221           Length:          915
Score:              113.50            Matches:          55
Percent Similarity: 43.90%             Conservative:     53
Best Local Similarity: 22.36%           Mismatches:       103
Query Match:        5.67%              Indels:          35
DB:                  6                 Gaps:           13

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-131-826A-294 (1-915)
OY      130 GACCGTACTTTCATTGTGCACAATATGAGAAGTG---CTGACACACTGGAAATGAATC 186
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Db      57 AspleuValPheIleIleAspSerSerArgSerValAsnThrHisArgTrAlaIysVal 76
QY      187 TATTACTT---GTTGAACAGTGTGGCTCACAATTCATCATGCCCCACAGTTG--AGAAATG 240
Db      77 LysGIuPheIleValAspIleLeuGlnPheLeuAspIleGlyProAspValThrArgVal 96
QY      241 TCCTTTATGTTGTTTCCACCCGGAACACCTTA-----ATGAACATG 285
Db      97 GlyLeuLeuGlnItyr-----GlySerThrValLysAsnGluPheSerLeuIysThr 113
QY      286 ACAGAGAAGACAGAAACAATCCGTCAGAGGCTTAGAAGATCCAGAAAGTTCTGCAGGA 345
Db      114 PheLysArgLysSerGluValGluArgAlaValLysArgMetArgHisIleuSerThrGly 133
QY      346 GGAGACACTTACATGCATGAAGAGATTGAAAGGCCACGTGAGCAGCATTTATTATGAAAC 405
Db      134 ThrMetThrGlyLeuAlaIleGlnItyr-----AlaLeuAsnIleAlaPheSerGlu 150
QY      406 AGACAAGAGTTCACAGG-----ACAGCCAGGCTCATCATTCGTTGATCGAT 450
Db      151 AlaGluGlyAlaArgProLeuArgGluAsnValProArgValIleMetIleValThrAsp 170
QY      451 GGAGAACTCCATGAAGATCTCTTTTCTATTTCAGAGAGGAGGCTTAATAGTCTCGAGAT 510
Db      171 GlyArgProGlnAspSerVal-----AlaGluValAlaIleLysAlaArgAsp 186
QY      511 CTGTGTCGAATGTTTACTGTGTGTGTG-----AAAGATTCAATGACACACAGCTG 564
Db      187 ThrGlyIleLeuIlePheAlaIleGlyAlaGlyAlaValAspPheAsnThrLeuIysSer 206
QY      565 GCCCGGATGGGGACAGTAGAGATCATGTGTTCCCGTAATGACGGCTTTACAGGCTGTG 624
Db      207 IleGlySerGluProHisGluAspHisValPheLeuValAlaAsn--PheSerGlnIle 225
QY      625 CAAGGCATCATCTCACTCAATTTTGAAGAGTCCGTCATCGAATTTTACAGCTGAACCA 684
Db      226 GluThrIleLeuThrSerValPheGlnIlyLysIleuCybThrAlaHisMetCybSerThrLeu 245
QY      685 TTCACCATATGTGCAGAGAGAGTCAATTTCAAGTTGTCGTAGAGAAACGGCTTCCGACAT 744
Db      246 GluHisAsnCybAla-----HisPheCybIleAsnIleProGlySerTyValCybArg 263
QY      745 GCCCGC-----AACGTGACAGAGGCTCTCTGCAGCTTCAAGATCATATGAC 789
Db      264 CybLysGlnGlyTyrIleLeuAsnSerArgGlnThrCys----ArgIleGlnAsp 281
QY      790 TCGTCACATCATATGAG 807
Db      282 LeuCybAlaMetGluAsp 287

RESULT 8
US-11-113-424-39
; Sequence 39, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangoli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113, 424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256, 704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311, 590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257, 314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311, 613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315, 617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307, 506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322, 358

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; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 956
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-39

Alignment Scores:
Pred. No.: 0.00224 Length: 956
Score: 113.50 Matches: 55
Percent Similarity: 43.90% Conservative: 53
Best Local Similarity: 22.36% Mismatches: 103
Query Match: 5.67% Indels: 35
DB: Gaps: 13

US-09-970-076-1_COPY_104_1207 (1-1104) x US-11-113-424-39 (1-956)
QY 130 GACCTGACTTCTTGGACAATCCGAAAGTGTG---CTGCACATGGAATGATC 186
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 57 AspleuValphelelleleapserSerArgSerValamnthrhlsaptryAlaVal 76
QY 187 TATTACTT---GTGAACAGTTGGCTCACAATTCAGCCCAAGTTG---AGAATG 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 77 LyeglunheilleValaplelleleuglnPheleuaplellyProapervalThArgVal 96
QY 241 TCCTTATTGTTTCTCCACCCGAGAACCACTTA-----ATCAAACTG 285
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 97 GlyleuLeuGlnTy-----GlySerThrValysangluPheSerLeuLySerThr 113
QY 286 ACAGAACAGACAGAACAAATCCGTCAGGCTAGAGAACCTCAGAAAGTTCTCCAGCA 345
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 114 PheleYarglyserSerGluValargAlaValysArgMetArgHsleuSerThcily 133
QY 346 GGAACACTTACATGATGATGAAGATTGAAAGGCCAGTGACAGATTATTAATAAAC 405
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 134 ThwerthrGlyleuAlaileGlnTy-----AlaLeuamilleAlaPheSerGlu 150
QY 406 AGACAGAGGATACAG-----ACAGCCAGCGTCATCATTTGCTTGATCAT 450
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 151 AlagluValylaaArgProleuArgGluamValProArgValIleMetIleValThrAsp 170
QY 451 GGAGAACTCCATGAAGATCTCTTTTCTATTCCAGAGAGGAGGCTAAATAGGTCGAGAT 510
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 171 GlyArgProGluamSerVal-----AlaGluValAlaAlaValysAlaArgAsp 186
QY 511 CTGTGCAATTTGTTACTGTGTGTGTG-----AAAGATTTCATGAGACACAGCTG 564
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 187 ThcGlylleuLeuIlePheAlaIleGlyValGlyGlnValaPhePheamnthrhleuYser 206
QY 565 GCCCGGATGGCGACAGTACATGATGATGTTTCCCGTGAATGACGGCTTTCAGGCTCTG 624
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 207 IleGlySerGluProHsGluAspHleValPheleuValAlaasn---PheSerGlnIle 225
QY 625 CAAGGACCTCATCACTCAATTTGAGAAAGCTCGTCAATTCGAAATTCAGACATGAACA 684
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 226 GluThrleuThrSerValPheGlnlylsPheucyThrAlaHsMetCysSerThleu 245
QY 685 TCACCATATGTGACAGAGACTTTCATGTTGCTGTGAGAGAAACGGCTTCCGACAT 744
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 246 GluHlsanCysAla-----HlsPheCysAlleamIleProGlySerTyValCysArg 263
QY 745 GCCCGC-----AACGTGACAGGGCTCTGACAGCTTCAGATCAATGAC 789
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 264 CysleuValnglyTyIleleuamSerAspGlnThrCys-----ArgIleGlnAsp 281
QY 790 TCGGTCACTCATGATGAG 807
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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DB 282 LeuCyAlaMetGluAsp 287

RESULT 9
US-10-601-368-24
; Sequence 24, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT FILING DATE: 2003-06-23
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 1141
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-601-368-24

Alignment Scores:
Pred. No.: 0.0041 Length: 1141
Score: 111.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 5.54% Indels: 38
DB: Gaps: 9

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-601-368-24 (1-1141)
QY 115 TGCTAGCGCGGATTTGACCTGTACTTCTTGGACAATCAGAAAGTGTGTCGACAC 174
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 159 CysGlnThrTyThrMetAspIleValIleValleuAspIlySeramSerIle---TyPro 177
QY 175 TGAATGAATCTATTACTTGTGGAACAGTTGGCTCACAATTC---ATCAGCCCA--- 228
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 178 TrpValGluValGlnHsPheleuIleamIleleuYlsYsPheTyIleGlyProGly 197
QY 229 CAGTTGAGATGTCCTTATTGTTTCTCCACCCGAGAACCAACTTAATGAATGACA 288
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 198 GlnIleGlnValGlyIleValGlnTyGlyGluAspAlaValHsGluPheHsleu--- 216
QY 289 GAAGACAGAGAACAAATCCGTCAGGCTGAGAACTCCAGAAAGTTCTGCCAGAGCA 348
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 217 AsnAspTyArgSerVallylsAspValValGluAlaHsSerHsIleGluGlnArgGly 236
QY 349 GACACTTACATGATGACAGATTGAA-----AGGCCAGTGACAGATTATAT 399
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 237 GlyThrGluThrArgThrAlaPheGlyIleGluPheAlaArgSerGluAlaPheGlnlys 256
QY 400 GAAACAGACAGAGGTCACAGACAGCGGTATCTTCTTGAATGAGAGACTC 459
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 257 GlyGlyArglySerGlyAlaLys-----LysValMetIleValIleThrAspGlyUser 274
QY 460 CATGAAGAT----- 468
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 275 HlsAspSerProAspLeuGluValIleArgGlnSerGluYlsAspAsnValThrArg 294
QY 469 -----CTCTTTTCTATCAGAGAGGAGGCTTAATAGCTTCGAGATCTT 513
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 295 TyAlaValAlaValleuGlyTyTyAsnArgArgGlyIleAsnProGluThrPheleu 314
QY 514 GGTCCATTTGTTTACTGTGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 561
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 315 AsnGluIleYsTyIleAlaSerAspProAspAspIlyHsIlePhePheamValThrAsp 334
QY 562 CTGCGCCGAGTTGGCAGACAGTAAAGATCATGTGTTTCCGTGAATGACGGCTTTCAGGCT 621
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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OY	469 -----	CTCTTTTCTATTGACAGGGAGGTATAGTCTTCAGATCTT	513
Dd	295 TylAlaValAlaValLeuGllyrTyTrAsnArgArglglYleAenProGlutThPhleu		314
OY	514 GGTGCATTTGTTACTGTGTGGTGGAAGAT-----	TTCATGACACACAG	561
Dd	315 AenGlutlleYerTyrlleAlaSerAspProAspIyShIShpheAenValThrAsp		334
OY	562 CTGGCCCCGAGTTGGCGACAGCAAGAATCATGTCTTCCCGTAATGACGGCTTCAGGCT	621	
Dd	335 GluAlaAlaLeu-----LysAspIleValAspAlaLeuGlYAspArgIllepser		351
OY	622 CTCGACAGC	630	
Dd	352 LeuGlucly	354	
 RESULT 12 US-11-057-047-6 Sequence 6, Application US/11057047 Publication NO. US20050260198A1 GENERAL INFORMATION: APPLICANT: Holerb, Vernon APPLICANT: Thurman, Joshua APPLICANT: Taube, Christian APPLICANT: Gelfand, Erwin APPLICANT: Gilkeson, Gary TITLE OR INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and FILE OF INVENTION: Methods Related Thereto CURRENT APPLICATION NUMBER: US/11/057,047 CURRENT FILING DATE: 2005-02-10 PRIORITY FILING DATE: 2004-02-10 PRIOR FILING DATE: 2004-02-10 PRIOR FILING DATE: 2004-12-14 PRIOR APPLICATION NUMBER: 60/636,239 PRIOR FILING DATE: 2004-05-13 PRIOR APPLICATION NUMBER: US04/015040 NUMBER OF SEQ ID NOS: 6 SOFTWARE: Patentin version 3.3 SEQ ID NO 6 LENGTH: 761 TYPE: PRT ORGANISM: Mus musculus US-11-057-047-6			
 Alignment Scores:			
Pred. No.:	0.00408	Length:	761
Score:	110.50	Matches:	71
Percent Similarity:	37.57%	Conservative:	59
Best Local Similarity:	20.52%	Mismatches:	99
Query Match:	5.52%	Indels:	117
DB:	7	Gaps:	20
 US-09-970-076-1_COPY_104_1207 (1-1104) x US-11-057-047-6 (1-761)			
OY	82 CAAGGGAGCGAGGAGATGGG-----		105
Dd	240 GluGlYAlaAspAlaGluAspIyHISerProGlYglnGlnLysArgLyelleVal		259
OY	106 ---GGTCCAGCTGTCTACGCCGAGATTGACCTGTACTTCAATTTGGACAAATCAGAGT		162
Dd	260 LeuAspProser-----GlySerMetAsnIleTyrlleuValLeuAspGlYSerAspser		277
OY	163 GTG-----	CTGCACACTGGAATGAATCTAT	189
Dd	278 IleglySerSerAsnPheThrclYAlaLysArgCySleuThrAsn-----		292
OY	190 TACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCACAGATTGAGATGCTTTATT		249
Dd	293 ---LeuIleGlYlulYValAlaIseryrclYValaIaPro-----ArgTyrclyleuLeu		309
OY	250 GTTTTCTCCACCAGGAGCAACTTAAATGAACCTGACAGACAGAG-----		297

[illegible]

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/ LENGTH: 1141
/ TYPE: PRF
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: (1)...(22)
US-10-601-368-6

Alignment Scores:
Pred. No.: 0 00996 Length: 1141
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 5.34% Indels: 38
DB: 6 Gaps: 9

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-601-368-6 (1-1141)
QY 115 TGTACGGCGGATTTGACCTGATCTTATTTGGACAATTCAGGAAGTGTGTCGACAC 174
Db 159 CysGlnThrTyrMetAspIleValIleValIleuAspGlySerAsnSerIle---TyrPro 177
QY 175 TGGAAATGAATCTATTACTTGTGGAAACAGTTGCTCAAAATTC---ATCAGCCCA--- 228
Db 178 TTPVALGluValGlnHisPheLeuIleAsnIleLeuLysPheTyrIleGlyProGly 197
QY 229 CAGTTGAGATGTCCTTTATGTTTCTCCACCCGAGGAACAACCTTAATGAACCTGACA 288
Db 198 GlnIleGlnValGlyValGlnTyrGlyGlnAspValValHisGluPheHisLeu--- 216
QY 289 GAAGACAGAGAACAAATCCGTCAGGCTTAGAAGAACTCCAGAAAGTGTGCGACAGGA 348
Db 217 AsnAspTyrArgSerValLysAspValValGluAlaIleAsnHisIleGlnIleAspGly 236
QY 349 GACACTTACATCATGATGAAGATTGAA-----AGGCCAGTGACAGATTATTAT 399
Db 237 GlyThrGluThrArgThrAlaPheGlyIleGluPheAlaArgSerGluAlaPheGlnLys 256
QY 400 GAAACAGACAAAGGTCACAGACAGACGCGTCATCTTGACTGATGAGAACCTC 459
Db 257 GlyGlyArgLysGlyAlaLys-----LysValMetIleValIleThrAspGlyGlnSer 274
QY 460 CATGAAGAT-----CTCTTTCTATTCAGAGAGGAGCTTAATAGTCTCGAGATCTT 513
Db 275 HisAspSerProAspLeuGlnLysValIleGlnGlnSerGluArgAspAsnValThrArg 294
QY 469 -----CTCTTTCTATTCAGAGAGGAGCTTAATAGTCTCGAGATCTT 513
Db 295 TyrAlaValAlaValLeuGlyTyrTyrAsnArgArgGlyIleAsnProGluThrPheLeu 314
QY 514 GGTGCAATTGTTACTGTGTGGTGTGAAGAT-----TTCAATGAGACACAG 561
Db 315 AenGluIleLysTyrIleAlaSerAspProAspAspLysHisPhePheAsnValThrAsp 334
QY 562 CTGGCCCGGATTCGGACAGTAAGATCATGTCTTCCGTGAATGACGGCTTCAGGCT 621
Db 335 GluAlaAlaLeu-----LysAspIleValAlaPheAlaLeuGlyAspArgIlePheSer 351
QY 622 CTGCAAGGC 630
Db 352 LeuGluGly 354

RESULT 14
US-10-601-368-4
/ Sequence 4, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
```

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/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FASTSEQ for Windows Version 3.0
/ SEQ ID NO 4
/ LENGTH: 1166
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-601-368-4

Alignment Scores:
Pred. No.: 0.01 Length: 1166
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 5.34% Indels: 38
DB: 6 Gaps: 9

US-09-970-076-1_COPY_104_1207 (1-1104) x US-10-601-368-4 (1-1166)
QY 115 TGTACGGCGGATTTGACCTGATCTTATTTGGACAATTCAGGAAGTGTGTCGACAC 174
Db 137 CysGlnThrTyrMetAspIleValIleValIleuAspGlySerAsnSerIle---TyrPro 155
QY 175 TGGAAATGAATCTATTACTTGTGGAAACAGTTGCTCAAAATTC---ATCAGCCCA--- 228
Db 156 TTPVALGluValGlnHisPheLeuIleAsnIleLeuLysPheTyrIleGlyProGly 175
QY 229 CAGTTGAGATGTCCTTTATGTTTCTCCACCCGAGGAACAACCTTAATGAACCTGACA 288
Db 176 GlnIleGlnValGlyValGlnTyrGlyGlnAspValValHisGluPheHisLeu--- 194
QY 289 GAAGACAGAGAACAAATCCGTCAGGCTTAGAAGAACTCCAGAAAGTGTGCGACAGGA 348
Db 195 AsnAspTyrArgSerValLysAspValValGluAlaIleAsnHisIleGlnIleAspGly 214
QY 349 GACACTTACATCATGATGAAGATTGAA-----AGGCCAGTGACAGATTATTAT 399
Db 215 GlyThrGluThrArgThrAlaPheGlyIleGluPheAlaArgSerGluAlaPheGlnLys 234
QY 400 GAAACAGACAAAGGTCACAGACAGACGCGTCATCTTGACTGATGAGAACCTC 459
Db 235 GlyGlyArgLysGlyAlaLys-----LysValMetIleValIleThrAspGlyGlnSer 252
QY 460 CATGAAGAT-----CTCTTTCTATTCAGAGAGGAGCTTAATAGTCTCGAGATCTT 513
Db 253 HisAspSerProAspLeuGlnLysValIleGlnGlnSerGluArgAspAsnValThrArg 272
QY 469 -----CTCTTTCTATTCAGAGAGGAGCTTAATAGTCTCGAGATCTT 513
Db 273 TyrAlaValAlaValLeuGlyTyrTyrAsnArgArgGlyIleAsnProGluThrPheLeu 292
QY 514 GGTGCAATTGTTACTGTGTGGTGTGAAGAT-----TTCAATGAGACACAG 561
Db 293 AenGluIleLysTyrIleAlaSerAspProAspAspLysHisPhePheAsnValThrAsp 312
QY 562 CTGGCCCGGATTCGGACAGTAAGATCATGTCTTCCGTGAATGACGGCTTCAGGCT 621
Db 313 GluAlaAlaLeu-----LysAspIleValAlaPheAlaLeuGlyAspArgIlePheSer 329
QY 622 CTGCAAGGC 630
Db 330 LeuGluGly 332

RESULT 15
US-10-601-368-3
/ Sequence 3, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
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1  TITLE OR INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
2
3  FILE REFERENCE: 07334-275001
4
5  CURRENT APPLICATION NUMBER: US/10/601,368
6
7  CURRENT FILING DATE: 2003-06-23
8
9  PRIOR APPLICATION NUMBER: US/09/561,263A
10
11 PRIOR FILING DATE: 2000-04-27
12
13 PRIOR APPLICATION NUMBER: US 09/322,790
14
15 PRIOR FILING DATE: 1999-05-28
16
17 NUMBER OF SEQ ID NOS: 40
18
19 SOFTWARE: FastSeq for Windows Version 3.0
20
21 SEQ ID NO 3
22
23     LENGTH: 1188
24
25     TYPE: PRT
26
27 ORGANISM: Homo sapiens
28
29 FEATURE:
30
31     NAME/KEY: SIGNAL
32
33     LOCATION: (1)...(22)
34
35     US-10-601-368-3

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Alignment Scores:	
Pred. No.:	1168
Score:	107.00
Percent Similarity:	37.93%
Best Local Similarity:	24.14%
Query Match:	5.34%
DB:	6
	9

US-09-970-076-1_COPY_104_1207 (1-1104) X US-10-601-368-3 (1-1188)

QY 115 TCGTACGGCGGAGATTTCACCTGTACTTCATTCTTTGGACAAATCCAGGAATGTCGTGCACAC 174
Db 159 CysgIntHrThyrmecaspIleValIleValLeuaspGlySeraspSerile---TyrPro 177
QY 175 TCGAATGAATCATTAATCTTGTGGGAACAGTTGGCTGCACAAATTC---ATCAGCCCA 228
Db 178 TTPValGIValGIghIshPheLeuIleashIleuLysPheTherIleGIProGly 197
QY 229 CAGTTGAGAATGCTCTTAATGTGTTTCTCCACCCGAGGAACAACCTTAATGAACCTGACA 288
Db 198 GlnIleGIhValGIValValGIhGlnTyrGIhGlyaspValValhIleGIhPhehIleu--- 216
QY 289 GAAAGCAGAGAACAAATCCGTCAGGCGTGAAGGCTGAGGAACCTCCAGAAAGTTGCCAGAGAGA 348
Db 217 AsnAspTyrArgSerValLysAspValValGIhValIleAspIshIleGIhGlnArgGly 236
QY 349 GACACTTACATGATGATGAAGATTGAA-----AGGCCAGTGACAGATTATAT 399
Db 237 GIYThrGIuThrArgThrAlaPheGIhIleGIuPhehIArgSerGIuAlaPheGIhLys 256
QY 400 GAAACAGACAAAGGTAACAGAGAACAGCCAGGCTCATCTTGCCTGTGACTGTAGAGAACTC 458
Db 257 GIyGIhArgLysPheGIhValLys-----LysValMetIleValIleThrAspGIhGlySer 274
QY 460 CATGAAGAT----- 468
Db 275 HisAspSerProAspLeuGIhLysValIleGIhGlnSerGIuArgAspAsnValThrArg 294
QY 469 -----CTCTTTTCTATTCAGAGAGAGAGCTTAATAGCTCCGATCTT 513
Db 295 TyrAlaValAlaValIleuGIhTyrTyrAsnArgArgGIhLysAspProGIuThrPheLeu 314
QY 514 GCGCAATGCTTAACTGTGTGGTGCAGAAAT-----TTCATAGAGACACAG 566
Db 315 AsnGIhIleLysTyrIleAlaSerAspProAspAspLysHisPhePheAsnValThrAsp 334
QY 562 CTGGCCCGGATCCCGGACAGTAAGATCATGTGTTTCCCGTAATGAAGCGCTTCAAGCT 621
Db 335 GluAlaIleLeu-----LysAspIleValAspAlaLeuGIhAspArgIlePheSer 351
QY 622 CTCGAAGGC 630
Db 352 LeuGIhGly 354

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GenCore version 5.1.6
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OM proteoin - protein search, using sw model

Run on: December 14, 2005, 11:02:37 ; Search time 33.1664 Seconds
(without alignments)
916.781 Million cell updates/sec

Title: US-09-970-076-2

Perfect score: 1914

Sequence: 1 MATERRALGIGFQWLSLAT.....VIKVEPPPESEENKIK 368

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/prodata/1/1aa/5 COMB.pep: *
2: /cgn2_6/prodata/1/1aa/6 COMB.pep: *
3: /cgn2_6/prodata/1/1aa/H_COMB.pep: *
4: /cgn2_6/prodata/1/1aa/PCITUS_COMB.pep: *
5: /cgn2_6/prodata/1/1aa/RE_COMB.pep: *
6: /cgn2_6/prodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	962.5	50.3	488	2	US-10-104-047-2639
2	166	8.7	1155	1	US-08-286-889-46
3	166	8.7	1155	1	US-08-485-618-46
4	166	8.7	1155	1	US-08-362-652-46
5	166	8.7	1155	1	US-08-605-672-46
6	166	8.7	1155	1	US-08-482-293A-46
7	166	8.7	1155	1	US-08-943-363-46
8	166	8.7	1155	2	US-09-193-043-46
9	166	8.7	1155	2	US-09-688-107A-46
10	166	8.7	1155	2	US-03-350-259-46
11	166	8.7	1161	1	US-08-485-618-53
12	166	8.7	1161	1	US-08-362-652-53
13	166	8.7	1161	1	US-08-605-672-53
14	166	8.7	1161	1	US-08-482-293A-53
15	166	8.7	1161	1	US-08-943-363-53
16	166	8.7	1161	2	US-09-193-043-53
17	166	8.7	1161	2	US-09-688-107A-53
18	166	8.7	1161	2	US-03-350-259-53
19	159.5	8.3	1151	1	US-08-286-889-37
20	159.5	8.3	1151	1	US-08-485-618-37
21	159.5	8.3	1151	1	US-08-362-652-37
22	159.5	8.3	1151	1	US-08-605-672-37
23	159.5	8.3	1151	1	US-08-482-293A-37
24	159.5	8.3	1151	1	US-08-943-363-37
25	159.5	8.3	1151	2	US-09-193-043-37
26	159.5	8.3	1151	2	US-09-688-107A-37
27	159.5	8.3	1151	2	US-09-350-259-37

28	159.5	8.3	1161	1	US-08-173-497-2	Sequence 2, Appl
29	159.5	8.3	1161	1	US-08-286-889-2	Sequence 2, Appl
30	159.5	8.3	1161	1	US-08-485-618-2	Sequence 2, Appl
31	159.5	8.3	1161	1	US-08-485-618-55	Sequence 55, Appl
32	159.5	8.3	1161	1	US-08-485-618-99	Sequence 99, Appl
33	159.5	8.3	1161	1	US-08-362-652-2	Sequence 2, Appl
34	159.5	8.3	1161	1	US-08-362-652-55	Sequence 55, Appl
35	159.5	8.3	1161	1	US-08-605-672-2	Sequence 2, Appl
36	159.5	8.3	1161	1	US-08-605-672-55	Sequence 55, Appl
37	159.5	8.3	1161	1	US-08-605-672-99	Sequence 99, Appl
38	159.5	8.3	1161	1	US-08-482-293A-2	Sequence 2, Appl
39	159.5	8.3	1161	1	US-08-482-293A-55	Sequence 55, Appl
40	159.5	8.3	1161	1	US-08-482-293A-99	Sequence 99, Appl
41	159.5	8.3	1161	1	US-08-943-363-2	Sequence 2, Appl
42	159.5	8.3	1161	1	US-08-943-363-55	Sequence 55, Appl
43	159.5	8.3	1161	1	US-08-943-363-99	Sequence 99, Appl
44	159.5	8.3	1161	2	US-09-193-043-2	Sequence 2, Appl
45	159.5	8.3	1161	2	US-09-193-043-55	Sequence 55, Appl

ALIGNMENTS

RESULT 1									
US-10-104-047-2639									
Sequence 2639, Application US/10104047									
Patent No. 6943241									
GENERAL INFORMATION:									
APPLICANT: HELIX RESEARCH INSTITUTE									
TITLE OF INVENTION: NO. 6943241el full length cDNA									
FILE REFERENCE: H1-A0105									
CURRENT APPLICATION NUMBER: US/10/104,047									
CURRENT FILING DATE: 2002-03-25									
PRIOR APPLICATION NUMBER:									
PRIOR FILING DATE:									
NUMBER OF SEQ ID NOS: 4096									
SOFTWARE: PatentIn Ver. 2.1									
BEO ID NO 2639									
LENGTH: 488									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-10-104-047-2639									
Query Match									
Best Local Similarity 50.3%; Score 962.5; DB 2; Length 488;									
Matches 190; Conservative 63; Mismatches 106; Indels 7; Gaps 3;									
QY	4	AERRALGIGFQWLSLATLVLCAGCGG-RREDGPACYGGFDLYFTIDKSGVYHHNNEI	62						
DB	3	AERSPARSPGSMWLPGLWMLVLSGPGGLRAQGPSCRAFDLYFVLDSGVSANMWIEL	62						
QY	63	YRVVEQLAKKEIPQRLMSFTVSTRTGTMKLTEDBEQRLQGLVLPBGDTYME	122						
DB	63	YRVVEQLAKKEIPQRLMSFTVSTRTGTMKLTEDBEQRLQGLVLPBGDTYME	122						
QY	123	GPERARQIYVEMKRGVTRVIALTDGELHDLFFYSERBRANRSRDGAIYVCGVKD	182						
DB	123	GPERARQIYVEMKRGVTRVIALTDGELHDLFFYSERBRANRSRDGAIYVCGVKD	182						
QY	183	FNETQLARLIDSDHVPVNDGFQALQGIHSLIKKSCIEILABPSTICAGSPQVVR	242						
DB	183	FNETQLARLIDSDHVPVNDGFQALQGIHSLIKKSCIEILABPSTICAGSPQVVR	242						
QY	243	GNGPRHARNDVLYCEFKINDSVTLAEKPSVEDTYLCPAPLIXEVMKAAALQVSMNDG	302						
DB	243	GNGPRHARNDVLYCEFKINDSVTLAEKPSVEDTYLCPAPLIXEVMKAAALQVSMNDG	302						
QY	244	GRGFMLGSRNGSVLCTYVMEITYTSVKPVSVDLNSMLCPAPLIXAGETLIDVSVFENG	300						
DB	244	GRGFMLGSRNGSVLCTYVMEITYTSVKPVSVDLNSMLCPAPLIXAGETLIDVSVFENG	300						
QY	303	LSRTSSVITTTTCHSGDGLATATLILFLLALMLMFWPCLCTVIIXEVPVPPA---	359						
DB	303	LSRTSSVITTTTCHSGDGLATATLILFLLALMLMFWPCLCTVIIXEVPVPPA---	359						
QY	301	KSVISGSLVYATBCSNGIAITVILVLLGLGLMMWPLCCKVVIVDPPPPAPAP	360						
DB	301	KSVISGSLVYATBCSNGIAITVILVLLGLGLMMWPLCCKVVIVDPPPPAPAP	360						
QY	360	-EESSE 364							
DB	360	-EESSE 364							

DB 361 KEEEEE 366

RESULT 2

US-08-286-889-46

Sequence 46, Application US/08286889

Patent No. 5470953

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Mich

TITLE OF INVENTION: No. 54709361 Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive, 6300 Sear Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286,889

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: P38,659

REFERENCE/DOCKET NUMBER: 27866/32168

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 1155 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-286-889-46

Query Match

Best Local Similarity 8.7%; Score 166; DB 1; Length 1155;

Best Local Similarity 28.2%; Pred. No. 1.1e-08;

Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GPDLVFILDKSGSV-LHNMNFIYFVEQLAHKFIISPOLRMSFIVFSTRTGLMK 94

DB 144 PCPCPGEMDIAPFLIDSGSISDSDFTQMKDFVYALMGQLASTSTSFSLMOYSNLIKTHFT 203

QY 95 LTEDR-----EOIRGLELEQLKVLPGDPTVMEHGFERRASEQIYENRQGYRTA-SVITAI 148

DB 204 FTEFSSLSPOSIVDAIVOLQ-----GLTYTASGIQKVKELFHSKNGARKSAKILIVY 258

QY 149 TDGELHEDLFFYSE--REANRSRDIGAIYVCVVD-FNE-TQLARI-----ADSKDHYF 199

DB 259 TDGQFRPDLERHVIPEAKA---GITRYALGVDAFREPALDELNTIGSAPSDHYF 315

QY 200 PVNDGFOALQGIHSLKSKSCIEILAEPTICAGSFQVVRNGNFRHARVD 253

DB 316 KVGN-FVALRSIORQIOEK-----IFALIGTSRSSSFQHEMSQGFSSALSM 364

RESULT 3

US-08-485-618-46

Sequence 46, Application US/08485618

Patent No. 5728533

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Van der Vieren, Monica

TITLE OF INVENTION: No. 572853361 Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive, 6300 Sear Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,618

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/32797

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 1155 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-485-618-46

Query Match

Best Local Similarity 8.7%; Score 166; DB 1; Length 1155;

Best Local Similarity 28.2%; Pred. No. 1.1e-08;

Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GPDLVFILDKSGSV-LHNMNFIYFVEQLAHKFIISPOLRMSFIVFSTRTGLMK 94

DB 144 PCPCPGEMDIAPFLIDSGSISDSDFTQMKDFVYALMGQLASTSTSFSLMOYSNLIKTHFT 203

QY 95 LTEDR-----EOIRGLELEQLKVLPGDPTVMEHGFERRASEQIYENRQGYRTA-SVITAI 148

DB 204 FTEFSSLSPOSIVDAIVOLQ-----GLTYTASGIQKVKELFHSKNGARKSAKILIVY 258

QY 149 TDGELHEDLFFYSE--REANRSRDIGAIYVCVVD-FNE-TQLARI-----ADSKDHYF 199

DB 259 TDGQFRPDLERHVIPEAKA---GITRYALGVDAFREPALDELNTIGSAPSDHYF 315

QY 200 PVNDGFOALQGIHSLKSKSCIEILAEPTICAGSFQVVRNGNFRHARVD 253

DB 316 KVGN-FVALRSIORQIOEK-----IFALIGTSRSSSFQHEMSQGFSSALSM 364

RESULT 4

US-08-362-652-46

Sequence 46, Application US/08362652

Patent No. 5766850

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Van der Vieren, Monica

TITLE OF INVENTION: No. 5766850e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-46

Query Match 8.7%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 1.1e-08;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
QY 37 PACYG-GFDLYFLIDSGSV-LHHMNEIYFVEQLAHKFIISPOLRMSFIYSTRGTTLMK 94
DB 144 PECPGQEMDIAPFLIDSGSIDQSDFTQMDPVKALMGQLASTSTSFIMQYSNLKTHFT 203
QY 95 LTEDR-----EQIRGLIELQKVLPGGDTYMHGFEFASQIYENRGYRTA-SVITIAL 148
DB 204 FTEFKSSLSPQSLVDALVQLQ-----GLFTYASGIQKVVELFHSKNGARKSAKKILIVI 258
QY 149 TDGELHEDLFFYSE--REANRSRDGAIVYCVGKVD-FNE-TOLARI-----ADSKDHF 199
DB 259 TDQCKRPDPLEYHVIVPEAKA---GIRVAIGVDAFREPTLQELNLTGSAFSDQHF 315
QY 200 PVNDGFOALOGIHSILKKSCEILAAPEPTICAGSFQVAVVNGFRHARNVD 253
DB 316 KVGN-FVALRSIQROIQEK----IFAIEGTESRSSSFQHEMSQEGFSSALSMD 364

RESULT 5
US-08-605-672-46
Sequence 46, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
CITY: Chicago
STATE: Illinois
STREET: 233 South Wacker Drive, 6300 Seear Tower

CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-46

Query Match 8.7%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 1.1e-08;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
QY 37 PACYG-GFDLYFLIDSGSV-LHHMNEIYFVEQLAHKFIISPOLRMSFIYSTRGTTLMK 94
DB 144 PECPGQEMDIAPFLIDSGSIDQSDFTQMDPVKALMGQLASTSTSFIMQYSNLKTHFT 203
QY 95 LTEDR-----EQIRGLIELQKVLPGGDTYMHGFEFASQIYENRGYRTA-SVITIAL 148
DB 204 FTEFKSSLSPQSLVDALVQLQ-----GLFTYASGIQKVVELFHSKNGARKSAKKILIVI 258
QY 149 TDGELHEDLFFYSE--REANRSRDGAIVYCVGKVD-FNE-TOLARI-----ADSKDHF 199
DB 259 TDQCKRPDPLEYHVIVPEAKA---GIRVAIGVDAFREPTLQELNLTGSAFSDQHF 315
QY 200 PVNDGFOALOGIHSILKKSCEILAAPEPTICAGSFQVAVVNGFRHARNVD 253
DB 316 KVGN-FVALRSIQROIQEK----IFAIEGTESRSSSFQHEMSQEGFSSALSMD 364

RESULT 6
US-08-482-293A-46
Sequence 46, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
CITY: Chicago
STATE: Illinois

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/
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/482,293A
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 46:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1155 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
US-08-482-293A-46

Query Match      8.7%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 1.1e-08;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GFDLYFLDKSGSV-LHNMNEYFVEQLAHKFIQPLMSFVFGSTGTYLTK 94
DB 144 PECFQEMDIAPFLIDSSGSDIDSDFTQMDPVALMGQLASTGSTPSLMQYNIKTHT 203
QY 95 LTEDR-----EQIRGLSELOKVLPGDPTVMHEGFERASEQIYENRQGYTA-SVIAL 148
DB 204 FTEFKSLSPQSLVDALVOLQ-----GLTYTASGIQVKVKELFHSKNGARKSAKKILIYI 258
QY 149 TDGELHEDLFFYSE--REANRSRDGAIVYCVGYKD-FNE-TQLARI-----ADSKDHYF 199
DB 259 TDGQKFRDPLEYRHVIPAERKA--GIRYALGVDAFREPTALQELNTIGSAPSDHYF 315
QY 200 PVNDGQALOGIHSILKSCIEILAAEPSTICAGSFQVVRGNGFRHARVD 253
DB 316 KYGN-FVALRSIORIOERK---IFAIGTESRSSSFQHEMSQEGFSSALSMD 364

RESULT 7
US-08-943-363-46
/ Sequence 46, Application US/08943363
/ Patent No. 5837478
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 114
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Seagr Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
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/ COMPUTER READABLE FORM:
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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
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/ APPLICATION NUMBER: US/08/943,363
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 46:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1155 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
US-08-943-363-46

Query Match      8.7%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 1.1e-08;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GFDLYFLDKSGSV-LHNMNEYFVEQLAHKFIQPLMSFVFGSTGTYLTK 94
DB 144 PECFQEMDIAPFLIDSSGSDIDSDFTQMDPVALMGQLASTGSTPSLMQYNIKTHT 203
QY 95 LTEDR-----EQIRGLSELOKVLPGDPTVMHEGFERASEQIYENRQGYTA-SVIAL 148
DB 204 FTEFKSLSPQSLVDALVOLQ-----GLTYTASGIQVKVKELFHSKNGARKSAKKILIYI 258
QY 149 TDGELHEDLFFYSE--REANRSRDGAIVYCVGYKD-FNE-TQLARI-----ADSKDHYF 199
DB 259 TDGQKFRDPLEYRHVIPAERKA--GIRYALGVDAFREPTALQELNTIGSAPSDHYF 315
QY 200 PVNDGQALOGIHSILKSCIEILAAEPSTICAGSFQVVRGNGFRHARVD 253
DB 316 KYGN-FVALRSIORIOERK---IFAIGTESRSSSFQHEMSQEGFSSALSMD 364

RESULT 8
US-09-193-043-46
/ Sequence 46, Application US/09193043
/ Patent No. 6251395
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ TITLE OF INVENTION: No. 6251395el Human 2
/ FILE REFERENCE: 27866/35004
/ CURRENT APPLICATION NUMBER: US/09/193,043
/ EARLIER FILING DATE: 1998-11-16
/ EARLIER APPLICATION NUMBER: 08/173,497
/ EARLIER FILING DATE: 1993-12-23
/ EARLIER APPLICATION NUMBER: 08/286,889
/ EARLIER FILING DATE: 1994-08-05
/ EARLIER APPLICATION NUMBER: 08/362,652
/ EARLIER FILING DATE: 1994-12-21
/ EARLIER APPLICATION NUMBER: 08/943,363
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EARLIER FILING DATE: 1997-10-03
 NUMBER OF SEQ ID NOS: 114
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO 46
 LENGTH: 1155
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-193-043-46

Query Match 8.7%; Score 166; DB 2; Length 1155;
 Best Local Similarity 28.2%; Pred. No. 1,1e-08;
 Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACG-GFDLYFIIDKSGSV-LHHMNEIYFVEQLAHKFIISPOLRMFSIVSTGTTLMK 94
 DB 144 PECGQEMDIAPFLIDSGSIDQSDFTQMKDFVAKLMQGLASTSTSFSLMYSNLTKHTFT 203
 QY 95 LTEDR-----EQIROGLEELQKVLPGDVTYMHGFERASQIYYENRGYRTA-SVIAL 148
 DB 204 FTEFKSSLSPQSLVDALVQLQ-----GLTYASGIQKVVKELFHSKNGARKSAKKILIVI 258
 QY 149 TDGELHEDLFFYSE--REANRSDLGAIYVCVGYKD-FNE-TOLARI-----ADSKDHF 199
 DB 259 TDGQKFRDPLEYRHVIVPEAKA---GIIRYALGVGDAFREPTALQELNTIGSAPSDHVF 315
 QY 200 PVNDGFQALOGIHSILKSCIEILAEPSITCAGSFQVVGNGRHRANVD 253
 DB 316 KVGN-FVALRSIQROIQEK----IFAIEGTERSSSSSFQHEMSQEGSSALSMD 364

RESULT 9
 US-09-688-307A-46
 Sequence 46, Application US/09688307A
 Patent No. 6432404
 GENERAL INFORMATION:
 APPLICANT: Gallatin, Michael W.
 TITLE OF INVENTION: No. 6432404e1 Human Beta-2
 FILE REFERENCE: 27866/36646
 CURRENT APPLICATION NUMBER: US/09/688.307A
 PRIOR FILING DATE: 2000-10-13
 PRIOR APPLICATION NUMBER: 09/193,043
 PRIOR FILING DATE: 1998-11-16
 PRIOR APPLICATION NUMBER: 08/605,672
 PRIOR FILING DATE: 1996-02-22
 PRIOR APPLICATION NUMBER: 08/173,497
 PRIOR FILING DATE: 1993-12-23
 PRIOR APPLICATION NUMBER: 08/286,889
 PRIOR FILING DATE: 1994-08-05
 PRIOR APPLICATION NUMBER: 08/362,652
 PRIOR FILING DATE: 1994-12-21
 PRIOR APPLICATION NUMBER: 08/943,363
 PRIOR FILING DATE: 1997-10-03
 NUMBER OF SEQ ID NOS: 114
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO 46
 LENGTH: 1155
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-688-307A-46

Query Match 8.7%; Score 166; DB 2; Length 1155;
 Best Local Similarity 28.2%; Pred. No. 1,1e-08;
 Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACG-GFDLYFIIDKSGSV-LHHMNEIYFVEQLAHKFIISPOLRMFSIVSTGTTLMK 94
 DB 144 PECGQEMDIAPFLIDSGSIDQSDFTQMKDFVAKLMQGLASTSTSFSLMYSNLTKHTFT 203
 QY 95 LTEDR-----EQIROGLEELQKVLPGDVTYMHGFERASQIYYENRGYRTA-SVIAL 148
 DB 204 FTEFKSSLSPQSLVDALVQLQ-----GLTYASGIQKVVKELFHSKNGARKSAKKILIVI 258

QY 149 TDGELHEDLFFYSE--REANRSDLGAIYVCVGYKD-FNE-TOLARI-----ADSKDHF 199
 DB 259 TDGQKFRDPLEYRHVIVPEAKA---GIIRYALGVGDAFREPTALQELNTIGSAPSDHVF 315
 QY 200 PVNDGFQALOGIHSILKSCIEILAEPSITCAGSFQVVGNGRHRANVD 253
 DB 316 KVGN-FVALRSIQROIQEK----IFAIEGTERSSSSSFQHEMSQEGSSALSMD 364

RESULT 10
 US-09-350-259-46
 Sequence 46, Application US/09350259
 Patent No. 6620915
 GENERAL INFORMATION:
 APPLICANT: Gallatin, Michael W.
 TITLE OF INVENTION: No. 6620915e1 Human 2
 FILE REFERENCE: 27866/35004
 CURRENT APPLICATION NUMBER: US/09/350,259
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: 09/193,043
 PRIOR FILING DATE: 1998-11-16
 PRIOR APPLICATION NUMBER: 08/173,497
 PRIOR FILING DATE: 1993-12-23
 PRIOR APPLICATION NUMBER: 08/286,889
 PRIOR FILING DATE: 1994-08-05
 PRIOR APPLICATION NUMBER: 08/362,652
 PRIOR FILING DATE: 1994-12-21
 PRIOR APPLICATION NUMBER: 08/943,363
 PRIOR FILING DATE: 1997-10-03
 NUMBER OF SEQ ID NOS: 114
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO 46
 LENGTH: 1155
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-350-259-46

Query Match 8.7%; Score 166; DB 2; Length 1155;
 Best Local Similarity 28.2%; Pred. No. 1,1e-08;
 Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACG-GFDLYFIIDKSGSV-LHHMNEIYFVEQLAHKFIISPOLRMFSIVSTGTTLMK 94
 DB 144 PECGQEMDIAPFLIDSGSIDQSDFTQMKDFVAKLMQGLASTSTSFSLMYSNLTKHTFT 203
 QY 95 LTEDR-----EQIROGLEELQKVLPGDVTYMHGFERASQIYYENRGYRTA-SVIAL 148
 DB 204 FTEFKSSLSPQSLVDALVQLQ-----GLTYASGIQKVVKELFHSKNGARKSAKKILIVI 258
 QY 149 TDGELHEDLFFYSE--REANRSDLGAIYVCVGYKD-FNE-TOLARI-----ADSKDHF 199
 DB 259 TDGQKFRDPLEYRHVIVPEAKA---GIIRYALGVGDAFREPTALQELNTIGSAPSDHVF 315
 QY 200 PVNDGFQALOGIHSILKSCIEILAEPSITCAGSFQVVGNGRHRANVD 253
 DB 316 KVGN-FVALRSIQROIQEK----IFAIEGTERSSSSSFQHEMSQEGSSALSMD 364

RESULT 11
 US-08-485-618-53
 Sequence 53, Application US/08485618
 Patent No. 5728533
 GENERAL INFORMATION:
 APPLICANT: Gallatin, W. Michael
 TITLE OF INVENTION: No. 5728533e1 Human 2 Integrin Alpha Subunit
 NUMBER OF SEQUENCES: 103
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 233 South Wacker Drive, 6300 Seear Tower
 CITY: Chicago
 STATE: Illinois

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/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/485,618
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32797
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 53:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1161 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
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US-08-485-618-53

Query Match
Best Local Similarity 28.2%; Score 166; DB 1; Length 1161;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GPDLVITLDSGSV-LHNMETIYFVEQLAHKFIISPOLMSPFVSTRTGLMK 94
DB 144 PCPCQEMDIAPFLIDSSGISIDSDFTQKDFVQALMGQLASTSTSFSLMQYSNLTHTFT 203
QY 95 LTEDR-----EQIRQGLELOKVLPGDPTVMHEGFERASEQIYYENRGYRTA-SVIAL 148
DB 204 FTEFKSLSPQSLVDAIVQLQ-----GLTYSAGIQKVKELPHSKNGARKSAKILYI 258
QY 149 TDGELHEDLFFYSE--REANRSRDGAIVYCVGKD-FNE-TOLARI-----ADSKDHF 199
DB 259 TDGQKFRDPLEYRHVIPAERKA---GIIRYAGVDAPREFPALQELNTIGSAPSQDHF 315
QY 200 PVNDGFQALQGIHSLKSCIEILAEPSITCAGSFQVYVRGNGFRARND 253
DB 316 KVGNG-FVALRSIORQIOEK---IFAIEGTESRSSSFQHEMSQEGFSALSMD 364

RESULT 12
US-08-362-652-53
/ Sequence 53, Application US/08362652
/ Patent No. 5766850
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 93
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
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/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.25
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/ APPLICATION NUMBER: US/08/362,652
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32391
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 53:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1161 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
US-08-362-652-53

Query Match
Best Local Similarity 28.2%; Score 166; DB 1; Length 1161;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GPDLVITLDSGSV-LHNMETIYFVEQLAHKFIISPOLMSPFVSTRTGLMK 94
DB 144 PCPCQEMDIAPFLIDSSGISIDSDFTQKDFVQALMGQLASTSTSFSLMQYSNLTHTFT 203
QY 95 LTEDR-----EQIRQGLELOKVLPGDPTVMHEGFERASEQIYYENRGYRTA-SVIAL 148
DB 204 FTEFKSLSPQSLVDAIVQLQ-----GLTYSAGIQKVKELPHSKNGARKSAKILYI 258
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DB 259 TDGQKFRDPLEYRHVIPAERKA---GIIRYAGVDAPREFPALQELNTIGSAPSQDHF 315
QY 200 PVNDGFQALQGIHSLKSCIEILAEPSITCAGSFQVYVRGNGFRARND 253
DB 316 KVGNG-FVALRSIORQIOEK---IFAIEGTESRSSSFQHEMSQEGFSALSMD 364

RESULT 13
US-08-605-672-53
/ Sequence 53, Application US/08605672
/ Patent No. 5817515
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-53

Query Match 8.7%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 1.1e-08;

Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

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DB	144	PECPGQEMDIAFLIDSGSIDQSDFTQMKDFVXALMGOLASTSTSFSLM	QYSNLTHTFT	203
QY	95	LTEDR-----EQROGLEELQKVLPGDPTMHEGFERASEQIYENRQVRTA-SVIT	AL	148
DB	204	FTEPKSLSPQSLVDAIVQLQ-----GLTYTASGIQVVKELPHSRNARKSKKTLIV	I	258
QY	149	TDGELHEDLFFYSE--REANRSRLGAIYCVGVKD-FNE-TQLARI-----ADSKDHVF		199
DB	259	TDGQKRDPLELVHNVPEAKA---GIRVAIGVGDAFREPTALQELANTIGSAPSGDHVF		315
QY	200	PVNDGFQALQGIHSILKKSCEIILAEPEPTICAGESFOVVVRNGFRIARNVD		253
DB	316	KVGN-FVALRSIQRIQEK----IFAIEGTESRSSSSFOHEMSQEGFSSALSMD		364

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%

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- 5: /cgn2_6/prodata/1/pubppa/us10B_PUBCOMB.pep:*
- 6: /cgn2_6/prodata/1/pubppa/us11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1914	100.0	368	6 US-11-047-278-2	Sequence 2, Appl1
2	1894	99.0	564	3 US-09-918-715-187	Sequence 187, App
3	1894	99.0	564	3 US-09-918-715-232	Sequence 232, App
4	1894	99.0	564	4 US-10-301-822-199	Sequence 199, App
5	1894	99.0	564	4 US-10-408-765A-1823	Sequence 1823, App
6	1894	99.0	564	4 US-10-474-794-187	Sequence 187, App
7	1894	99.0	564	4 US-10-474-794-232	Sequence 232, App
8	1894	99.0	564	5 US-10-979-159-187	Sequence 187, App
9	1894	99.0	564	5 US-10-979-159-232	Sequence 232, App
10	1894	99.0	564	5 US-11-047-278-6	Sequence 6, Appl1
11	1889	98.7	403	3 US-09-833-245-621	Sequence 621, App
12	1870	97.7	403	3 US-09-833-245-620	Sequence 620, App
13	1793	93.7	562	3 US-09-918-715-194	Sequence 194, App
14	1793	93.7	562	3 US-09-918-715-301	Sequence 301, App
15	1793	93.7	562	4 US-10-474-794-194	Sequence 194, App
16	1793	93.7	562	4 US-10-474-794-301	Sequence 301, App
17	1793	93.7	562	5 US-10-979-159-194	Sequence 194, App
18	1793	93.7	562	5 US-10-979-159-301	Sequence 301, App
19	1661	86.8	551	4 US-10-038-307-18	Sequence 18, Appl1
20	1661	86.8	551	4 US-10-201-292-18	Sequence 18, Appl1
21	1649	86.2	333	3 US-09-796-753-12	Sequence 12, Appl1
22	1649	86.2	333	4 US-10-038-307-2	Sequence 2, Appl1
23	1649	86.2	333	4 US-10-201-292-2	Sequence 2, Appl1
24	1649	86.2	333	6 US-11-047-278-8	Sequence 8, Appl1
25	1649	86.2	345	4 US-10-038-307-24	Sequence 24, Appl1
26	1649	86.2	345	4 US-10-201-292-24	Sequence 24, Appl1
27	1649	86.2	564	4 US-10-038-307-20	Sequence 20, Appl1

28	1649	86.2	564	4 US-10-201-292-20	Sequence 20, Appl1
29	1636	85.5	328	4 US-10-038-307-26	Sequence 26, Appl1
30	1636	85.5	328	4 US-10-201-292-26	Sequence 26, Appl1
31	1634.5	85.4	322	4 US-10-038-307-22	Sequence 22, Appl1
32	1634.5	85.4	342	4 US-10-201-292-22	Sequence 22, Appl1
33	1629	85.1	543	4 US-10-038-307-14	Sequence 14, Appl1
34	1629	85.1	543	4 US-10-038-307-16	Sequence 16, Appl1
35	1629	85.1	543	4 US-10-201-292-16	Sequence 16, Appl1
36	1629	85.1	543	4 US-10-201-292-16	Sequence 16, Appl1
37	1619	84.6	543	4 US-10-038-307-10	Sequence 10, Appl1
38	1619	84.6	543	4 US-10-201-292-10	Sequence 10, Appl1
39	1548	80.9	529	4 US-10-201-292-36	Sequence 36, Appl1
40	1488	77.7	534	4 US-10-038-307-12	Sequence 12, Appl1
41	1488	77.7	534	4 US-10-201-292-12	Sequence 12, Appl1
42	1434.5	74.9	504	4 US-10-201-292-34	Sequence 34, Appl1
43	1307	68.3	479	4 US-10-201-292-32	Sequence 32, Appl1
44	1193	62.3	460	4 US-10-201-292-28	Sequence 28, Appl1
45	1183	61.8	460	4 US-10-201-292-30	Sequence 30, Appl1

ALIGNMENTS

RESULT 1					
US-11-047-278-2					
; Sequence 2, Application US/11047278					
; Publication No. US20050196407A1					
; GENERAL INFORMATION:					
; APPLICANT: Young, John A.T.					
; APPLICANT: Bradley, Kenneth A.					
; APPLICANT: Collier, Robert J.					
; APPLICANT: Mogridge, Jeremy S.					
; TITLE OF INVENTION: Anthrax Toxin Receptor					
; FILE REFERENCE: 960296.97745					
; CURRENT APPLICATION NUMBER: US/11/047,278					
; CURRENT FILING DATE: 2005-01-31					
; PRIOR APPLICATION NUMBER: US/09/970,076					
; PRIOR FILING DATE: 2001-10-03					
; PRIOR APPLICATION NUMBER: 60/251,481					
; PRIOR FILING DATE: 2000-12-05					
; NUMBER OF SEQ ID NOS: 10					
; SOFTWARE: PatentIn Ver. 2.1					
; SEQ ID NO 2					
; LENGTH: 368					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-11-047-278-2					
Query Match					
Best Local Similarity 100.0%; Score 1914; DB 6; Length 368;					
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MATERRALGIGFOWLSLATLVILICAGGARGREDGGPACYGFDLYIILDKSGSVLHHNN	60		
DB	1	MATERRALGIGFOWLSLATLVILICAGGARGREDGGPACYGFDLYIILDKSGSVLHHNN	60		
QY	61	EIYFYEQIAHKFISQGLMSFIVFSTRGTTLMKLTEDBEOIRQIEELQKVLPGSDTYN	120		
DB	61	EIYFYEQIAHKFISQGLMSFIVFSTRGTTLMKLTEDBEOIRQIEELQKVLPGSDTYN	120		
QY	121	HSGFERASQIYKNNQGRVTSVIALTDGELHEDLFYSEBEARSRDLGIVYCVGV	180		
DB	121	HSGFERASQIYKNNQGRVTSVIALTDGELHEDLFYSEBEARSRDLGIVYCVGV	180		
QY	181	KQFNETQIARIDSQDHPVNDGFOALQGIHSLIKSCIBILAEPSTICAGSEFOVY	240		
DB	181	KQFNETQIARIDSQDHPVNDGFOALQGIHSLIKSCIBILAEPSTICAGSEFOVY	240		
QY	241	VRNGGRHARNDRVLCRKINDSVTLNKPSPVEVTYLLCPAPILKEGKRAALQVSN	300		
DB	241	VRNGGRHARNDRVLCRKINDSVTLNKPSPVEVTYLLCPAPILKEGKRAALQVSN	300		
QY	301	DGSLFSSVITTTTCSDGSLIALILFLILLALALLMFWPLCCTVYIKVPPPAE	360		
DB	301	DGSLFSSVITTTTCSDGSLIALILFLILLALALLMFWPLCCTVYIKVPPPAE	360		

```
Db      301 DGLSFSSSVITTTTHCSGSIATLAILFLLLALALLMFWPLCCTVIKEVPPPAE 360
Qy      361 ESEENKIK 368
Db      361 ESEENKIK 368
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RESULT 2

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US-09-918-715-187
; Sequence 187, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Bert Vogelstein
; APPLICANT: Brad St. Croix
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-187
```

```
Query Match      99.0%; Score 1894; DB 3; Length 564;
Best Local Similarity 100.0%; Pred. No. 8.7e-182;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 MATARRALGIGFQWLSLTLVLIICAGGGRREDGPGACYGFDLYFIIDKSGSVLHNN 60
Db      1 MATARRALGIGFQWLSLTLVLIICAGGGRREDGPGACYGFDLYFIIDKSGSVLHNN 60
Qy      61 EIIYFVEQLAHKFISPOLMSFIVSTGTTLTKLTEDREQIRQGLEELQKVLPGDITYM 120
Db      61 EIIYFVEQLAHKFISPOLMSFIVSTGTTLTKLTEDREQIRQGLEELQKVLPGDITYM 120
Qy      121 HEGFERASEQIYYENRQGYRTASVITLALTDGELHEDLPFYSEREANRSDLGAIYVCV 180
Db      121 HEGFERASEQIYYENRQGYRTASVITLALTDGELHEDLPFYSEREANRSDLGAIYVCV 180
Qy      121 HEGFERASEQIYYENRQGYRTASVITLALTDGELHEDLPFYSEREANRSDLGAIYVCV 180
Db      121 HEGFERASEQIYYENRQGYRTASVITLALTDGELHEDLPFYSEREANRSDLGAIYVCV 180
Qy      181 KOFNETQLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIILAEPTICAGESFOYV 240
Db      181 KOFNETQLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIILAEPTICAGESFOYV 240
Qy      241 VGNNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMRAALQVSNM 300
Db      241 VGNNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMRAALQVSNM 300
Qy      301 DGLSFSSSVITTTTHCSGSIATLAILFLLLALALLMFWPLCCTVIKEVPPPAE 360
Db      301 DGLSFSSSVITTTTHCSGSIATLAILFLLLALALLMFWPLCCTVIKEVPPPAE 360
Qy      361 ESEE 364
Db      361 ESEE 364
```

RESULT 3

```
US-09-918-715-232
; Sequence 232, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
```

```
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 232
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-232
```

```
Query Match      99.0%; Score 1894; DB 3; Length 564;
Best Local Similarity 100.0%; Pred. No. 8.7e-182;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 MATARRALGIGFQWLSLTLVLIICAGGGRREDGPGACYGFDLYFIIDKSGSVLHNN 60
Db      1 MATARRALGIGFQWLSLTLVLIICAGGGRREDGPGACYGFDLYFIIDKSGSVLHNN 60
Qy      61 EIIYFVEQLAHKFISPOLMSFIVSTGTTLTKLTEDREQIRQGLEELQKVLPGDITYM 120
Db      61 EIIYFVEQLAHKFISPOLMSFIVSTGTTLTKLTEDREQIRQGLEELQKVLPGDITYM 120
Qy      121 HEGFERASEQIYYENRQGYRTASVITLALTDGELHEDLPFYSEREANRSDLGAIYVCV 180
Db      121 HEGFERASEQIYYENRQGYRTASVITLALTDGELHEDLPFYSEREANRSDLGAIYVCV 180
Qy      121 HEGFERASEQIYYENRQGYRTASVITLALTDGELHEDLPFYSEREANRSDLGAIYVCV 180
Db      121 HEGFERASEQIYYENRQGYRTASVITLALTDGELHEDLPFYSEREANRSDLGAIYVCV 180
Qy      181 KOFNETQLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIILAEPTICAGESFOYV 240
Db      181 KOFNETQLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIILAEPTICAGESFOYV 240
Qy      241 VGNNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMRAALQVSNM 300
Db      241 VGNNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMRAALQVSNM 300
Qy      301 DGLSFSSSVITTTTHCSGSIATLAILFLLLALALLMFWPLCCTVIKEVPPPAE 360
Db      301 DGLSFSSSVITTTTHCSGSIATLAILFLLLALALLMFWPLCCTVIKEVPPPAE 360
Qy      361 ESEE 364
Db      361 ESEE 364
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RESULT 4

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US-10-301-822-199
; Sequence 199, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgate, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MP001-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
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/ PRIOR FILING DATE: 2001-12-10
/ PRIOR APPLICATION NUMBER: US 60/361, 978
/ PRIOR FILING DATE: 2002-03-05
/ PRIOR APPLICATION NUMBER: US 60/381, 988
/ PRIOR FILING DATE: 2002-05-20
/ NUMBER OF SEQ ID NOS: 228
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 199
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-301-822-199

Query Match          99.0%; Score 1894; DB 4; Length 564;
Best Local Similarity 100.0%; Pred. No. 8.7e-182;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATERRALGIGFOWLSLATLVLCAGGGRREDGPGACGFDLYFILDKSGSVLHHN 60
DB 1 MATERRALGIGFOWLSLATLVLCAGGGRREDGPGACGFDLYFILDKSGSVLHHN 60
QY 61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIRQGLELOKVLPGGDTYM 120
DB 61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIRQGLELOKVLPGGDTYM 120
QY 121 HEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYSERANRSRDGAIIVCGV 180
DB 121 HEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYSERANRSRDGAIIVCGV 180
QY 181 KDFNETQLARIADSKDHPVNDGFOALQGIHSHILKSCIEILAAEPSTICAGESFOV 240
DB 181 KDFNETQLARIADSKDHPVNDGFOALQGIHSHILKSCIEILAAEPSTICAGESFOV 240
QY 241 VRNGGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGKKAALQVSMN 300
DB 241 VRNGGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGKKAALQVSMN 300
QY 301 DGLSFISSSVIITTHCSGDSIIAIIALLIFLLALALMLWFWPLCCTVLIKEVPPPAE 360
DB 301 DGLSFISSSVIITTHCSGDSIIAIIALLIFLLALALMLWFWPLCCTVLIKEVPPPAE 360
QY 361 ESEE 364
DB 361 ESEE 364

RESULT 5
US-10-408-765A-1823
/ Sequence 1823, Application US/10408765A
/ Publication NO. US20040101874A1
/ GENERAL INFORMATION:
/ APPLICANT: Ghosh, Soumitra S.
/ APPLICANT: Fahy, Eoin D.
/ APPLICANT: Zhang, Bing
/ APPLICANT: Gibson, Bradford W.
/ APPLICANT: Taylor, Steven W.
/ APPLICANT: Glenn, Gary M.
/ APPLICANT: Warnock, Dale E.
/ TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
/ FILE REFERENCE: 660088.465
/ CURRENT APPLICATION NUMBER: US/10/408, 765A
/ NUMBER OF SEQ ID NOS: 3077
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1823
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-408-765A-1823

Query Match          99.0%; Score 1894; DB 4; Length 564;
Best Local Similarity 100.0%; Pred. No. 8.7e-182;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATERRALGIGFOWLSLATLVLCAGGGRREDGPGACGFDLYFILDKSGSVLHHN 60
DB 1 MATERRALGIGFOWLSLATLVLCAGGGRREDGPGACGFDLYFILDKSGSVLHHN 60
QY 61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIRQGLELOKVLPGGDTYM 120
DB 61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIRQGLELOKVLPGGDTYM 120
QY 121 HEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYSERANRSRDGAIIVCGV 180
DB 121 HEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYSERANRSRDGAIIVCGV 180
QY 181 KDFNETQLARIADSKDHPVNDGFOALQGIHSHILKSCIEILAAEPSTICAGESFOV 240
DB 181 KDFNETQLARIADSKDHPVNDGFOALQGIHSHILKSCIEILAAEPSTICAGESFOV 240
QY 241 VRNGGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGKKAALQVSMN 300
DB 241 VRNGGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGKKAALQVSMN 300
QY 301 DGLSFISSSVIITTHCSGDSIIAIIALLIFLLALALMLWFWPLCCTVLIKEVPPPAE 360
DB 301 DGLSFISSSVIITTHCSGDSIIAIIALLIFLLALALMLWFWPLCCTVLIKEVPPPAE 360
QY 361 ESEE 364
DB 361 ESEE 364

RESULT 6
US-10-474-794-187
/ Sequence 187, Application US/10474794
/ Publication NO. US20040213793A1
/ GENERAL INFORMATION:
/ APPLICANT: Carson-Walter, Eleanor
/ APPLICANT: St. Croix, Brad
/ APPLICANT: Vogelstein, Bert
/ APPLICANT: Kinzler, Kenneth
/ TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
/ FILE REFERENCE: 1107.00179
/ CURRENT APPLICATION NUMBER: US/10/474, 794
/ PRIOR FILING DATE: 2003-10-14
/ PRIOR APPLICATION NUMBER: 60/282, 850
/ PRIOR FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: 60/308, 829
/ PRIOR FILING DATE: 2001-08-01
/ NUMBER OF SEQ ID NOS: 359
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 187
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-474-794-187

Query Match          99.0%; Score 1894; DB 4; Length 564;
Best Local Similarity 100.0%; Pred. No. 8.7e-182;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATERRALGIGFOWLSLATLVLCAGGGRREDGPGACGFDLYFILDKSGSVLHHN 60
DB 1 MATERRALGIGFOWLSLATLVLCAGGGRREDGPGACGFDLYFILDKSGSVLHHN 60
QY 61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIRQGLELOKVLPGGDTYM 120
DB 61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIRQGLELOKVLPGGDTYM 120
QY 121 HEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYSERANRSRDGAIIVCGV 180
DB 121 HEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYSERANRSRDGAIIVCGV 180
QY 181 KDFNETQLARIADSKDHPVNDGFOALQGIHSHILKSCIEILAAEPSTICAGESFOV 240
```

```

Db      181 KQNETQLARIADSKDHPVNDGFOALQGIHSHILKSCIEILAEPSITCAGESFOV 240
        241 VRNGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGMKAALQVSMN 300
        241 VRNGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGMKAALQVSMN 300
Qy      301 DGLSFSSSVIITTTTCHSDGSIILAILLFLLLALALLMFWPMLCCTVIKEVPPPAE 360
        301 DGLSFSSSVIITTTTCHSDGSIILAILLFLLLALALLMFWPMLCCTVIKEVPPPAE 360
Db      361 ESSE 364
        361 ESSE 364

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RESULT 7
US-10-474-794-232
; Sequence 232, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 232
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-232

```

```

Query Match      99.0%; Score 1894; DB 4; Length 564;
Best Local Similarity 100.0%; Pred. No. 8.7e-182;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MATERRALGIGFOMSLATLVILICAGGGRREDGPGACGFDLYFIIDKSGSVLHHNN 60
        1 MATERRALGIGFOMSLATLVILICAGGGRREDGPGACGFDLYFIIDKSGSVLHHNN 60
Db      61 EIYFVEQLAHKFIISPOLMSFIVFSTRGTITLTKLTEDREQIRQGLEBLQKVLPGDITY 120
        61 EIYFVEQLAHKFIISPOLMSFIVFSTRGTITLTKLTEDREQIRQGLEBLQKVLPGDITY 120
Qy      121 HGFEPASQIYYENRQGYRTASVITLALTDGELHEDLFYSSREARNSRLGAIYVCV 180
        121 HGFEPASQIYYENRQGYRTASVITLALTDGELHEDLFYSSREARNSRLGAIYVCV 180
Db      121 HGFEPASQIYYENRQGYRTASVITLALTDGELHEDLFYSSREARNSRLGAIYVCV 180
        121 HGFEPASQIYYENRQGYRTASVITLALTDGELHEDLFYSSREARNSRLGAIYVCV 180
Qy      181 KQNETQLARIADSKDHPVNDGFOALQGIHSHILKSCIEILAEPSITCAGESFOV 240
        181 KQNETQLARIADSKDHPVNDGFOALQGIHSHILKSCIEILAEPSITCAGESFOV 240
Db      181 KQNETQLARIADSKDHPVNDGFOALQGIHSHILKSCIEILAEPSITCAGESFOV 240
        181 KQNETQLARIADSKDHPVNDGFOALQGIHSHILKSCIEILAEPSITCAGESFOV 240
Qy      241 VRNGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGMKAALQVSMN 300
        241 VRNGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGMKAALQVSMN 300
Db      241 VRNGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGMKAALQVSMN 300
        241 VRNGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGMKAALQVSMN 300
Qy      301 DGLSFSSSVIITTTTCHSDGSIILAILLFLLLALALLMFWPMLCCTVIKEVPPPAE 360
        301 DGLSFSSSVIITTTTCHSDGSIILAILLFLLLALALLMFWPMLCCTVIKEVPPPAE 360
Db      301 DGLSFSSSVIITTTTCHSDGSIILAILLFLLLALALLMFWPMLCCTVIKEVPPPAE 360
        301 DGLSFSSSVIITTTTCHSDGSIILAILLFLLLALALLMFWPMLCCTVIKEVPPPAE 360
Qy      361 ESSE 364
        361 ESSE 364
Db      361 ESSE 364

```

```

RESULT 8
US-10-979-159-187
; Sequence 187, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-979-159-187

```

```

Query Match      99.0%; Score 1894; DB 5; Length 564;
Best Local Similarity 100.0%; Pred. No. 8.7e-182;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MATERRALGIGFOMSLATLVILICAGGGRREDGPGACGFDLYFIIDKSGSVLHHNN 60
        1 MATERRALGIGFOMSLATLVILICAGGGRREDGPGACGFDLYFIIDKSGSVLHHNN 60
Db      61 EIYFVEQLAHKFIISPOLMSFIVFSTRGTITLTKLTEDREQIRQGLEBLQKVLPGDITY 120
        61 EIYFVEQLAHKFIISPOLMSFIVFSTRGTITLTKLTEDREQIRQGLEBLQKVLPGDITY 120
Qy      121 HGFEPASQIYYENRQGYRTASVITLALTDGELHEDLFYSSREARNSRLGAIYVCV 180
        121 HGFEPASQIYYENRQGYRTASVITLALTDGELHEDLFYSSREARNSRLGAIYVCV 180
Db      121 HGFEPASQIYYENRQGYRTASVITLALTDGELHEDLFYSSREARNSRLGAIYVCV 180
        121 HGFEPASQIYYENRQGYRTASVITLALTDGELHEDLFYSSREARNSRLGAIYVCV 180
Qy      181 KQNETQLARIADSKDHPVNDGFOALQGIHSHILKSCIEILAEPSITCAGESFOV 240
        181 KQNETQLARIADSKDHPVNDGFOALQGIHSHILKSCIEILAEPSITCAGESFOV 240
Db      181 KQNETQLARIADSKDHPVNDGFOALQGIHSHILKSCIEILAEPSITCAGESFOV 240
        181 KQNETQLARIADSKDHPVNDGFOALQGIHSHILKSCIEILAEPSITCAGESFOV 240
Qy      241 VRNGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGMKAALQVSMN 300
        241 VRNGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGMKAALQVSMN 300
Db      241 VRNGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGMKAALQVSMN 300
        241 VRNGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGMKAALQVSMN 300
Qy      301 DGLSFSSSVIITTTTCHSDGSIILAILLFLLLALALLMFWPMLCCTVIKEVPPPAE 360
        301 DGLSFSSSVIITTTTCHSDGSIILAILLFLLLALALLMFWPMLCCTVIKEVPPPAE 360
Db      301 DGLSFSSSVIITTTTCHSDGSIILAILLFLLLALALLMFWPMLCCTVIKEVPPPAE 360
        301 DGLSFSSSVIITTTTCHSDGSIILAILLFLLLALALLMFWPMLCCTVIKEVPPPAE 360
Qy      361 ESSE 364
        361 ESSE 364
Db      361 ESSE 364

```

```

RESULT 9
US-10-979-159-232
; Sequence 232, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159

```


Db 121 HEGFERASEQIYYENKQGYRTASVIALITDGELEHEDLFFYSERANRSDLAIVYCVGV 180
QY 181 KDFNETOLARIADSKDHVPVNDGFOALOGIHSILKSCIEILAAPESTICAGESFOVV 240
Db 181 KDFNETOLARIADSKDHVPVNDGFOALOGIHSILKSCIEILAAPESTICAGESFOVV 240
QY 241 VANGNFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKAAIQVSNV 300
Db 241 VANGNFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKAAIQVSNV 300
QY 301 DGLSFISSSVIITTHCSGDSIIAIALILFLLLALALLMFWPLCCTVYIIKEVPPPAE 360
Db 301 DGLSFISSSVIITTHCSGDSIIAIALILFLLLALALLMFWPLCCTVYIIKEVPPPAE 360
QY 361 ESE 363
Db 361 ESE 363

RESULT 12
US-09-833-245-620
; Sequence 620, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 620
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (320)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (331)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (368)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-620

Query Match 97.7%; Score 1870; DB 3; Length 403;
Best Local Similarity 99.2%; Pred. No. 1.4e-179;
Matches 360; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MATERRALGIGFOWLSLATLVLCAGGGRREDGPGACYGFDLYIILDKSGSVLHHNN 60
Db 1 MATERRALGIGFOWLSLATLVLCAGGGRREDGPGACYGFDLYIILDKSGSVLHHNN 60
QY 61 ELYYFVEQLAHKISPOLRMSFIVFSTRGTTLMKLTEDREQIRQGLELOKVLPGDITYM 120
Db 61 ELYYFVEQLAHKISPOLRMSFIVFSTRGTTLMKLTEDREQIRQGLELOKVLPGDITYM 120
QY 121 HEGFERASEQIYYENKQGYRTASVIALITDGELEHEDLFFYSERANRSDLAIVYCVGV 180
Db 121 HEGFERASEQIYYENKQGYRTASVIALITDGELEHEDLFFYSERANRSDLAIVYCVGV 180
QY 181 KDFNETOLARIADSKDHVPVNDGFOALOGIHSILKSCIEILAAPESTICAGESFOVV 240

Db 181 KDFNETOLARIADSKDHVPVNDGFOALOGIHSILKSCIEILAAPESTICAGESFOVV 240
QY 241 VANGNFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKAAIQVSNV 300
Db 241 VANGNFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKAAIQVSNV 300
QY 301 DGLSFISSSVIITTHCSGDSIIAIALILFLLLALALLMFWPLCCTVYIIKEVPPPAE 360
Db 301 DGLSFISSSVIITTHCSGDSIIAIALILFLLLALALLMFWPLCCTVYIIKEVPPPAE 360
QY 361 ESE 363
Db 361 ESE 363

RESULT 13
US-09-918-715-194
; Sequence 194, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FaestSeq for Windows Version 3.0
; SEQ ID NO 194
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-918-715-194

Query Match 93.7%; Score 1793; DB 3; Length 562;
Best Local Similarity 96.1%; Pred. No. 1.4e-171;
Matches 342; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 9 LGIGFOWLSLATLVLCAGGGRREDGPGACYGFDLYIILDKSGSVLHHNNIYFVBO 68
Db 7 LGAGLRGLCVAAVLVVCAGHGRREDGPGACYGFDLYIILDKSGSVLHHNNIYFVBO 66
QY 69 LAHKFISPOLRMSFIVFSTRGTTLMKLTEDREQIRQGLELOKVLPGDITYMHGFERAS 128
Db 67 LAHKFISPOLRMSFIVFSTRGTTLMKLTEDREQIRQGLELOKVLPGDITYMHGFERAS 126
QY 129 EOIYYENKQGYRTASVIALITDGELEHEDLFFYSERANRSDLAIVYCVGVDFNETOL 188
Db 127 EOIYYENKQGYRTASVIALITDGELEHEDLFFYSERANRSDLAIVYCVGVDFNETOL 186
QY 189 ARIADSKDHVPVNDGFOALOGIHSILKSCIEILAAPESTICAGESFOVVVANGNFRH 248
Db 187 ARIADSKDHVPVNDGFOALOGIHSILKSCIEILAAPESTICAGESFOVVVANGNFRH 246
QY 249 ARNVDRVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKAAIQVSNVDSFISS 308
Db 247 ARNVDRVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKAAIQVSNVDSFISS 306
QY 309 SVIITTHCSGDSIIAIALILFLLLALALLMFWPLCCTVYIIKEVPPPAESEE 364
Db 307 SVIITTHCSGDSIIAIALILFLLLALALLMFWPLCCTVYIIKEVPPPAESEE 362
RESULT 14
US-09-918-715-301

```
; Sequence 301, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918, 715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Mouse
US-09-918-715-301
```

```
Query Match          93.7%; Score 1793; DB 3; Length 562;
Best Local Similarity 96.1%; Pred. No. 1,4e-171;
Matches 342; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 9 LGIGFQWLSATVTLVLCAGGGRRRDEGPAICYGFDLYFLDKSGSVLHHMNEIYYFVEQ 68
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 7 LGAGLRGLCVAAVLVLCAGHGRREDGPGACYGFDLYFLDKSGSVLHHMNEIYYFVEQ 66
QY 69 LAHKFISPOLRMSFIVFSTRTGTLMLKLTEDREQIRQGLELOKYLPGGDTYMHGFERAS 128
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 LAHRFISPOLRMSFIVFSTRTGTLMLKLTEDREQIRQGLELOKYLPGGDTYMHGFERAS 126
QY 129 EQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDGAIYVCVGDVDFNETOL 188
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 127 EQIYENSQGYRTASVIALTDGELHEDLFFYSERANRSRDGAIYVCVGDVDFNETOL 186
QY 189 ARIADSKDHYFPVNDGFQALQGIHSHILKKSCEIILAEPSSTICAGESFQVVRGNGFRH 248
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 187 ARIADSKDHYFPVNDGFQALQGIHSHILKKSCEIILAEPSSTICAGESFQVVRGNGFRH 246
QY 249 ARVNDVLCSEFKINDSVTLNEKPSVEDPYLLCPAPILKEVGKALQVSMNDGLSFIS 308
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 247 ARVNDVLCSEFKINDSVTLNEKPSVEDPYLLCPAPILKEVGKALQVSMNDGLSFIS 306
QY 309 SVIITTHCSGDSIIALIALILFLALALALMLMFWPLCCTVIIKEVPPPEESSEE 364
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 307 SVIITTHCSGDSIIALIALILFLALALALMLMFWPLCCTVIIKEVPPPEESSEE 362
```

```
RESULT 15
US-10-474-794-194
; Sequence 194, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carlson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194
```

```
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-474-794-194
```

```
Query Match          93.7%; Score 1793; DB 4; Length 562;
Best Local Similarity 96.1%; Pred. No. 1,4e-171;
Matches 342; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 9 LGIGFQWLSATVTLVLCAGGGRRRDEGPAICYGFDLYFLDKSGSVLHHMNEIYYFVEQ 68
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 7 LGAGLRGLCVAAVLVLCAGHGRREDGPGACYGFDLYFLDKSGSVLHHMNEIYYFVEQ 66
QY 69 LAHKFISPOLRMSFIVFSTRTGTLMLKLTEDREQIRQGLELOKYLPGGDTYMHGFERAS 128
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 LAHRFISPOLRMSFIVFSTRTGTLMLKLTEDREQIRQGLELOKYLPGGDTYMHGFERAS 126
QY 129 EQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDGAIYVCVGDVDFNETOL 188
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 127 EQIYENSQGYRTASVIALTDGELHEDLFFYSERANRSRDGAIYVCVGDVDFNETOL 186
QY 189 ARIADSKDHYFPVNDGFQALQGIHSHILKKSCEIILAEPSSTICAGESFQVVRGNGFRH 248
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 187 ARIADSKDHYFPVNDGFQALQGIHSHILKKSCEIILAEPSSTICAGESFQVVRGNGFRH 246
QY 249 ARVNDVLCSEFKINDSVTLNEKPSVEDPYLLCPAPILKEVGKALQVSMNDGLSFIS 308
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 247 ARVNDVLCSEFKINDSVTLNEKPSVEDPYLLCPAPILKEVGKALQVSMNDGLSFIS 306
QY 309 SVIITTHCSGDSIIALIALILFLALALALMLMFWPLCCTVIIKEVPPPEESSEE 364
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 307 SVIITTHCSGDSIIALIALILFLALALALMLMFWPLCCTVIIKEVPPPEESSEE 362
```

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Search completed: December 14, 2005, 11:58:58
Job time : 112.034 secs
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Db 121 HEGFERASQIYENKQRTASVIALDGDHEDLPFYSEBANSRSDLAIVYCVG 180
Qy 181 KQNETQLARIDSKCHVPVNDGPNALGGIHSILKSCIEILAEPTICAGSEFOV 240
Db 181 KQNETQLARIDSKCHVPVNDGPNALGGIHSILKSCIEILAEPTICAGSEFOV 240
Qy 241 VAGNGFRHARNDRVLCSEKINDSVTLNEKPSVEDTYLCPAPILKEYGMKALQVSN 300
Db 241 VAGNGFRHARNDRVLCSEKINDSVTLNEKPSVEDTYLCPAPILKEYGMKALQVSN 300
Qy 301 DGLSFSSSVITTTTCSGSIALLLILFLILALALIMWEPCLCTVITIKVPPPE 360
Db 301 DGLSFSSSVITTTTCSGSIALLLILFLILALALIMWEPCLCTVITIKVPPPE 360
Qy 361 ESEE 364
Db 361 ESEE 364
```

```
RESULT 2
US-11-080-026-4
; Sequence 4, Application US/11080026
; Publication No. US20050260192A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Shimooka, Motomu
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; FILE REFERENCE: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: CFBF-P02-021
; CURRENT APPLICATION NUMBER: US/11/080,026
; PRIOR FILING DATE: 2005-03-15
; PRIOR APPLICATION NUMBER: 09/945,265
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,700
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-026-4
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Query Match 7.6%; Score 145.5; DB 7; Length 1152;
Best Local Similarity 26.2%; Pred. No. 1,4e-05;
Matches 60; Conservative 45; Mismatches 81; Indels 43; Gaps 12;
Qy 44 DLYFLDKSGSVL-HHMEIYYFVEQLAHKFIPOLRMSFIVSTRTGTLMLKLTED---- 98
Db 150 DIAFLDLSGSGSIHPHFRMKKEVST-----VMEQLKSKSTLFS-----LMQVSEFRH 199
Qy 99 -----RQIRQGLEELQKVLPGDVTWHEGFERASEQIYENKQRTA-SVIALT 149
Db 200 FTFKEFQNNPNRSLVKPIQLL--GRTHATGIRKVBELFITGARKNAFKIIVIT 257
Qy 150 DGLHEDLPFYSE--REARSRLGAIYCVGVKDNENQOLAR-----TADS--KHVP 200
Db 258 DGEKFDPLGYEDVIEADRE--GVIRYVIGVGDVFRSEKSKQELINTJASKPRDHVQ 314
Qy 201 VNDGPNALGGIHSILKSCIEILAEPTICAGSEFOVVRNGFRHA 249
Db 315 VNN-FBALKTQQLREK-----IFAIGTOTGSSSFEHMSQEGFSAA 358
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```
RESULT 3
US-11-186-284-26
; Sequence 26, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
```

```
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John B.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; FILE REFERENCE: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 60/381,988
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 3063
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-26
```

```
Query Match 6.8%; Score 131; DB 7; Length 3063;
Best Local Similarity 29.8%; Pred. No. 0.0014;
Matches 59; Conservative 38; Mismatches 75; Indels 26; Gaps 13;
Qy 44 DLYFLDKSGSVL-HHMEIYYFVEQLAHKFIPOLRMSFIVSTRTGTLMLKLTED---- 97
Db 440 DLYFLDLSGSGSIHPHFRMKKEVST-----VMEQLKSKSTLFS-----LMQVSEFRH 199
Qy 98 DQEQIRQGLEELQKVLPGDVTWHEGFERASEQIYENKQRTA-SVIALT 153
Db 500 VEDII-----EAINTFPYKSGSTNKGKMTYVREKIFVPSK-GSRSNVPEKWMILLTDGK- 552
Qy 154 HEDLPFYSEBANSRSDLAIVYCVGVKDNENQOLARID--SKHVPVNDGPNALGGI 211
Db 553 SSDAF---RDPALKLRNSDVEIFAVGVDAVRSLEALASPAETHVTEVD-FDAFORI 608
Qy 212 IHSILKSCIEI---LAA 226
Db 609 SFELVQSTCLRIEQLAA 626
```

```
RESULT 4
US-11-057-047-2
; Sequence 2, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilkeson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; FILE REFERENCE: Methods Related Thereof
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057,047
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; PRIOR FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
```



```

; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-057-047-2

Query March 5, 94; Score 113.5; DB 7; Length 739;
Beet local similarity 19.6%; Pred. No. 0.0076;
Matches 66; Conservative 63; Mismatches 109; Indels 99; Gaps 17;

Dy 28 QGGRREDG-GPA-----CYGFPDYILDKSGS-----LHHMNEIYFVEOLAH 71
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dy 218 EGVADDEHGEGEQQRKIVLDPSSGMIIYVLVDSOSIGASNFGAKKCLVNIIEKVAS 277
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dy 72 KPIFQQLMSTIVESTRGTTLMKLTE---DREQIRQGLEEL---QKVLFGSDTYMHG 123
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dy 278 YGVNP-RYGLVATYATYPKIWKVSEADSNADWYTKOLINEYDHDKLXSGTWT----- 330
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dy 124 FERASEQIYYENR-----QGY-RTASVITALLDG-----ELHEDLFFYSE 162
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dy 331 -KKALQAVYSWMSWEDVPRPEGMMNRTRVITLLMTDGLHNMCGDPTVIADIRDLVYIGKD 389
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dy 163 REANRSRLGAIIVYCVG--VKDFNETQIARIADSKDHVPFNPDSFOALQGIHHSILKSC 220
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dy 390 RKNRPEDLDVYVFCVGLPNQVAINALASKKDNQDHVFKYKD-MENLEDVFFYGMIDES 447
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dy 221 IEIIAAEBSITCAGESFQVVVVRGNGFRHARVNDVRLCSFKINDSVTLNEKPSVEDTYLL 280
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dy 448 -----QSLSLC-----GMVMEHRKGTD-----YHKQPMQAKISV-- 476
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Dy 281 CPAPIKKEVGKKALQVSMNDGLSFISSVITTTTHC 317
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dy 477 ----IRPSKGHSCMG-----AVSSEFVLTIAHC 502
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 5
US-11-057-047-1
; Sequence 1, Application US/11057047
; Publication No. US20050260198A1
GENERAL INFORMATION:
APPLICANT: Holters, Vernon
APPLICANT: Thurman, Joshua
APPLICANT: Taube, Christian
APPLICANT: Gelband, Erwin
APPLICANT: Gilkeson, Gary
TITLE OF INVENTION: Inhibition of Factor B. The Alternative Complement Pathway and
TITLE OF INVENTION: Methods Related Thereto
FILE REFERENCE: 2848-66
CURRENT APPLICATION NUMBER: US/11/057_047
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,594
PRIOR FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: 60/636,239
PRIOR FILING DATE: 2004-12-14
PRIOR APPLICATION NUMBER: US04/015040
PRIOR FILING DATE: 2004-05-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LENGTH: 764
TYPE: PRT
ORGANISM: Homo sapiens
US-11-057-047-1

Query Match      5.9% Score 113.5 DB 7 Length 764;
Best Local Similarity 19.6%, Pred.No.0.0079;
Matches    66; Conservative   63; Mismatches 109; Indels 99; Gaps 17;

28 OCGRRDDG-GPA-----CYGGFDLYFILDKSGSV-----LHHWNBEIYFEOLAH 71
       |||               :||:||||          :|::|
Db     EGVADNEDHGHEEQKKRIIVLDPSGSNNIIYLVDSDSIGSNFTGAKKCLVNIIEKYAS 302
       |                  :|:|              :|:|
Qy     KFISSQLMSPISFYSTRGTTLMKLT---DREQIRGLEEL----OKVLPGSPTYNHGG 123
       :                 ::|             :|:|

```

```

Db      YGVPR--RYGLVTYATYTKIKWKKVSEADSSNADWTQKLNELNYEDHKLKSGTNT----- 355
Oy      124 PERASEQIYYENR-----OGY-RTASVIITALTDG-----ELHEDIEFTYE 162
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      356 -KKALQAVYSMMWSWEPDVPBEGSMNRTRHVIIIMTGILHNMGDPITVIDEIRDLXYIGKD 414
Oy      163 REARNSRLGAIIVYCVG--VVDENFNTOLARIADSODHYFPVVDGFQALQGIIHSILKKS 220
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db      415 RKNRPEDYLDVYVFVGPLVNOVNINALASKDONQHVFVKVD-MENLEDVFOQMDIES- 472
Oy      221 IEILLAEPSTTCAGESPQVVVRGNNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEEDYLL 280
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      473 -----QLSLSC-----GMWEHRKGTD-----YHKQPQAKTISV-- 501
Oy      281 CPAPLKEVGKMKALQVMSNDGLSTISSVIIITTHC 317
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      502 ----IRPSKGHSCMG-----AVSYEFVLTAAHC 527

RESULT 6
US-10-821-234-1034
; Sequence 1034, Application US/10821234
; Publication No. US2005025511A41
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1034
; LENGTH: 798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1034
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Query Match	5.9%	Score 113.5	DB 6	Length 798
Similarity	19.6%	Pred. No. 0.0085		
Matches	66	Conservative	63	Mismatches 109, Indels 99, Gaps 17
Qy	OGGRREDS-GPA-----	CYGFPLPYFLIDKSGSV----	LHHNMEIYFVEYQLAH	71
Db	EGVDAEDDHGGEQQRKIVLDPSSMMIYLVLDSDSDISGANSFPGAKKCLVNLLEKVAS			336
Qy	72 KFISFQLMSTFVSTRGTTLMKLT-----	DREQIRQGLEI----	QKVLPGQDTYMHG	123
Db	337 YGVPR--RYGLVATYATYPKIWKVSEADSSNADWTQKLTNEINVEDHKLKSGTNT-----			389
Qy	124 FERASEQIYYENR-----	QGY-RTASVITLITDG-----	ELHEDLFFYSE	162
Db	390 -KKALQAVIYSSMMSWPDVPRGSMNTRIVILIMTGLHNMGGDPITVVIDEIRDLIYIGKD			448
Qy	163 REANRSRDLGAIIVYCVG--VKDFNETQLARLADSKDHVFPVNDGFOALQGIHLSILKKS			220
Db	449 RKNPREDLVDVYFVGVPLVNVQVININALASKKDNGHAFKVD--MENLEDVYQIMDES-			506
Qy	221 IEILAAESTICAGESFOVYVRGNGFRARANDVRLCSFKINDSVTLNEKPSVEDTYLL			280
Db	507 -----QSLSLC-----	GNMWERKRGTD-----	YHKQPMQAKISV--	535
Qy	281 CPAPILKEVGMKALQVSMNDGLSFSSSVIITTHC			317
Db	536 ----IRPSKGHSCHG-----	AVSYSEFVLTAAHC		561

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/ Sequence 294, Application US/10131826A
/ Publication No. US20050245730A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: DeForge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvarcoff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Geritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Guirney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P330R1C128
/ CURRENT APPLICATION NUMBER: US/10/131,826A
/ PRIOR FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: 60/049911
/ PRIOR FILING DATE: 1997-06-18
/ PRIOR APPLICATION NUMBER: 60/056914
/ PRIOR FILING DATE: 1997-08-26
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059115
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059117
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059122
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059184
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059352
/ PRIOR FILING DATE: 1997-09-19
/ PRIOR APPLICATION NUMBER: 60/059588
/ PRIOR FILING DATE: 1997-09-19
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 294
/ LENGTH: 915
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-131-826A-294

Query Match      5.9%; Score 113.5; DB 6; Length 915;
Best Local Similarity 22.4%; Pred. No. 0.01;
Matches 55; Conservative 53; Mismatches 103; Indels 35; Gaps 13;

QY 44 DLYFLIDKSGSV-LHHMNEIYF-VEQLAHKFIISPOL-RMSFVIFSTRTGTL-----MKL 95
DB 57 DLVFIIDSSRSVNTHDYAKKEFIVDILQFLDIGPVTRVGLQY---GSTVKNERSLKT 113
QY 96 TEDREQIROGLELEQKVLPGGDTYMHGFEFASBOQIYENRQGYR-----TASVIALTD 150
DB 114 FRKSEVERAVAKRMHLSTGTMGLAIQY---ALNIAFSEAGARPLRENVPRVIMIVTD 170
QY 151 GELHEDLFFYSERENRSDLGAIYCVGV--KDFNETQLARIADSKDHVPNDGFQAL 208
DB 171 GRPODSV---AEVAKKADTGILIFALGVGVDFMTLKSIGSEPHEDHVFIVAN--FSOI 225
QY 209 OGIIHSILKKSCEIILAAEPSTICAGESFQVVVRNGGFHAR-----NVDRLVCSFKIND 263
DB 226 ETLTVSFQKCLCTAHWCSTLEHNCA--HFCINIPGSYVCRCKOGYILNSDQTTCC--RIOD 281
```

```
QY 264 SVTLNE 269
DB 282 LCAMED 287

RESULT 8
US-11-113-424-39
/ Sequence 39, Application US/11113424
/ Publication No. US20050260713A1
/ GENERAL INFORMATION:
/ APPLICANT: Gangolli et al.
/ TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-225
/ CURRENT APPLICATION NUMBER: US/11/113,424
/ PRIOR FILING DATE: 2005-04-21
/ PRIOR APPLICATION NUMBER: 60/256,704
/ PRIOR FILING DATE: 2000-12-19
/ PRIOR APPLICATION NUMBER: 60/311,590
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: 60/257,314
/ PRIOR FILING DATE: 2000-12-20
/ PRIOR APPLICATION NUMBER: 60/311,613
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: 60/315,617
/ PRIOR FILING DATE: 2001-08-29
/ PRIOR APPLICATION NUMBER: 60/307,506
/ PRIOR FILING DATE: 2001-07-24
/ PRIOR APPLICATION NUMBER: 60/322,358
/ PRIOR FILING DATE: 2001-09-14
/ PRIOR APPLICATION NUMBER: 60/294,075
/ PRIOR FILING DATE: 2001-05-29
/ PRIOR APPLICATION NUMBER: 60/288,153
/ PRIOR FILING DATE: 2001-05-02
/ NUMBER OF SEQ ID NOS: 190
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 39
/ LENGTH: 956
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-113-424-39

Query Match      5.9%; Score 113.5; DB 7; Length 956;
Best Local Similarity 22.4%; Pred. No. 0.01;
Matches 55; Conservative 53; Mismatches 103; Indels 35; Gaps 13;

QY 44 DLYFLIDKSGSV-LHHMNEIYF-VEQLAHKFIISPOL-RMSFVIFSTRTGTL-----MKL 95
DB 57 DLVFIIDSSRSVNTHDYAKKEFIVDILQFLDIGPVTRVGLQY---GSTVKNERSLKT 113
QY 96 TEDREQIROGLELEQKVLPGGDTYMHGFEFASBOQIYENRQGYR-----TASVIALTD 150
DB 114 FRKSEVERAVAKRMHLSTGTMGLAIQY---ALNIAFSEAGARPLRENVPRVIMIVTD 170
QY 151 GELHEDLFFYSERENRSDLGAIYCVGV--KDFNETQLARIADSKDHVPNDGFQAL 208
DB 171 GRPODSV---AEVAKKADTGILIFALGVGVDFMTLKSIGSEPHEDHVFIVAN--FSOI 225
QY 209 OGIIHSILKKSCEIILAAEPSTICAGESFQVVVRNGGFHAR-----NVDRLVCSFKIND 263
DB 226 ETLTVSFQKCLCTAHWCSTLEHNCA--HFCINIPGSYVCRCKOGYILNSDQTTCC--RIOD 281

RESULT 9
US-10-601-368-24
/ Sequence 24, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
```



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/ PRIOR FILING DATE: 2004-12-14
/ PRIOR APPLICATION NUMBER: US04/015040
/ PRIOR FILING DATE: 2004-05-13
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 6
/ LENGTH: 761
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-11-057-047-6

Query Match
Best Local Similarity 20.5%; Score 110.5; DB 7; Length 761;
Matches 71; Conservative 59; Mismatches 99; Indels 117; Gaps 20;

QY 28 OGGRREDG-----GPACYGFDLYFLDKSGSV-----LHWNNEIY 63
DB 240 EGADADGDGSPGQGRKIVLDPG--GSANITIVLDGSDISGNSNTGAKRLTN----- 292
QY 64 YFVEQLAHKRFISPOLMSFIVFSTRTGTTMLKLTEDR-----EQIROGLEBELQVLP 115
DB 293 -LIEKVASYGVR--RYGLLTVAIVPKVLVRVSDERSDADWYTEKLNQISYEDHKLKSG 349
QY 116 GDTYHMEGRASEQIYY-----ENRQGY-RTASVITALTDEGLH-----EDL 157
DB 350 TMT-----KRALQAVYSMMWSMAGDAPRPGMNRTRHVIIMTDG-LHNGGNPVTVIODI 402
QY 158 FPFYSE--REANRERD--LGAIVYCVG--VKDFNETQLARIADSKDHVPFVNDGFOALQGI 211
DB 403 RALDDGRDPKPREYLDVYVGVGPLVDSVININALSKKDEHNVFVKD-MEDLENV 461
QY 212 IHSILKSCIEILAEPSITCAGESFOVYVNGGPFHARNVRLCSFKINDSVTLNEKP 271
DB 462 FYQMIDET-----KSLSLC-----GMVWEHKKGNDYHKQPMQAKISVT---RP 501
QY 272 FSVEDTYLLCPAFLKEVCKKALQVSMNDGLSFISSVIITTHC 317
DB 502 LKQHER---CMGAV-----VSEYFLTPAHC 524

RESULT 13
US-10-601-368-6
/ Sequence 6, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 6
/ LENGTH: 1141
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: (1)...(22)
US-10-601-368-6

Query Match
Best Local Similarity 24.1%; Score 107; DB 6; Length 1141;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

QY 39 CYGFPDLYFLDKSGSVLHHMNEIYFVEQLAHKRF-ISP-QLRMSFIVFSTRTGTTMLKLT 96
DB 159 CQTYMDIYVLDDGNSNI-YPWVEVOHFLINILKKFYIGPQIQGVGVYGDVVEHFEHL- 216
```

```
QY 97 EDREIQROGLEBELQVLPFGDTYHMEGRF--RASEQIYYENRQGYRTASVITALTDEGL 153
DB 217 NDYRSVKDVEAASHIEQRGTETRTARGIETPARSEAFQKGRKAK--KVMIVITDGS 274
QY 154 HED-----LFFYSEEARNSRDLGAIYCVGVKD-----FNETQ 187
DB 275 HDSPDLKVIQOSERDNTRYAVAVLGYNRRGINPETFLNEIKYIASDPDDKHFPNVTD 334
QY 188 LARIADSKDHVPFVNDGFOALQG 210
DB 335 EAAL---KDIYDALGDRIFSLG 354

RESULT 14
US-10-601-368-4
/ Sequence 4, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ LENGTH: 1166
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-601-368-4

Query Match
Best Local Similarity 24.1%; Score 107; DB 6; Length 1166;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

QY 39 CYGFPDLYFLDKSGSVLHHMNEIYFVEQLAHKRF-ISP-QLRMSFIVFSTRTGTTMLKLT 96
DB 137 CQTYMDIYVLDDGNSNI-YPWVEVOHFLINILKKFYIGQIQGVGVYGDVVEHFEHL- 194
QY 97 EDREIQROGLEBELQVLPFGDTYHMEGRF--RASEQIYYENRQGYRTASVITALTDEGL 153
DB 195 NDYRSVKDVEAASHIEQRGTETRTARGIETPARSEAFQKGRKAK--KVMIVITDGS 252
QY 154 HED-----LFFYSEEARNSRDLGAIYCVGVKD-----FNETQ 187
DB 253 HDSPDLKVIQOSERDNTRYAVAVLGYNRRGINPETFLNEIKYIASDPDDKHFPNVTD 312
QY 188 LARIADSKDHVPFVNDGFOALQG 210
DB 313 EAAL---KDIYDALGDRIFSLG 332

RESULT 15
US-10-601-368-3
/ Sequence 3, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
```

```

; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1188
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(22)
US-10-601-368-3

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```

Query Match      5.6%; Score 107; DB 6; Length 1188;
Best Local Similarity 24.1%; Pred. No. 0.061;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

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QY 39 CYGQFDLYFLIDKSGSVLHHNEIYVFVEQLAHKF-ISP-QLRMSFTVFSTRGTTLMKLT 96
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 159 CQTYMDIVIVLDGSNSI-YPMVEVQHFLINILKKFYIGPCQIQGVVQYGEDVVEHFL- 216
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 97 EDREQIRQGLEELQKVLPGDLYMHGEF--RASEQIYYENRQGYRTASVITATDDEL 153
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 217 NDYRSVADVEAASHLEQRGSTETRTAFGIEPARSEAFQKGRKGA--KVMIVITDGS 274
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 154 HED-----LFFYGERBANRSRDLGAIYVCYVKD----FNETQ 187
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 275 HDSPDLEKVIQSERDVTTRYAVAVLGYNRKGINPETFLNELKYLASDPDDKHFRVNTD 334
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 188 LARIADSKDHVPVNDGFOALQG 210
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 335 EAAL---KDIYDALGDRIFSLEG 354
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

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Search completed: December 14, 2005, 11:59:26
 Job time : 6.40815 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:01:37 ; Search time 258.362 Seconds
(without alignments)
2531.884 Million cell updates/sec

Title: US-09-970-076-2

Perfect score: 1914
Sequence: 1 MATERRALDGTGOWLSLAT.....VITKEVPPAPSESENKIK 368

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool/US09970076/runac_14122005_11850_20999/app_query.fasta_1.2410
-DB=Isued_Patents_NA -OPMT=fastcap -SUFFIX=rm1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US09970076 -CCGN_1_1_535 -runac_14122005_11850_20999 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -MAIN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/lna/1.COMB.seq:*
2: /cgn2_6/ptodata/1/lna/5.COMB.seq:*
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4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/lna/H.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/PCTUS.COMB.seq:*
7: /cgn2_6/ptodata/1/lna/PP.COMB.seq:*
8: /cgn2_6/ptodata/1/lna/RE.COMB.seq:*
9: /cgn2_6/ptodata/1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1392	72.7	1609	3	US-09-620-312D-8
2	962.5	50.3	2234	3	US-10-104-047-669
3	891	46.6	3981	3	US-09-799-451-250
4	859	44.9	1492	3	US-09-774-528-297
5	859	44.9	1492	3	US-10-120-988-297
6	240	12.5	450	3	US-10-131-827-8330
7	166	8.7	3519	2	US-08-286-889-45
8	166	8.7	3519	2	US-08-485-618-45
9	166	8.7	3519	2	US-08-362-652-45

10	166	8.7	3519	2	US-08-605-672-45	Sequence 45, Appl
11	166	8.7	3519	2	US-08-482-293A-45	Sequence 45, Appl
12	166	8.7	3519	2	US-08-943-363-45	Sequence 45, Appl
13	166	8.7	3519	3	US-09-193-043-45	Sequence 45, Appl
14	166	8.7	3519	3	US-09-688-307A-45	Sequence 45, Appl
15	166	8.7	3519	3	US-09-350-259-45	Sequence 45, Appl
16	166	8.7	3803	2	US-08-485-618-52	Sequence 52, Appl
17	166	8.7	3803	2	US-08-362-652-52	Sequence 52, Appl
18	166	8.7	3803	2	US-08-605-672-52	Sequence 52, Appl
19	166	8.7	3803	2	US-08-482-293A-52	Sequence 52, Appl
20	166	8.7	3803	2	US-08-943-363-52	Sequence 52, Appl
21	166	8.7	3803	3	US-09-193-043-52	Sequence 52, Appl
22	166	8.7	3803	3	US-09-688-307A-52	Sequence 52, Appl
23	166	8.7	3803	3	US-09-350-259-52	Sequence 52, Appl
24	159.5	8.3	2499	2	US-08-485-618-96	Sequence 96, Appl
25	159.5	8.3	2499	2	US-08-605-672-96	Sequence 96, Appl
26	159.5	8.3	2499	2	US-08-482-293A-96	Sequence 96, Appl
27	159.5	8.3	2499	2	US-08-943-363-96	Sequence 96, Appl
28	159.5	8.3	2499	3	US-09-193-043-96	Sequence 96, Appl
29	159.5	8.3	2499	3	US-09-688-307A-96	Sequence 96, Appl
30	159.5	8.3	2499	3	US-09-350-259-96	Sequence 96, Appl
31	159.5	8.3	3528	2	US-08-286-889-36	Sequence 36, Appl
32	159.5	8.3	3528	2	US-08-485-618-36	Sequence 36, Appl
33	159.5	8.3	3528	2	US-08-362-652-36	Sequence 36, Appl
34	159.5	8.3	3528	2	US-08-605-672-36	Sequence 36, Appl
35	159.5	8.3	3528	2	US-08-482-293A-36	Sequence 36, Appl
36	159.5	8.3	3528	2	US-08-943-363-36	Sequence 36, Appl
37	159.5	8.3	3528	3	US-09-193-043-36	Sequence 36, Appl
38	159.5	8.3	3528	3	US-09-688-307A-36	Sequence 36, Appl
39	159.5	8.3	3528	3	US-09-350-259-36	Sequence 36, Appl
40	159.5	8.3	3597	2	US-08-485-618-54	Sequence 54, Appl
41	159.5	8.3	3597	2	US-08-362-652-54	Sequence 54, Appl
42	159.5	8.3	3597	2	US-08-605-672-54	Sequence 54, Appl
43	159.5	8.3	3597	2	US-08-482-293A-54	Sequence 54, Appl
44	159.5	8.3	3597	2	US-08-943-363-54	Sequence 54, Appl
45	159.5	8.3	3597	3	US-09-193-043-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-09-620-312D-8
; Sequence 8, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Felyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Uian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghaast
; APPLICANT: Dymnanc, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP28
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_fl_genes Version 1.0

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/ SEQ ID NO 8
/ LENGTH: 1609
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (309)..(1202)
US-09-620-312D-8

Alignment Scores:
Pred. No.: 2,046-160 Length: 1609
Score: 1392.00 Matches: 267
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 99.26% Mismatches: 0
Query Match: 72.73% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-2 (1-368) x US-09-620-312D-8 (1-1609)

QY 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
Db 309 ATGGCCACCGCGGAGCGGAGAGCCCTCGGATCGCTTCCAGTGGCTCTTTGGCCACT 368

QY 21 LeuValLeuIleCysAlaGlyGlnGlyGlyArgGluAspGlyGlyProAlaCysTyr 40
Db 369 CTGGTCTCATCTGCGCGGCGAAGGGGACGACGAGGAGATGGGGGTCCAGCTTCTAC 428

QY 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60
Db 429 GCGGGATTGACCTGACTTCACTTGTGACAAATCAGAAAGTGTGTGACCACTGGAAAT 488

QY 61 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
Db 489 GAAATTAATTAATCTTGTGGACAGTGGCTCAAAATTCATCAGCCCAAGTTGAAAG 548

QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
Db 549 TCTTTATTGTTTTCCTCCACCCGAGAGAACAACTTAATGAAATGACAGAGACAGAGA 608

QY 101 GlnIleArgGlnGlyLeuGlnGluLeuValLeuProGlyValAspThrTyrMet 120
Db 609 CAATCGCTCAAGGCTTAGAAGAACTCCAGAAAGTCTGCGAGAGAGACACTTACAG 668

QY 121 HisGluGlyPheGlnuArgAlaSerGlnGlnIleTyrTyrGlnuAspArgGlnGlyTyrArg 140
Db 669 CATGAAGATTGAAAGCGCCAGTAGACAGATTTATTATGAAACAGACAGAGTACAG 728

QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyr 160
Db 729 ACAGCCAGCGTCACTATTGCTTGAATGAGAACTCCATGAAATCTCTTTTCTAT 788

QY 161 SerGluuArgGluuAspArgSerArgAspLeuGluAlaIleValTyrCysValGlyVal 180
Db 789 TCAGAGAGGAGGCTAATAGCTTCAGAGATCTTGAGTGTGTTTAACTGTGTGTGTGTG 848

QY 181 LysAspPheAsnGlnuThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
Db 849 AAAAGATTTCAATAGACACACAGCTGCGCCGATGGCCGACAGTAAAGATCATGTGTTCC 968

QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
Db 909 GTGAAATGACGGCTTTCAGGCTTCGCAAGGCATCATCACTCAATTTTGAAGAAGTCTCG 968

QY 221 IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyLysSerPheGlnValVal 240
Db 969 ATCGAAATTTCTACACACTGAACCATCCACCAATATGTGCAAGAGAGATTCATTTCAGTGTGC 1028

QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
Db 1029 GTGAGAGGAAACGGCTTCCGACATGCCCGGACAGTGGACAGGGTCTCTGCACTTCAAG 1088

QY 261 IleAsnAspSerValThrLeuAsnGlu 269
Db 1155 AsnAspSerValThrLeuAsnGlu 269
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Db 1089 ATCAATGACTCGGTGACACTCAGTAAG 1115

RESULT 2
US-10-104-047-669
/ Sequence 669, Application US/10104047
/ Patent No. 6943241
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: No. 6943241el full length cDNA
/ FILE REFERENCE: H1-A0105
/ CURRENT APPLICATION NUMBER: US/10/104,047
/ CURRENT FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER:
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 669
/ LENGTH: 2234
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-104-047-669

Alignment Scores:
Pred. No.: 1,886-107 Length: 2234
Score: 962.50 Matches: 190
Percent Similarity: 69.13% Conservative: 63
Best Local Similarity: 51.91% Mismatches: 106
Query Match: 50.29% Indels: 7
DB: 3 Gaps: 3

US-09-970-076-2 (1-368) x US-10-104-047-669 (1-2234)

QY 4 AlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThrLeuValLeu 23
Db 535 GCGAGCGGCTCCCGCGCGCGAGCCCGGAGACTGGCTTCCCGCGGTGGCTGTG 594

QY 24 IleCysAlaGlyGlnGlyGly--ArgArgGluAspGlyGlyProAlaCysTyrGlyGly 42
Db 595 GTGCTACGCGGCTCCCGGGGGCTGCTGCGGCCAGAGACACCCCTCGCAGAAAGGCC 654

QY 43 PheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsnGluIle 62
Db 655 TTTGATCTCTTACTTGTCTGAGCAAGTCTGGAGTGTGGCAAAATTAATGATGAAAT 714

QY 63 TyrTyrPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSerPhe 82
Db 715 TATATTCGTACAGCAACTTCCGAGAGATTTGTGAGCCCTGAAATGATGATTCCTTC 774

QY 83 IleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlnGluIle 102
Db 775 ATTGTGTTTCTTCTCAAGCACTATTATTGTGCCATTGAGTGAACAGAGCAAAATC 834

QY 103 ArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyLysAspThrTyrMetHisGlu 122
Db 835 AGTAAAGCTTGAGAGATTAAACGTGTAGCTCCAGTAGAGACATATATTCATGAA 894

QY 123 GlyPheGluArgAlaSerGlnGlnIleTyrTyrGlnuAspArgGlnGlyTyrArgThrAla 142
Db 895 GGCATTAAGCTAGCCAAATGACAAAT-----CAGAAAGCAGAGAGCTTGAAGAACTCC 948

QY 143 SerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGlu 162
Db 949 AGTATCATATATGCTCTGACAGATGGACAGTGGACCGCTGTGCTCATCATATGACAG 1008

QY 163 ArgGluAlaAspArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAsp 182
Db 1009 AAAAGGCAAAAGATATCCAGGTCACTGGGCTAGTGTATGTGTGTGTGTGTGTGTGAT 1068

QY 183 PheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPheProValAsn 202
Db 1069 TTTGAACAAAGCACAGCTTAAAGAAATGCTGATTTCCAGAGACAGATTTTCCCTGTCAAA 1128

QY 203 AspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCysIleGlu 222
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Db      1129 GGTGATTTGAGGCTTTAAAGAAATATTCTATCTACTAGCTCATGTACTGAA 1188
Qy      223 ILLEUUAIALAGUPROSEThrIleCysAlaGlyIleuSerPheGlnValValArg 242
Db      1189 ATCTTAATAATGAGCCCTCAAGTCTGTGTGGGAGAAATTTCAAGATGCTTAACT 1248
Qy      243 GLVAsngIlyPheArgHisAlaArgAsnValAspArgValIleuCysSerPheIleAsn 262
Db      1249 GGAAGAGGATTCATGCTGGGAGCTCGAATGGCAGTCTTCTGCACTTACACTGTAAAT 1308
Qy      263 AspSerValThrIleuAsngIlyuysProPheSerValGluAspThrIlyIleuCysPro 282
Db      1309 GAAACATATACAGAGTGTAAACAGTAAGTACAGCTTAATCTTAAGCTTTGCTT 1368
Qy      283 ALAProIleuIlyuysGluValGlyMetLysAlaIleuGlnValSerMetAsnAspGly 302
Db      1369 GCACCTATCTCGATTAAGCTGGAAACTCTTGATCTTTCAGTACCTTTAATGGAGA 1428
Qy      303 LeuSerPheIleSerSerSerValIleIleThrThrIleCysSerAspGlySerIle 322
Db      1429 AAATCTGCTATTCAGATCATTAATGTACACAGCCACAGAAATGTTAAAGGAGTCGA 1488
Qy      1489 GCCATCATTTGTTTGGTGTACTGCTACTCTGGGAGTCGGTTTGATGTGGTGT 1548
Qy      343 TrpProIleuCysCysThrValIleIleIlyGluValProProProAla----- 359
Db      1549 TGCCCCCTTTCGCAAAAGGTGTTAATTAAGATCTCCACACACCCGCCCTGCACCA 1608
Qy      360 ---GluGluSerGluGlu 364
Db      1609 AAAGAGAGGAAGAAAGAA 1626

RESULT 3
US-09-799-451-250
; Sequence 250, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qiang A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yundong
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Keena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pc_fl_genes Version 2.0
; SEQ ID NO 250
; LENGTH: 3981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (297)..(1118)
US-09-799-451-250
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Alignment Scores:
Pred. No.: 2,87e-98 Length: 3981
Score: 891.00 Matches: 172
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 46.55% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-2 (1-368) x US-09-799-451-250 (1-3981)
Qy      193 AspSerLysAspHisValIlePheProValAsnAspGlyPheGlnIleuGlnIlyIle 212
Db      3 GACAGTAAGGATCATGTGTTCCCGTAAGAAGAGCGCTTACAGGCTCGCAAGCATATC 62
Qy      213 HisSerIleuIlyuysSerCysIleGlnIleuAlaIleuProSerThrIleCys 232
Db      63 CACTCAATTTTGAAGAAGTCTGCATCGAAATTCAGACCTGAACCATCCACCATATGT 122
Qy      233 ALAGlyIleuSerPheGlnValValArgGlyAsngIlyPheArgHisAlaArgAsnVal 252
Db      123 GCAGAGAGTCATTTCAAGTGTGTGAGAGAAAGCGCTTCGACATGCGCCGACATGTG 182
Qy      253 AspArgValIleuCysSerPheIlyIleAsnAspSerValThrIleuAsngIlyuysProPhe 272
Db      183 GACAGGCTCTCTGCAGCTTCAAGATCAATGACTCGGTCACTCAATGAGAAAGCCTTT 242
Qy      273 SerValGluAspThrIlyIleuIleuCysProAlaProIleuIlyuysGluValGlyMetLys 292
Db      243 TCTGTGAAGATCTTAATTAATGTTCTGTCAGCCGCTATTTAAAGAAAGTTGGCATGAAA 302
Qy      293 ALAlaIleuGlnValSerMetAsnAspGlyLeuSerPheIleSerSerValIleIle 312
Db      303 GCTGCACTCCAGGTGACATGAAGAGAGGCTCTCTTTATCTTCAGTTGTGATCATATC 362
Qy      313 ThrThrThrIleCysSerAspGlySerIleIleuAlaIleuIleuIleuPheIleu 332
Db      363 ACCACACACACAGCTTCTGACGTTCCATCTGCGCATGCGCCCTGCTGAGCCGTTCTCTG 422
Qy      333 LeuIleuAlaIleuIleuIleuTrpTrpPheTrpProIleuCysCysThrValIleIleLys 352
Db      423 CTCCTAGCCCTGGCTCTCTCTGTGTGTCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 482
Qy      353 GluValProProProProAlaGluGluSerGluGlu 364
Db      483 GAGTCCCTTCACCCCTCGAGAGAGTGAAGAA 518

RESULT 4
US-09-774-528-297
; Sequence 297, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qiang A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pc_fl_genes Version 2.0
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Seq ID	NO	297	Seq ID	NO	297
1	LENGTH:	1492	1	LENGTH:	1492
2	TYPE:	DNA	2	TYPE:	DNA
3	ORGANISM:	Homo sapiens	3	ORGANISM:	Homo sapiens
4	FEATURE:		4	FEATURE:	
5	NAME/KEY:	CDS	5	NAME/KEY:	CDS
6	LOCATION:	(179) .. (1434)	6	LOCATION:	(179) .. (1434)
7	US-09-774-528-297		7	US-09-774-528-297	
Alignment Scores:					
Pred. NO.:	4.97e-95	Length:	1492		
Score:	859.00	Matches:	165		
Percent Similarity:	71.47%	Conservative:	58		
Best Local Similarity:	52.88%	Mismatches:	83		
Query Match:	44.88%	Indels:	6		
DB:	3	Gaps:	2		
US-09-770-076-2 (1-368) x US-09-774-528-297 (1-1492)					
QY	57	HISHETPRASGNIILetYrYrPheValGIUNLeuAlaHisbysPheIleSerPro	76		
		
DB	16	AATACTGATTGAATTTATATATTCGTACAGCACTGGCAGAGATTGTGACCCCT	75		
QY	77	GlnLeuArgMetSerPheIleValPheSerThrArgGIYThrThreUmetbysLeuThr	96		
		
DB	76	GAATAGAGATTATCTTTCATTGTGTGTTTCTTCACAGCAACTATATTTGGCATTAACT	135		
QY	97	GIuAPARgIUGInIleArgGInGIeUGInGIeUGInLIuValLeuProGIyGIY	116		
		
DB	136	GGAGACAGAGCGCAAAATCAGTAAAGGCTTGAGAGATTAAACGTGTAGTCCAGTAGGA	195		
QY	117	AsPThrTYrMeHIGInLIuYrPheGIuArgAlaSerGIuGInLIeTYrTYrGIuABnArg	136		
		
DB	196	GAGACATATATTCCTAGTAAAGCACTAAAGCTAGCAAGAACAAATTT-----CGAAAGCA	249		
QY	137	GIuGIYTYrArgThrAlaSerValIleIleAlaLeuThrAspGIyGIuLeuHISGIuAsp	156		
		
DB	250	GGAGGCTTGAACAACTCCAGTATCATATTTGCTCTGACAGATGGCAAGTTGACAGGCTG	309		
QY	157	LeuPhePheTYrSerGIuArgGIuAlaAsnArgSerArgAspLeuGIYAlaIleValTYr	176		
		
DB	310	GGCCATCATATGACAGAGAAAGGCAAGATATCCAGGTCACCTGGGGCTAGTGTTAT	369		
QY	177	CysValGIYValIleAspPheAsnGIuThrGInLeuAlaArgIleAlaAspSerIleAsp	196		
		
DB	370	TGTGTGGGGCTCTTGATTTTGAACAAGCACACCTTGAAAGATTCGTGATTCAGAGAG	429		
QY	197	HisValPheProValAsnAspGIYPheGInAlaLeuGInLIYIleHisSerIleLeu	216		
		
DB	430	CAAGTTTTCCTGTCACAAAGTGATTTCAAGGCTCTTAAAGAAATTAATTTCTATCTA	469		
QY	217	LYuSISeSCysIleGIuIleLeuAlaAlaGIuProSerThrIleCysAlaGIyGIuSer	236		
		
DB	490	GCTCAGTCACTGATCAATAATCCATGAAGATGGCACCCCTCAAGTGTGTGTGGGGAGAA	549		
QY	237	PheGInValValIleArgGIYAsnGIYPheArgHisIleAlaArgbAnValAspArgValLeu	256		
		
DB	550	TTTCAGATGTGCTTAAGTGGAAGAGATTCATCTGGGCGAGTCSGAATGCGAGGTGCTC	609		
QY	257	CysSerPheLYuIleAsnAspSerValThrLeuAsnGIuYrProPheSerValGIuAsp	276		
		
DB	610	TGCACCTTACCTGTAAATGAACAATATACACAGAGGTAAACCGATGAAGTCAAGCTT	668		
QY	277	ThrTYrLeuLeuCysProAlaProIleLeuLYeGIuValGIYmetbysAlaAlaLeuGIn	296		
		
DB	670	AATTCATATGCTTGTCTGTCGACCTATCTCGAATAAAGCTGGAGAACTCTTATGTTCA	722		
QY	297	ValSerMetAsnAspGIYLeuSerPheIleSerSerSerValIleIleThrThrHis	316		
		
DB	730	GTGAGCTTTAATGAGAAATCTGTCATTTCAAGATCATTAATTTGACAGCCAGAA	789		
QY	317	CysSerAspGIYSerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeu	336		
		

Db	790	TGTTCTCAACGGGATGCGACCCATCTTTGTTTGGTTCACGCACTCCGGGATC	845
Qy	337	AlaLeuLeuTrpTrpPheTrpProLeuCysCysThrValIleIleIleYsGIuValIProPro	356
Db	850	GGTTTATGTATGGTGGTTTGGCCCTTGTCTGCAAAAGTGGTTATTAAAGATCTCCACCA	909
Qy	357	Pro-----ProIaGIuGIuSerGIuGIu 364	
Db	910	CCACCCCCCTGCAACCAAAAGAGAGAGAGAGA 945	
RESULT 5			
US-10-120-988-297			
Sequence 297, Application US/10120988			
Patent No. 6919193			
GENERAL INFORMATION:			
APPLICANT: Tang, Y. Tom			
APPLICANT: Goodrich, Ryle			
APPLICANT: Liu, Chenghua			
APPLICANT: Ren, Feiyan			
APPLICANT: Wang, Dunrui			
APPLICANT: Drmanac, Radoje T			
TITLE OF INVENTION: No. 6919193el Nucleic Acids and			
FILE REFERENCE: 802CON			
CURRENT APPLICATION NUMBER: US/10/120,988			
PRIOR FILING DATE: 2002-04-11			
PRIOR FILING DATE: 2001-01-30			
NUMBER OF SEQ ID NOS: 441			
SOFTWARE: pc_fl_genes Version 2.0			
SEQ ID NO 297			
LENGTH: 1492			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (79)..(1434)			
US-10-120-988-297			
Alignment Scores:			
Pred. No.: 4,97e-95 Length: 1492			
Score: 859.00 Matches: 165			
Percent Similarity: 71.47% Conservative: 58			
Best local Similarity: 52.88% Mismatches: 83			
Query Match: 44.88% Indels: 2			
DB: 3 Gaps: 6			
US-09-970-076-2 (1-368) x US-10-120-988-297 (1-1492)			
Qy	57	HisHisTrpAsnGluLeuTyrTrpPheValGIuGIuLeuValHisIleYsPheIleSerPro	76
Db	16	AAATAACGATGGATGAAATTTATATATTTCGACACCAACTGGGAGAGATTTGTAGCCCT	75
Qy	77	GlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetIleValThr	96
Db	76	GAATAGAGATTAATCTTCTTCTTGTGTTTCTTCTCAAGCAACATATATTTCACATACT	135
Qy	97	GluAspArgGIuGIuIleArgGlnGlyLeuGIuLeuGIuValLeuProGIyGIy 116	
Db	136	GGAACAAGAGGCAAAATCAGTAAAGGCTTGAGAGATTAAAAACGTTAAGTCCAGTAGGA	195
Qy	117	AspThrTyrMetHisGluGlyPheGIuArgIaSerGIuGIuIleTyrTyrGIuAsnArg	135
Db	196	GAGACATATATCCATCAATCAAGACTTAAAGCTAAGCGAATGAACAAATTT-----CAGAAAGCA	245
Qy	137	GlnGIyTyrArgThrIaSerValIleIleIaIaLeuThrAspGIyGIuLeuHisGIuAsp	156
Db	250	GAGGGCTTGAAACCTCCAGTATCATTAATGCTTGCACAGATGGCAAGTTGGACGGCTG	307
Qy	157	LeuPhePheTyrSerGIuArgGIuIaAsnArgSerArgAspLeuGIyValIleValTyr	175
Db	310	GTGCATCATATGCAGAAAGAGGCAAAAGATATCCAGGTCACTTGGGGCTAGTGTAT	364

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QY 177 CysValGlyValIysAspPheAenGluThrGlnLeuAlaArgIleAlaAspSerIysAsp 196
   |||||
Db 370 TGTGTGGGGCTCTTGAATTTTGAACAAGCAGCTTAAAGAAATGCTGTATTCACAGAG 429
   |||||
QY 197 HisValPheProValAsnAspGlyPheGlnAlaLeuGlnIleIleHisSerIleLeu 216
   |||||
Db 430 CAAGTTTCCCTCTCAAGGATGATTTCAAGCTCTTAAAGAAATTAATTAATTCATACTA 489
   |||||
QY 217 LysLysSerCysIleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSer 236
   |||||
Db 490 GCTCAGCAGTACTAGTAAATCTAGAAATTCAGCCCTCAAGTCTGTGTGTGGGGAGAA 549
   |||||
QY 237 PheGlnValValAlaArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeu 256
   |||||
Db 550 TTTCAAGTTTCTTAAGTGAAGAAGATTCATGCTGGGCACTGGGAATGGCAGTGTCTC 609
   |||||
QY 257 CysSerPheLysIleAsnAspSerValThrLeuAsnGlyLysProPheSerValGluAsp 276
   |||||
Db 610 TGCATTACACTGTAAATGAACAATATACAGAGGTAAACACAGTAAGTATACAGCTT 669
   |||||
QY 277 ThrTyrLeuLeuCysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGln 296
   |||||
Db 670 AATTCATAGCTTGTCTGTCGACCTATCTGAATTAAGCTGAGAACTTGTGATGTTTCA 729
   |||||
QY 297 ValSerMetAsnAspGlyLeuSerPheIleSerSerSerValIleIleThrThrHis 316
   |||||
Db 730 GTACGCTTAAATGAGGAAATCTGTATTCAGATCATTAATTTGTCACAGCAGAA 789
   |||||
QY 317 CysSerAspGlySerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeu 336
   |||||
Db 790 TGTTCATACGGATCGCAGCATCATGTTATTTGTGTATCTGACTACCTGGGGATC 849
   |||||
QY 337 AlaLeuLeuThrTrpPheTrpProLeuCysCysThrValIleIleLysGluValProPro 356
   |||||
Db 850 GGTTCATAGTGTGGTTTGGCCCTTGTCTGCAAAAGTGTATTAAGATCTCTCAACA 909
   |||||
QY 357 Pro-----ProAlaGluGluSerGluGlu 364
   |||||
Db 910 CCACCCCCCTGACCAAAAGAGAGAAAGAA 945
   |||||

RESULT 6
US-10-131-827-8330
; Sequence 8330, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Monigemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCES: 50612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8330
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-8330

Alignment Scores:
Pred. No.: 7,1e-20 Length: 450
Score: 240.00 Matches: 45
Percent Similarity: 65.17% Conservative: 13
Best Local Similarity: 50.56% Mismatches: 30
Query Match: 12.54% Indels: 1
DB: 3 Gaps: 0

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US-09-970-076-2 (1-368) x US-10-131-827-8330 (1-450)

QY 279 LeuLeuCysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSer 298
   |||||
Db 16 ATCTTGTGCTCCGACCTATCTCGAATTAAGCTGGAGAACTCTTGATGTTTCAGTGAGC 75
   |||||
QY 299 MetAsnAspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSer 318
   |||||
Db 76 TTTAAATGAGGAAATCTGTCAATTCAGATCATTAATGTCACAGCAGAAATGTTCT 135
   |||||
QY 319 AspGlySerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeu 338
   |||||
Db 136 AACGGATGACAGCCATCATTTGTTATTTGTTACTGCTACTCTGGGGATCGGTTTG 195
   |||||
QY 339 LeuTrpTrpPheTrpProLeuCysCysThrValIleIleLysGluValProProProP 358
   |||||
Db 196 ATCTGTTGTTTGTGTCCTTGTCTGTAAGTGTATTAAGGATCTCCACACACCCC 255
   |||||
QY 358 AlaGluGluSerGluGluAsnLys 366
   |||||
Db 256 CCTGCACCAAAAGAGAGAGAA 280
   |||||

RESULT 7
US-08-286-889-45
; Sequence 45, Application US/08286889
; Patent No. 5470953
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Mich
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Bornun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,889
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: P38,659
; REFERENCE/DOCKET NUMBER: 27866/32168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3519 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 52..3519
US-08-286-889-45

Alignment Scores:
Pred. No.: 2.42e-09 Length: 3519

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Score:	166.00	Matches:	66
Percent Similarity:	46.15%	Conservative:	422
Best Local Similarity:	28.21%	Mismatch:	96
Query Match:	8.67%	Indels:	30
DB:	2	Gaps:	12

US-09-970-076-2 (1-368) X US-08-286-889-45 (1-3519)

Oy 37 ProAlaCySvTYGlyL---GlyPheAapLeuTYrPheIleLeuAAspYsSerGlySerVal 55
 Db 481 CCAAGTGTCCAGGACCAAGAGATGAGCACTTGGCTTCCTGATTGATGATGGCTCCGGCAGCATT 540
 Oy 56 ---LeuH1sH1sTPAsnGlnIleTYrPheValGlnGlnLeuAlaH1sYsPheIle 74
 Db 541 GATCAAAATGACTTATCCAGCATGGAAGGACTTCGTCAAAGCTTGTATGGCCAGCTGGCG 600
 Oy 75 SerProGlnLeuAAspMetSerPheIleValPheSerThrArgGlyThrThrLeuMetYs 94
 Db 601 AGCACCAGACCTCGTTCTCCCTGATGACATCTCAAAACATCCTGAAGCTCATTTTACC 660
 Oy 95 LeuThrGluAspArg-----GlnGlnIleArgGlnIleGlnGlnLeu 109
 Db 661 TTCACGGATTCAGAGACAGCAGCTGAGCCTCGAGCCTGATGGATGCATGCATGCCAGCTC 720
 Oy 110 GlnIysValLeuProGlyGlyAspThrTYrMetH1sGlnGlyPheGlnArgAlaSerGln 129
 Db 721 CAA-----GGCTGACGTACACAGCCTCGGGCATCCGAAGAGTGCGTAA 765
 Oy 130 GlnIleTYrTYrGluAsnArgGlnGlyTYrArgThrAla---SerValIleIleAlaLeu 148
 Db 766 GAGCATTTTTCATGACAGAAATGGGGCCGAAAAAGTCCAGAGAAATACTAATTGTCATC 825
 Oy 149 ThrAspGlyGlnLeuH1sGlnAspLeuPhePheTYrSerGln-----ArgGlnAlaAsn 166
 Db 826 ACAGATGGGACAGAAATTCAGAAACCCCTCGAGTAAAGACATGTCATCCCTGAAGCGAG 885
 Oy 167 ArgSerArgAspLeuGlyValAlaIleValTYrCyValGlyValIlysAsp---PheAsnGln 185
 Db 886 AAAGCT-----CGGATCATTCGCTATGCTATAGGGGTGGAGATGCTCTCCGGGAA 936
 Oy 186 ---ThrGlnLeuAlaArgIle-----AlaAspSerIysAspH1sValPhe 199
 Db 937 CCCACTGGCCTTCAGAGAGCTGAACACCATTTGGCTCAGCTCCCTCGGAGAGACCACTGGTTC 996
 Oy 200 ProValAsnAspGlyPheGlnIleAlaGlnGlnGlyIleIleH1sSerIleLeuIysIysSer 219
 Db 997 AAGGTGGGCAAT---TTTGTAGACTTCGACAGCATCCAGCGGCAAAATTCAGAGAAA--- 105
 Oy 220 CyvIleGlnIleLeuAlaIleAspProSerThrIleCyAlaGlyGlnSerPheGlnVal 239
 Db 1051 -----ATCTTGGCCATTGAAGGACCGAATCAAGGTCAAGTAGTTCCTTCAGCAC 110
 Oy 240 ValValaArgGlyAsnGlyPheArgH1sAlaArgAsnValAsp 253
 Db 1102 GAGATGTCACAAGAGGTTTACGCTCAGCTCTTCATAGTAT 1143

RESULT 8
US-08-485-618-45

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1 GENERAL INFORMATION:
2
3 APPLICANT: Gallatin, W. Michael
4
5 APPLICANT: Van der Vliet, Monica
6
7 TITLE OF INVENTION: No. 5728533e1 Human 2 Integrin Alpha Subunit
8
9 NUMBER OF SEQUENCES: 103
10
11 CORRESPONDENCE ADDRESS:
12
13 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
14
15 STREET: 233 South Wacker Drive, 6300 Sear Tower
16
17 CITY: Chicago
18
19 STATE: Illinois
20
21 COUNTRY: United States
22
23 ZIP: 60606-6402
24
25 COMPUTER READABLE FORM:
26
27

```

```

1 MEDIUM TYPE: Floppy disk
2
3 COMPUTER: IBM PC compatible
4
5 OPERATING SYSTEM: PC-DOS/MS-DOS
6
7 SOFTWARE: Patent In Release #1.0, Version #1.25
8
9 CURRENT APPLICATION DATA:
10
11 APPLICATION NUMBER: US/08/485,618
12

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CLASSIFICATION: 435
PRIOR APPLICATION DATE: US 08/173,497
APPLICATION NUMBER: DATA
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,885
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,655
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/33
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
MAILING ADDRESS:

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; NAME/KEY: CDS
; LOCATION: 52..3519
US-08-485-618-45

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Alignment Scores:	
Pred. No.:	2,42e+09
Score:	166.00
Percent Similarity:	46.15%
Best Local Similarity:	28.21%
Query Match:	6.67%
PR:	2
Length:	351
Matches:	66
Conservative:	42
Mismatches:	96
Indels:	30
Gaps:	12

US-09-970-076-2 (1-368) x US-08-485-618-45 (1-3519

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Oy      37  prolaCyGyTgYgY--GlyPheAspLeuTyrPheIleLeuAspLysSerGlySerIle 55
Db      481  CCAGAGTGTCCAGGACAAAGATGGACATTCGCTTTCCGATGGATGGCTCCGGACACATT 540
Oy      56  ---LeuHisIeTxDpAngIuIeTyrTyrPheValGIuGIuLeuIaHisLysPheIle 74
Db      541  GATCAAAAGTCACTTACCCCAAGATGAAGACATTGTCAAAGCTTTGATGGGCCAGTTGGCG 600
Oy      75  SerProGIuLeuArgMetSerPheIleValPheSerThiArgGIYThiThiLeuMetLys 94
Db      601  AGCASCACACACCTGTTCTCCCTGATGCAATCTCAAAATCCTGAAGATCTATTTCAC 660
Oy      95  LeuThiGIuAspArg-----GluGIuIleArgGIuGIuLeuGIuLeu 109
Db      661  TTTCACGGAATTCAAAGACAGCCTGAGCCTCAGAGCCTGTGGATGCATGTCGACAGCTC 720
Oy      110  GlnLysValLeuProGIuGIuAspThiThiThiMetHisGIuGIuPheGIuIaGlaSerGIu 129
Db      721  CAA-----GGCCTGACGTACACAGCCTCGGGCATCCAGAAAGGTGTGAA 765
Oy      130  GlnIleTyrTyrGIuAsnAspArgGlnIleTyrIaGlyThiAla---SerValIleIleAlaLeu 148
Db      766  GAGCATATTTCATGCAAGATGGGCGCCGAAAGATGTCACAGAAAGTACTAAATGTGCATC 825
Oy      149  ThiArgGIuGIuLeuHisGIuAspLysPhePheTyrSerGIu-----ArgGIuIaAsn 166

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Db 826 ACAGATGGGCAAAATTACAGACCCCTGGAGTATAGACATGTCTATCCCTGAAGCAG 885
Qy 167 ArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValysAsp---PheAsnGlu 185
Db 886 AAAGCT-----GGATCATTCGCTATGAGGGGGGAGATGCCCTTCGGGAA 936
Qy 186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 199
Db 937 CCCACTGCCCTACAGAGCTGAACACCATTTGGCTCAGCTCCCTCCGACAGACAGCTGTC 996
Qy 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 219
Db 997 AAGGTGGGCAAT---TTGTAGCACTTCGACGATCCAGCGGCAAAATTTCAGAGAAA--- 1050
Qy 220 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyIleGlySerPheGlnVal 239
Db 1051 -----ATCTTTGCCATTGAAGAGAACCGAATCAAGTCAAGTCAAGTCTCTTCAGCAC 1101
Qy 240 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 253
Db 1102 GAAGTGCACAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 9

US-08-362-652-45
; Sequence 45, Application US/08362652
; Patent No. 5766850

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652

FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/32391

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SRO ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 3519 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 52..3519

US-08-362-652-45

Alignment Scores:

Pred. No.: 2,42e-09 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.67% Indels: 30
DB: 2 Gaps: 12

US-09-970-076-2 (1-368) x US-08-362-652-45 (1-3519)

Qy 37 ProAlaCysTyrGly---GlyPheAspLeuTyrPheIleLeuAspLysSerGlySerVal 55
Db 481 CCAGAGTGTCCAGAGACAGAGATGACATTTCTCTTCTGATGATGCTCCGACAGATT 540
Qy 56 ---LeuHisThrPheAsnGluIleTyrTyrPheValGlnGlnLeuAlaHisLysPheIle 74
Db 541 GATCAAGATGATTTACCCAGATGAAGACTTGTCAGAACTTTGATGGCCAGTTGGCG 600
Qy 75 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 94
Db 601 AGCAGCAGACGCTCGTCTCTCCATGACATTAACAACATCTGAAGATCTATTTTACC 660
Qy 95 LeuThrGlnAspArg-----GlnGlnIleArgGlnGlyLeuGluLeu 109
Db 661 TTCACGGAAATTCAGACGACCTGAGCCCTCAGAGCCTGTGGATGCCATCGTCCAGCTC 720
Qy 110 GlnLysValLeuProGlyGlyAspThrTyrMetHisGlnGlyPheGlnArgAlaSerGlu 129
Db 721 CAA-----GGCTGACGTACAGACCTCGGGGATCCAGAAAGTGTGAAA 765
Qy 130 GlnIleTyrGlnAsnArgGlnGlyTyrArgThrAla---SerValIleIleAlaLeu 148
Db 766 GACATATTTCATGACAGATGGGGCCCGAAAGTCCAGAGATCAATTCATTCATC 825
Qy 149 ThrAspGlyGlnLeuHisGlnAspLeuPhePheTyrSerGlu-----ArgGluAlaAsn 166
Db 826 ACAGATGGGCAAAATTACAGACCCCTGGAGTATAGACATGTCAATCCCTGAAGCAGAG 885
Qy 167 ArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValysAsp---PheAsnGlu 185
Db 886 AAAGCT-----GGATCATTCGCTATGAGGGGGGAGATGCCCTTCGGGAA 936
Qy 186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 199
Db 937 CCCACTGCCCTACAGAGCTGAACACCATTTGGCTCAGCTCCCTCCGACAGACAGCTGTC 996
Qy 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 219
Db 997 AAGGTGGGCAAT---TTGTAGCACTTCGACGATCCAGCGGCAAAATTTCAGAGAAA--- 1050
Qy 220 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyIleGlySerPheGlnVal 239
Db 1051 -----ATCTTTGCCATTGAAGAGAACCGAATCAAGTCAAGTCAAGTCTCTTCAGCAC 1101
Qy 240 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 253
Db 1102 GAAGTGCACAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 10
US-08-605-672-45
; Sequence 45, Application US/08605672
; Patent No. 5817515

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA: US 08/362,652
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-605-672-45
Alignment Scores:
Pred. No.: 2,42e-09 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 92
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.67% Indels: 30
DB: 2 Gaps: 12
US-09-970-076-2 (1-368) x US-08-605-672-45 (1-3519)
QY 37 ProAlaCyetyrGly---GlyPheAerPLeuTyPheIleuAerPLeuSerGlySerVal 55
DB 481 CCAAGATGTCACAGACAGACAGATGACATTCCTTCTGATTAATGCTCCGACAGATT 540
QY 56 ---LeuHieHietrPangluIleTyTyPheValGluGluLeuAlaHiePheIle 74
DB 541 GATCAAGTCACTTCCACAGATGAGTCACTGCAAAAGCTTGATGGCCAGTTGGCC 600
QY 75 SerProGluLeuArgIleSerPheIleValPheSerThrArgIleTyHrThiLeuMetIy 94
DB 601 AGCAGACAGACCTGCTTCCTGATGCAATACCAAACTCTGAAAGACTCAATTTTACC 660
QY 95 LeuThiGluAerArg-----GluGluIleArgGluGluGluGluGluLeu 109
DB 661 TTACACGGAATTCAAGACAGACCTGAGACCTGATGATGCAATCCATCCAGCTC 720
QY 110 GlnLysValLeuProGluGlyAerThrTyTyrMetHieGluGluPheGluArgAlaSerGlu 129
DB 721 CAA-----GGCCTGACGTACACAGCTCGGACATCCAGAAAGTGGTGA 765
QY 130 GlnIleTyTyTyrGluAerArgGluGluGluTyTyArgThiAla---SerValIleIleAlaLeu 148
DB 766 GAGCTATTTCATAGCAAGATGGGGCCGAAAGATGTCAGAAAGATCAATTTGTCATC 825

QY 149 ThrAerGlyGluLeuHieGluAerPLeuPhePheTySerGlu-----ArgGluAlaAen 166
DB 826 ACAGATGGGCAAAATTCAGAGACCCCTGAGATATAGCATGTATCCCTGAGACAGAG 885
QY 167 ArgSerAerAerPLeuGlyAlaIleValTyTyCysValGlyValLysAer---PheAenglu 185
DB 886 AAGACT-----GGATCTTCCTGATGCTATGAGGGGTGGAGATGCTTCGCGGAA 936
QY 186 ---ThrGluLeuAlaArgIle-----AlaAerSerLysAerPheValPhe 199
DB 937 CCCACTGCCCTTCAGAGCTGAACACCATTTGGCTCAGCTCCCTCCAGACCAACGTTTC 996
QY 200 ProValAerAerGlyPheGluAlaLeuGluGlyIleIleHieSerIleLeuLysSer 219
DB 997 AAGTGGGCAAT---TTGTAGCACTTCGACAGATCCAGCGCAAAATTCAGAGAA--- 1050
QY 220 CysIleGluIleLeuAlaGluProSerThrIleCysAlaGlyGluSerPheGluVal 239
DB 1051 -----ATCTTGGCACTTGAAGAACCGAATCAAGGTCAAGTATGTTCTTTCAGCAC 1101
QY 240 ValValAerGlyAerGlyPheAerGlyAlaAerAerValAer 253
DB 1102 GAGATGTCACAGAAAGTTTCAGCTCAGCTCCTCATGTGAT 1143
RESULT 11
US-08-482-293A-45
Sequence 45, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

```

FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-482-293A-45

Alignment Scores:
Pred. No.: 2,42e-09      Length: 3519
Score: 166.00           Matches: 66
Percent Similarity: 46.15%      Conservative: 42
Best Local Similarity: 28.21%    Mismatches: 96
Query Match: 8.67%             Indels: 30
DB: 2                     Gaps: 12

US-09-970-076-2 (1-368) x US-08-482-293A-45 (1-3519)

Qy 37 ProAlaCySTyrgly---GlyPheAplLeuTyrrPheileuAplYsSerGlySerVal 55
Db 481 CCAAGAGTGTCCAGACAAAGATGACATTGCTTCTGATTGATGCTCCGGCAGCAT 540
Qy 56 ---LeuHish1eTPraNgliuleTyrrTyrrPheValGluGlnleuAlah1slyPheile 74
Db 541 GATCAAAAGTACCTTACCACAGATGACATTCCTCAAGCTTGATGGCCAGTGGCG 600
Qy 75 SerProGlnleuAryMetSerPheileValPheSerThrArglyThrThrleuMetly 94
Db 601 AGCACCAAGCACTGCTTCTCCCTGATGCAATACCAAACTCCGAAGACTCATTTACC 660
Qy 95 LeuThrGluAparg-----GluGlnleAryGlnGlnleuGluGlu 109
Db 661 TTCACGGAAATTCAGAGCAGCCTGAGCCCTCAGAGCTGTGATGTCATGCTCAGCTC 720
Qy 110 GlnlyValleuProGlyAparThrTyrrMech1sGluGlyPheGluAglaserGlu 129
Db 721 CAA-----GGCTGACGTACACAGCCCTGGCATCCGAAAGTGTGAAA 765
Qy 130 GlnleTyrrGluAparGlnGlyTyrrArgThra---SerValleleAla 148
Db 766 GAGGTATTTCATGCAAGAAATGGGGCCGAAAGTCCCAAGAAATGATTCATTCATC 825
Qy 149 ThrAparGlyleuHish1sGluAparleuPhePheTyrrSerGlu----ArgGluAla 166
Db 826 ACAGATGGGCAAAATTCAGAGACCCCTGGAGTATAGACATGTCATCCCTGAAGCAGAG 885
Qy 167 ArgSerArgAparleuGlyAlaValleValTyrrCyrrValGlyVallyApar---PheA 185
Db 886 AAAGCT-----GGGATCATTCGCTATGCTATAGAGGGGAGGATGCTTCGGGAA 936
Qy 186 ---ThrGlnleuAlaArglyle-----AlaAparSerlyAparHishValPhe 199
Db 937 CCCACTGCCCTACAGAGCTGACACATTCGCTGAGCTCCCTGCGAGACACAGCTTTC 996
Qy 200 ProValAparAparGlyPheGlnAlaLeuGlnGlyleleHishSerleleuAllySer 219
Db 997 AAGGTGGGCAAT---TTGTAGACATTCGCGAGCTCAGAGGCAAAATTCAGAGAAA--- 1050
Qy 220 CysleleGlnleuAlaGluPProSerThrleCyrrAglGlySerPheGlnVal 239
Db 1051 -----ATCTTGCCATTGAGAGAAACCAATCAAGGTCAGTACTCTTCCTTCAGCAC 1101
Qy 240 ValValArgGlyAengGlyPheAryHish1AparGluValApar 253
Db 1102 GAATGTCAAGAAAGTTTCACTGCTGCTCTCATGAT 1143

RESULT 12
US-08-943-363-45
Sequence 45, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: Van der Vlieten, Monica
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:

```

```

ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-943-363-45

Alignment Scores:
Pred. No.: 2,42e-09      Length: 3519
Score: 166.00           Matches: 66
Percent Similarity: 46.15%      Conservative: 42
Best Local Similarity: 28.21%    Mismatches: 96
Query Match: 8.67%             Indels: 30
DB: 2                     Gaps: 12

US-09-970-076-2 (1-368) x US-08-943-363-45 (1-3519)

Qy 37 ProAlaCySTyrgly---GlyPheAplLeuTyrrPheileuAplYsSerGlySerVal 55
Db 481 CCAAGAGTGTCCAGACAAAGATGACATTGCTTCTGATTGATGCTCCGGCAGCAT 540
Qy 56 ---LeuHish1eTPraNgliuleTyrrTyrrPheValGluGlnleuAlah1slyPheile 74
Db 541 GATCAAAAGTACCTTACCACAGATGACATTCCTCAAGCTTGATGGCCAGTGGCG 600
Qy 75 SerProGlnleuAryMetSerPheileValPheSerThrArglyThrThrleuMetly 94
Db 601 AGCACCAAGCACTGCTTCTCCCTGATGCAATACCAAACTCCGAAGACTCATTTACC 660
Qy 95 LeuThrGluAparg-----GluGlnleAryGlnGlnleuGluGlu 109
Db 661 TTCACGGAAATTCAGAGCAGCCTGAGCCCTCAGAGCTGTGATGTCATGCTCAGCTC 720
Qy 110 GlnlyValleuProGlyAparThrTyrrMech1sGluGlyPheGluAglaserGlu 129
Db 721 CAA-----GGCTGACGTACACAGCCCTGGCATCCGAAAGTGTGAAA 765

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; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3516)
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-688-307A-45

Alignment Scores:
Pred. No.: 2,42e-09 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.67% Indels: 30
DB: 3 Gaps: 12

US-09-970-076-2 (1-368) x US-09-688-307A-45 (1-3519)
Qy ProLaCyTyrGly---GlyPheApyLeuTyRpheIleuApyLysSerGlySerVal 55
Db 481 CCAAGAGTGTCCAGACAAAGAGATGGACATTCCTTCTGATGATGCTCCGCGACAT 540
Qy 56 ---LeuH1stRpaNgLuIleTyTyRpheValGluGlnLeuAlaH1slyvPheIle 74
Db 541 GATCAAGTGAATTTACCCAGATGAGAACTTCGTCAAAGCTTGATGGCGCAGTTGGCG 600
Qy 75 SerProGlnLeuApyMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 94
Db 601 AGCACCGACACCTGTTCTCTCCGTGATCAATCAACATCTGAAAGACTCATTTTACC 660
Qy 95 LeuThrGluApyArg-----GluGlnIleArgGlnGlyLeuGluGlnLeu 109
Db 661 TTCACGGAATTTCAAGACAGACAGCTGAGCCCTCAGAGCTGGGATGCCATCTCCACTC 720
Qy 110 GlnIleValLeuProGlyApyThrTyRmechIleGluGlyPheGluArgAlaSerGlu 129
Db 721 CAA-----GGCTGACGTACACAGCTCGGCGACACAGAAAGTGTGAA 765
Qy 130 GlnIleTyTyRglnApyArgGlnGlyTyArgThrAla---SerValIleIleAlaLeu 148
Db 766 GAGCTATTTCATAGCAAGAAATGGGGCCGAAAGTCCCAAGAAATTAATGTGATC 825
Qy 149 ThrApyGlyGluLeuH1sGluApyLeuPhePheTyRserGlu-----ArgGluAlaAsn 166
Db 826 ACAGATGGCGCAAAATTCAGAGACCCCTGAGATAGACATGTCATCTCTGAAGCAGAG 885
Qy 167 ArgSerArgApyLeuGlyAlaIleValTyRcysValGlyValIlyApyR---PheAsnGlu 185
Db 886 AAAGCT-----GGGATCATTCGCTATGCTATAGGGGGTGGAGATGCTTCGGGAA 936
Qy 186 ---ThrGlnLeuAlaArgIle-----AlaApySerLysApyPheIleValPhe 199
Db 937 CCCACTGCCCTACAGAGACGTGAACACCATGGCTCCTCCCTGCGAGACACAGTCTTC 996
Qy 200 ProValApyApyGlyPheGlnAlaLeuGlnGlyTyRleuH1sSerIleLeuLysLysSer 219
Db 997 AAGGTGGGCAAT---TTTGACACTTCGCGACATCCAGCGCGCAATTCAGAGAAA--- 1050
Qy 220 CysIleGluIleLeuAlaAlaGluPProSerThrIleCysAlaGlyLysSerPheGlnVal 239
Db 1051 -----ATCTTGCCATTGAGAAAGAAATGCAAGATCAAGTCAAGTCAAGTCTTCACAC 1101
Qy 240 ValValArgGlyApyGlyPheApyGlyAlaArgApyValApy 253
Db 1102 GAGATGTCACAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 15
US-09-350-259-45
; Sequence 45: Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vlieten, Monica
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; TITLE OF INVENTION: No. 6620915el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 45
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3516)
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-350-259-45

Alignment Scores:
Pred. No.: 2,42e-09 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.67% Indels: 30
DB: 3 Gaps: 12

US-09-970-076-2 (1-368) x US-09-350-259-45 (1-3519)
Qy 37 ProLaCyTyrGly---GlyPheApyLeuTyRpheIleuApyLysSerGlySerVal 55
Db 481 CCAAGAGTGTCCAGACAAAGAGATGGACATTCCTTCTGATGATGCTCCGCGACAT 540
Qy 56 ---LeuH1stRpaNgLuIleTyTyRpheValGluGlnLeuAlaH1slyvPheIle 74
Db 541 GATCAAGTGAATTTACCCAGATGAGAACTTCGTCAAAGCTTGATGGCGCAGTTGGCG 600
Qy 75 SerProGlnLeuApyMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 94
Db 601 AGCACCGACACCTGTTCTCTCCGTGATCAATCAACATCTGAAAGACTCATTTTACC 660
Qy 95 LeuThrGluApyArg-----GluGlnIleArgGlnGlyLeuGluGlnLeu 109
Db 661 TTCACGGAATTTCAAGACAGACAGCTGAGCCCTCAGAGCTGGGATGCCATCTCCACTC 720
Qy 110 GlnIleValLeuProGlyApyThrTyRmechIleGluGlyPheGluArgAlaSerGlu 129
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Qy 130 GlnIleTyTyRglnApyArgGlnGlyTyArgThrAla---SerValIleIleAlaLeu 148
Db 766 GAGCTATTTCATAGCAAGAAATGGGGCCGAAAGTCCCAAGAAATTAATGTGATC 825
Qy 149 ThrApyGlyGluLeuH1sGluApyLeuPhePheTyRserGlu-----ArgGluAlaAsn 166
Db 826 ACAGATGGCGCAAAATTCAGAGACCCCTGAGATAGACATGTCATCTCTGAAGCAGAG 885
Qy 167 ArgSerArgApyLeuGlyAlaIleValTyRcysValGlyValIlyApyR---PheAsnGlu 185
Db 886 AAAGCT-----GGGATCATTCGCTATGCTATAGGGGGTGGAGATGCTTCGGGAA 936
Qy 186 ---ThrGlnLeuAlaArgIle-----AlaApySerLysApyPheIleValPhe 199
Db 937 CCCACTGCCCTACAGAGACGTGAACACCATGGCTCCTCCCTGCGAGACACAGTCTTC 996
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OM protein - nucleic search, using frame_plus_p2n model

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(without alignments)
2581.163 Million cell updates/sec

Title: US-09-970-076-2

Perfect score: 1914

Sequence: 1 MATERRALGIGFQWLSLAT.....VIVKEVPPPEASESENKIK 368

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications_NA_Main: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1914	100.0	1454	US-10-133-937-58	Sequence 59, Appl1
3	1914	100.0	1454	US-10-159-563-58	Sequence 58, Appl1
4	1894	99.0	5540	US-09-918-715-176	Sequence 176, Appl1
5	1894	99.0	5540	US-09-918-715-231	Sequence 231, Appl1
6	1894	99.0	5540	US-10-301-822-198	Sequence 198, Appl1
7	1894	99.0	5540	US-10-474-794-176	Sequence 176, Appl1
8	1894	99.0	5540	US-10-474-794-231	Sequence 231, Appl1

9	1894	99.0	5540	US-10-979-159-176	Sequence 176, App
10	1894	99.0	5540	US-10-979-159-231	Sequence 231, App
11	1894	99.0	5540	US-11-047-278-5	Sequence 5, Appl1
12	1793	93.7	5220	US-09-918-715-186	Sequence 186, Appl1
13	1793	93.7	5220	US-09-918-715-300	Sequence 300, App
14	1793	93.7	5220	US-10-474-794-186	Sequence 186, App
15	1793	93.7	5220	US-10-474-794-300	Sequence 300, App
16	1793	93.7	5220	US-10-979-159-186	Sequence 186, App
17	1793	93.7	5220	US-10-979-159-300	Sequence 300, App
18	1661	86.8	1674	US-10-038-307-17	Sequence 17, Appl1
19	1661	86.8	1674	US-10-201-292-17	Sequence 17, Appl1
20	1650	86.2	1650	US-10-038-307-11	Sequence 13, Appl1
21	1650	86.2	1650	US-10-038-307-15	Sequence 15, Appl1
22	1650	86.2	1650	US-10-201-292-13	Sequence 13, Appl1
23	1650	86.2	1650	US-10-201-292-15	Sequence 15, Appl1
24	1649	86.2	1056	US-10-038-307-23	Sequence 23, Appl1
25	1649	86.2	1056	US-10-201-292-23	Sequence 23, Appl1
26	1649	86.2	1713	US-10-038-307-19	Sequence 19, Appl1
27	1649	86.2	1713	US-10-201-292-19	Sequence 19, Appl1
28	1649	86.2	2112	US-11-047-278-7	Sequence 7, Appl1
29	1649	86.2	2272	US-09-796-753-11	Sequence 11, Appl1
30	1649	86.2	2272	US-10-038-307-1	Sequence 1, Appl1
31	1649	86.2	2272	US-10-201-292-1	Sequence 1, Appl1
32	1649	86.2	2333	US-10-198-846-9957	Sequence 9957, App
33	1640	85.7	1650	US-10-038-307-9	Sequence 9, Appl1
34	1640	85.7	1650	US-10-201-292-9	Sequence 9, Appl1
35	1636	85.5	1008	US-10-038-307-25	Sequence 25, Appl1
36	1636	85.5	1008	US-10-201-292-25	Sequence 25, Appl1
37	1634.5	85.4	1047	US-10-038-307-21	Sequence 21, Appl1
38	1634.5	85.4	1047	US-10-201-292-21	Sequence 21, Appl1
39	1548	80.9	1608	US-10-062-674-1757	Sequence 1757, App
40	1520	79.4	2397	US-10-038-307-11	Sequence 11, Appl1
41	1509	78.8	1623	US-10-201-292-11	Sequence 11, Appl1
42	1509	78.8	1623	US-10-201-292-13	Sequence 13, Appl1
43	1423	74.3	1534	US-10-037-270-8	Sequence 8, Appl1
44	1392	72.7	1609	US-10-117-722-8	Sequence 8, Appl1
45	1392	72.7	1609	US-10-117-722-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-11-047-278-1
; Sequence 1, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Antitoxin Receptor
; FILE REFERENCE: 960296, 97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (104)..(1207)
US-11-047-278-1
Alignment Scores:
Pred. No.: 4,876-229
Score: 1914.00
Percent Similarity: 100.00%
Length: 1414
Matches: 368
Conservative: 0

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DB 624 TCAGAGAGGAGGCTTAATAGATCTCGAGATCTTGCGCAATGGTTAATCTGTGGTG 663
QY 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
DB 684 AAGATTTCATAGACACAGCTGGCCGGATTGGCGAGTAAGATCATGTGTTTCCC 743
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuValLysSerCys 220
DB 744 GTCAATGACCGCTTTCAGGCTTCGCAAGGCATCATCAATTTTGAAGAGTCTGCG 803
QY 221 IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyLysSerPheGlnValVal 240
DB 804 ATCGAATTCCTAGACGTGAACCATCCACATATGTGACAGAGAGTCATTTCAAGTTGTC 863
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
DB 864 GTGAGAGGAAACGGCTTCGACATGCCGCAAGCTGACAGGGCTCTGCGACCTTCAG 923
QY 261 IleAsnAspSerValThrLeuAsnGlyLysProPheSerValGluAspThrTyrLeuLeu 280
DB 924 ATCAATGACTCGGTCACTCAATGAGAACCTTTTCTGTGGAAGACACTTATTTACTG 983
QY 281 CysProAlaProIleLeuLysGlyValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
DB 984 TGTCACGCGCTTATCTTAAGAAGATTGTCATGAAGCTGCTCCAGGTCACATGAAC 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
DB 1044 GATGGCTCTCTTTTATCTCAGATTCGTATCATCCACACACACTTTCTGACGCT 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuTyr 340
DB 1104 TCCATCTGGCCATCGCCCTGCTGATCTCTGCTCTGCTCTGCTCTGCTCTGCTG 1163
QY 341 ThrPheThrProLeuCysCysThrValIleIleIleGlyValProProProAlaGlu 360
DB 1164 TGGTTCTGGCCCTCTGCTGCTGCTGATTAATCAAGAGGCTCCCTCCACCCCTGCGAG 1223
QY 361 GluSerGlyGluAsnLysIleLys 368
DB 1224 GAGAGTGAGGAAATTAATAATA 1247

RESULT 3
US-10-159-563-58
; Sequence 58, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Melzer, Paul
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-58

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Pred. No.: 5,1e-229 Length: 1454
Score: 1914.00 Matches: 368
Percent Similarity: 100.004 Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-970-076-2 (1-368) x US-10-159-563-58 (1-1454)

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DB 144 ATGGCCACGGCGGAGGAGGAGGCTCGGCATGCGCTCCAGTGGCTCTTTGGCCACT 203
QY 21 LeuValLeuIleCysAlaGlyGlnGlyArgArgGluAspGlyGlyProAlaCysTyr 40
DB 204 CTGGTCTCATCTGCGCCGGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCCTCTAC 263
QY 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerAlaLeuHisIleTyrAsn 60
DB 264 GGGGATTGACCTGTATCTTCAATTTGACCAATTCAGAAAGTGTGTGACCCACTGAAT 323
QY 61 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
DB 324 GAAATCTATTACTTTGTGAAACGTTGGCTCAACAATTCATCAGCCCAAGTTGAAATG 383
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
DB 384 TCCTTATTATTGTTTCTCCACCGAGGAAACACTTATGAACTGACAGAAACAGAA 443
QY 101 GlnIleArgGlnGlyLeuGlnGlnLysValLeuProGlyGlyAspThrTyrMet 120
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DB 504 CATGAAGATTTCAGAGGCGGCAATGACATTTATTAAGAAACAGACAGGTTACAGG 563
QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGluAspLeuPheTyr 160
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QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyValAlaIleValTyrCysValGlyVal 180
DB 624 TCAGAGAGGAGGCTTAATAGATCTCGAGATCTTGCGCAATGGTTAATCTGTGGTG 663
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DB 744 GTCAATGACCGCTTTCAGGCTTCGCAAGGCATCATCAATTTTGAAGAGTCTGCG 803
QY 221 IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyLysSerPheGlnValVal 240
DB 804 ATCGAATTCCTAGACGTGAACCATCCACATATGTGACAGAGTCATTTCAAGTTGTC 863
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
DB 864 GTGAGAGGAAACGGCTTCGACATGCCGCAAGCTGACAGGGCTCTGCGACCTTCAG 923
QY 261 IleAsnAspSerValThrLeuAsnGlyLysProPheSerValGluAspThrTyrLeuLeu 280
DB 924 ATCAATGACTCGGTCACTCAATGAGAACCTTTTCTGTGGAAGACACTTATTTACTG 983
QY 281 CysProAlaProIleLeuLysGlyValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
DB 984 TGTCACGCGCTTATCTTAAGAAGATTGTCATGAAGCTGCTCCAGGTCACATGAAC 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
DB 1044 GATGGCTCTCTTTTATCTCAGATTCGTATCATCCACACACACTTTTCTGACGCT 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuTyr 340
DB 1104 TCCATCTGGCCATCGCCCTGCTGATCTCTGCTCTGCTCTGCTCTGCTCTGCTG 1163

QY 341 TrpPheTrpProLeuCySeThrValIleIleIleGluValProProProAlaGlu 360
DB 1164 TGGTTCGGCCCTCTGCTGCACTGATTCAGAGAGTCCCTCCACCTGCGAG 1223
QY 361 GluSerGluGluAsnIleIleIle 368
DB 1224 GAGAGTGAGGAAATGAAATGAAA 1247
RESULT 4
US-09-918-715-176
/ Sequence 176, Application US/09918715
/ Publication No. US20030017157A1
/ GENERAL INFORMATION:
/ APPLICANT: Brad St. Croix
/ APPLICANT: Bert Vogelstein
/ APPLICANT: Kenneth Kinzler
/ TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
/ FILE REFERENCE: 1107.00134
/ CURRENT APPLICATION NUMBER: US/09/918, 715
/ PRIOR FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: 60/222,599
/ PRIOR FILING DATE: 2000-08-02
/ PRIOR APPLICATION NUMBER: 60/224,360
/ PRIOR FILING DATE: 2000-08-11
/ PRIOR APPLICATION NUMBER: 60/282,850
/ PRIOR FILING DATE: 2000-04-11
/ NUMBER OF SEQ ID NOS: 358
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 176
/ LENGTH: 5540
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-918-715-176
Alignment Scores:
Pred. No.: 1,486-225 Length: 5540
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.96% Indels: 0
DB: 3 Gaps: 0
US-09-970-076-2 (1-368) x US-09-918-715-176 (1-5540)
QY 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
DB 144 ATGGCCACGGCGGAGCGAGAGCCCTCGCATCGCTTCAGTGGCTCTTTGGCCACT 203
QY 21 LeuValLeuIleCySaIaGlyGlnIleGlyArgArgGluAspGlyGlyProAlaCybTyx 40
DB 204 CTGGTCTCATCTGCGCCCGGCAAGGGGAGCGCAGGAGATGGGGGTCCAGCTCTCAG 263
QY 41 GlyIlePheAspLeuTyrrPheIleLeuAspLeuSerGlySerValLeuHisIleTPAan 60
DB 264 GGGGGAATTTGACCTGTAATTCATTTTGGCAAAATCGAAGTGTGCTGCACCACTGAAAT 323
QY 61 GluIleTyrrPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80
DB 324 GAATCTAATTAATCTTTGGAAACAGTTGGCTCACAAATTCACAGCCACGTTGAGAAATG 383
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLeuSerLeuThrGluAspArgGlu 100
DB 384 TCTTTATTTGTTTCTTCCACCCGAGAAACAACCTTAATGAAATGACAGAAAGACAGAA 443
QY 101 GlnIleArgGlnIleLeuGlnIleLeuGlnIleValLeuProGlyGlyAspThrTyrrMet 120
DB 444 CAATCCGTCAGAGCCCTAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG 503
QY 121 HisGluGlyPheGluArgAlaSerGluGlnIleTyrrTyrrGluAsnArgGlnIleTyrrArg 140
DB 504 CATGAAGGATTTGAAAGGCGCAGATGAGCAGATTTATTTATGAAACAGAAAGGATCAGG 563

QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyx 160
DB 564 ACAGCCAGGCGTCATGATGCTTTGACTGATGAGAACTCCATGAAGATCTTTTTCAT 623
QY 161 SerGluArgGluAlaAspArgSerArgAspLeuGlyAlaIleValTyrrCybValGlyVal 180
DB 624 TCAGAGAGGAGGCTTAATGATGCTTCGAGATCTTGGCAATGTTTACTGTGTGGTGG 683
QY 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
DB 684 AAGATTTCAATGAGACACACGCTGCCGAGATGGCGGACAGTAAAGATCATGTGTTTCC 743
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnIleIleHisSerIleLeuIleLysSerCyS 220
DB 744 GTGAATGACGCGCTTCAGGCTCTGCAGAGCATCATCTCAATTTTGAAGAGTCTCC 803
QY 221 IleGluIleLeuAlaGluProSerThrIleCySaIaGlyGluSerPheGlnValI 240
DB 804 ATCGAAATTTGACGAGCTGAACCATTCACCATATGTGCAGAGAGTCATTTCAAGTTGTC 863
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCySerPheLys 260
DB 864 GTGAGAGGAAACGCTTCGACATGCCCGCAACGTGACAGGGTCTCTGCAAGCTTCAAG 923
QY 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrrLeu 280
DB 924 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGGAAGATCTTATTTACTG 983
QY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaIleLeuGlnValSerMetAn 300
DB 984 TGTCCAGCGCTATCTTAAGAAAGTGCATGAAAGCTGCACTCCAGGTCAAGCATGAAC 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCySerAspGly 320
DB 1044 GATGGCTCTCTTTATCTCCAGTCTGTGCATCATCACCAACACAGTGTGACGGT 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuTrp 340
DB 1104 TCCATCTTGCCATGCGCCCTGCTGATCCGTTCCTGCTCTGAGCCCTGCTCTCTG 1163
QY 341 TrpPheTrpProLeuCySeThrValIleIleIleGluValProProProAlaGlu 360
DB 1164 TGGTTCGGCCCTCTGCTGCACTGATTCAGAGAGTCCCTCCACCTGCGAG 1223
QY 361 GluSerGluGlu 364
DB 1224 GAGAGTGAGGAA 1235
RESULT 5
US-09-918-715-231
/ Sequence 231, Application US/09918715
/ Publication No. US20030017157A1
/ GENERAL INFORMATION:
/ APPLICANT: Brad St. Croix
/ APPLICANT: Bert Vogelstein
/ APPLICANT: Kenneth Kinzler
/ TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
/ FILE REFERENCE: 1107.00134
/ CURRENT APPLICATION NUMBER: US/09/918, 715
/ PRIOR FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: 60/222,599
/ PRIOR FILING DATE: 2000-08-02
/ PRIOR APPLICATION NUMBER: 60/224,360
/ PRIOR FILING DATE: 2000-08-11
/ PRIOR APPLICATION NUMBER: 60/282,850
/ PRIOR FILING DATE: 2000-04-11
/ NUMBER OF SEQ ID NOS: 358
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 231
/ LENGTH: 5540
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-918-715-231

Alignment Scores:

Pred. No.: 1,48e-225 Length: 5540
 Score: 1894.00 Matches: 364
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.96% Indels: 0
 DB: 3 Gaps: 0

US-09-970-076-2 (1-368) x US-09-918-715-231 (1-5540)

```

QY 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaTrp 20
DB 144 ATGGCCACGGCGGAGGCGAGAGCCCTCGGCATCGGCTTCACAGTGGCTCTTTGGCCACT 203

QY 21 LeuValLeuIleCySaAlaGlyIngIyGlyArgArgGluAspGlyGlyProAlaCyArg 40
DB 204 CTGGTCTCATCTGCGCGCGGCAAGGGGGAACGACAGGAGGATGGGGGTCCAGCCTGCTAC 263

QY 41 GlyGlyPheAspLeuTrpPheIleLeuAspLeuSerGlySerValLeuHisIleTrpAsn 60
DB 264 GGGGATTGACCTGATCTTCTTATTTGGACAATCAGAAATGCTGTGACACCACTGGAAT 323

QY 61 GluIleTyTrPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80
DB 324 GAATCTATTACTTGTGGAAACAGTTGGCTCAAAATTCATGACCCACAGTTGAGAAATG 383

QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetIleLeuThrGluAspArgGlu 100
DB 384 TCTTTATTGTTTCTCCACCAGGAAACAACCTTAATGAACTGACAGAAAGACAGAA 443

QY 101 GlnIleArgGlnIleLeuGluLeuGlnIleValLeuProGlyGlyAspThrTrpMet 120
DB 444 CAATCCGTCAGAGCCCTAGAAAGACTCCAGAAAGTTCTGACAGAGAGACACTTACATG 503

QY 121 HisGluGlyPheGluArgAlaSerGluGlnIleTyTrPheGluAsnArgGlnIyTyArg 140
DB 504 CATGAAGATTGTAAGAGGCGCAAGTGAAGATTTATTATGAAACAGACAGAGGTACAG 563

QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTy 160
DB 564 ACAGCCAGCGCTCATCTGCTTGTGACTGATGAGAACTCCATGAAGATCTCTTTCTAT 623

QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyArgValGlyVal 180
DB 624 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCATCTTTAATGCTGTGAGTGTG 683

QY 181 LysAspPheAsnGluTrpGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
DB 684 AAGGATTTCAATAGACACAGCTGGCCCGGATTTGGACAGTAAAGATCATGTGTTCCC 743

QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIySylSerCy 220
DB 744 GTGATATGAGCGCTTTTCAGGCTCTGCAAGGATCATCATCAATTTTGAAGAGTCTCG 803

QY 221 IleGluIleLeuAlaIleGluProSerThrIleCySaAlaGlyGluSerPheGlnVal 240
DB 804 ATCGAAATCTTACAGCTGAAACATCCATATGTCAGAGAAAGCATTTCAAGTTGTC 863

QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCySerPheLys 260
DB 864 GTGAGAGGAAACGGCTTCCACATGCCCCGCAAGTGAACAGGGTCTCTGACACTTCAG 923

QY 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyLeuLeu 280
DB 924 ATCAATGACTCGGTCACTCAATGAGAAACCTTTTCTGTGGAAGTACTTATTATCTG 983

QY 281 CysProAlaProIleLeuLysGluValGlyMetIleAlaIleGlnIleValSerMetAsn 300
DB 984 TGTCCAGCGCTTATCTTAAAGAAAGTGGCATGAAAGCTGCACTCCAGGTCACATGAAAC 1043

QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
  
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DB 1044 GATGGCTCTCTTTATCTCCAGTTCTGTCATCATCACCACACACTGTTTCAGCGT 1103

QY 321 SerIleLeuAlaIleAlaIleLeuIleLeuPheLeuLeuAlaIleLeuTrp 340
DB 1104 TCCATCTGTCGATGCGCCCTGCTGATCCGTTCTGCTCTGACCTGCTCTCTCTG 1163

QY 341 TrpPheTrpProLeuCySaThrValIleIleLysGluValProProProAlaGlu 360
DB 1164 TGGTTTGACCCCTCTGCTGCACTGATTCATGAGAGGTCCCTCCACCCCTGCCAG 1223

QY 361 GluSerGluGlu 364
DB 1224 GAGAGTGAAGAA 1235

RESULT 6
US-10-301-822-198
; Sequence 198, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144) ... (1838)
US-10-301-822-198

Alignment Scores:
Pred. No.: 1,48e-225 Length: 5540
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.96% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2 (1-368) x US-10-301-822-198 (1-5540)

QY 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaTrp 20
DB 144 ATGGCCACGGCGGAGGCGAGAGCCCTCGGCATCGGCTTCACAGTGGCTCTTTGGCCACT 203

QY 21 LeuValLeuIleCySaAlaGlyIngIyGlyArgArgGluAspGlyGlyProAlaCyArg 40
DB 204 CTGGTCTCATCTGCGCGCGGCAAGGGGGAACGACAGGAGGATGGGGGTCCAGCCTGCTAC 263

QY 41 GlyGlyPheAspLeuTrpPheIleLeuAspLeuSerGlySerValLeuHisIleTrpAsn 60
DB 264 GGGGATTGACCTGATCTTCTTATTTGGACAATCAGAAATGCTGTGACACCACTGGAAT 323

QY 61 GluIleTyTrPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80
  
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DB 324 GAAATCTATTACTTTGTGGAACAGTGGCTCACAAATTCATCGCCACAGTTGAGAAAG 383
QY Serphe11eValPheSerThraGlyYThrThrLeuMetLysLeuThrGluAspArgGlu 100
DB 384 TCCCTTATTGTTTCTCCACCCGAGGAAACACTTAATGAAATGACAGAAAGACAGAGAA 443
QY Gln11eArgGlnGlyLeuGluGluLeuGlnLysValLeuProGlyGlyAspThrTyrmec 120
DB 444 CAATTCGTCAGAGCCTTAGAAGAACTCCAGAAAGTTCTGCGAGGAGAGACCTTACAG 503
QY H1sgLuglyPheGluArgAlaSerGluGln11eTyTyTyGluAsnArgGlnGlyTyArg 140
DB 504 CATGAAGGATTGAAAGGCGCAGTGCAGATTTATTATGAAACAGACAGAGGTCACAG 563
QY ThrAlaSerVal11e11eAlaLeuThrPheGlyGluLeuH1sgLysAspLeuPhePheTy 160
DB 564 ACAGCCAGGCTCATCTGCTTGACTGATGAGAACTCCATGAAAGATCTTTTCTAT 623
QY SerGluArgGluAlaAsnArgSerArgAspLeuGlyAla11eValTyTyCysValGlyVal 180
DB 624 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCGCAATTGTTTACTGTGTGTGTG 683
QY LysAspPheAsnGlyThrGlnLeuAlaArg11eAlaAspSerLysAspH1sValPhePro 200
DB 684 AAAGATTTCATATGACACACAGCTGCCGCGATTGCCGACAGTAAGATCATGTGTTCCC 743
QY ValAsnAspGlyPheGlnAlaLeuGlnGly11eH1sSer11eLeuLysLysSerCys 220
DB 744 GTGAATGACGGCTTTCAGGCTTCGCAAGGCATCATCTCAATTTTGAAAGAGTCTGC 803
QY 11eGlu11eLeuAla11eValProSerThr11eCysAlaGlyGlySerPheGlnVal1 240
DB 804 ATCGAATTCCTACACACTGAAACCATCCATATGTGCGAGAGATCATTTCAAGTTGTC 863
QY ValArgGlyAsnGlyPheArgH1sAlaArgAsnValAspArgValLeuCysSerPheLys 260
DB 864 GTGAGAGGAAACCGCTTCCACATGCCGCGCACAGTGCACAGGTCCTGCACTGACAG 923
QY 11eAsnAspSerVal11eLeuAsnGlyLysProPheSerValGluAspThrTyTyLeu 280
DB 924 ATCAATGACTCGGCTCACATCAATGAGAAACCTTTTCTGTGGAAGATTTATTATCAG 983
QY CysProAlaPro11eLeuLysGluValGlyMetLysAla11eLeuGlnValSerMetAsn 300
DB 984 TGTCACGCGCTTATCTTAAAGAAAGTTGGCATTAAGAGTGCATCCAGGTCACAGAAC 1043
QY AspGlyLeuSerPhe11eSerSerSerVal11e11eThrThrThi1sCysSerAspGly 320
DB 1044 GATGGCCTCTCTTTATCTCCAGTTCGTGATCATCACACACACACTGTTCTGACGGT 1103
QY Ser11eLeuAla11eAlaLeuLeu11eLeuPheLeuLeuLeuAlaLeuAlaLeuTyP 340
DB 1104 TCCATCTGCGCATCGCCCTGCTGATCTGTCTCTGCTTACCTTACCTGCTCTCTG 1163
QY TrpPheTrpProLeuCysCysThrVal11e11eLysGluValProProProAlaGlu 360
DB 1164 TGGTTCTGGCCCTCTGCTGCTGCACTGTGATATCAAGAGAGTCCCTCCACCCCTGCGAG 1223
QY 361 GluSerGluGlu 364
DB 1224 GAGAGTCAGGAA 1235
RESULT 7
US-10-474-794-176
; Sequence 176, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
```

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; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-474-794-176

Alignment Scores:
Pred. No.: 1,486-225 Length: 5540
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.96% Indels: 0
DB: 8 Gaps: 0

US-09-970-076-2 (1-368) x US-10-474-794-176 (1-5540)
QY 1 MetAlaThrAlaGluArgH1sLeuGly11eGlyPheGlnTrpLeuSerLeuAlaThr 20
DB 144 ATGGCCAGCGCGGAGGAGGAGAGCCTCGGCATCGGCTTCAGATGCTCTTGGCCACT 203
QY 21 LeuValLeu11eCysAlaGlyGlnGlyValArgGluAspGlyGlyProAlaCysTy 40
DB 204 CTGGGCTCATCTGGCGCGGCAAGGGGACGAGGAGAGATGGGGTCCAGCTGCTAC 263
QY 41 GlyGlyPheAspLeuTyTyPhe11eLeuAspLysSerGlySerValLeuH1sH1sTrpAn 60
DB 264 GCGGATTTGACCTGACTTCAATTTTGACAAATCAGAAAGTGTGTCACCACTGGAAT 323
QY 61 Gln1eTyTyTyPheValGluGlnLeuAlaH1sLysPhe11eSerProGlnLeuArgMet 80
DB 324 GAAATCTATTACTTTGTGGAACAGTTGCTCACAAATTCATCAGCCACAGTTGAGAAATG 383
QY 81 Serphe11eValPheSerThraGlyYThrThrLeuMetLysLeuThrGluAspArgGlu 100
DB 384 TCCCTTATTGTTTCTCCACCCGAGGAAACACTTAATGAAATGACAGAAAGACAGAGAA 443
QY Gln11eArgGlnGlyLeuGluGluLeuGlnLysValLeuProGlyGlyAspThrTyrmec 120
DB 444 CAATTCGTCAGAGCCTTAGAAGAACTCCAGAAAGTTCTGCGAGGAGAGACCTTACAG 503
QY 101 Gln11eArgGlnGlyLeuGluGluLeuGlnLysValLeuProGlyGlyAspThrTyrmec 140
DB 504 CATGAAGGATTGAAAGGCGCAGTGCAGATTTATTATGAAACAGACAGAGGTCACAG 563
QY 141 ThrAlaSerVal11e11eAlaLeuThrPheGlyGluLeuH1sgLysAspLeuPhePheTy 160
DB 564 ACAGCCAGGCTCATCTGCTTGACTGATGAGAACTCCATGAAAGATCTTTTCTAT 623
QY AAGCCAGGCTCATCTGCTTGACTGATGAGAACTCCATGAAAGATCTTTTCTAT 623
DB 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAla11eValTyTyCysValGlyVal 180
DB 624 TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGTCGCAATTGTTTACTGTGTGTGTG 683
QY LysAspPheAsnGlyThrGlnLeuAlaArg11eAlaAspSerLysAspH1sValPhePro 200
DB 684 AAAGATTTCATATGACACACAGCTGCCGCGATTGCCGACAGTAAGATCATGTGTTCCC 743
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGly11eH1sSer11eLeuLysLysSerCys 220
DB 744 GTGAATGACGGCTTTCAGGCTTCGCAAGGCATCATCTCAATTTTGAAAGAGTCTGC 803
QY 221 11eGlu11eLeuAla11eValProSerThr11eCysAlaGlyGlySerPheGlnVal1 240
DB 804 ATCGAATTCCTACACACTGAAACCATCCATATGTGCGAGAGATCATTTCAAGTTGTC 863
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QY 241 ValArgGlyAseNGlyPheArgHisAlaArgAsnValAspArgValLeuCySerPheLys 260
DB 864 GTGAGAGGAAACGGCTTCCGACATGCGCCGCACTGAGCAGGCTCTTGCAGCTTCAAG 923
QY 261 IleAsnAspSerValThrLeuAsnGlyLeuProPheSerValGluAspThrTyrLeuLeu 280
DB 924 ATCAATGACTCGGTCACACTCAATGAGAGCCCTTTCTGTGGAAGATCTTATTACTG 983
QY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaLeuGlnValSerMetAsn 300
DB 984 TGTCACAGCGCTATCTTAAAGAGTTGGATGAACTGACCTCCAGGTGAGATTAAC 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
DB 1044 GATGGCTCTCTTATCTTCAAGTTCTGTATCTATCCACACACACTGTTCTGACGGT 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTyr 340
DB 1104 TCCATCTGCGCATCGCCCTGCTGATCTCTGCTCTGCTGCTGCTGCTGCTGCTG 1163
QY 341 TrpPheTrpProLeuCySerThrValIleIleIleGluValProProProAlaGlu 360
DB 1164 TGGTTCTGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1223
QY 361 GluSerGluGlu 364
DB 1224 GAGAGTGAGGAA 1235

RESULT 8

US-10-474-794-231
; Sequence 231, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carlson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474.794
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-474-794-231

Alignment Scores:

Prod. No.: 1.48e-225 Length: 5540
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.96% Indels: 0
DB: 8 Gaps: 0

US-09-970-076-2 (1-368) x US-10-474-794-231 (1-5540)

QY 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
DB 144 ATGGCCACGGCGGAGCGGAGCGCTCGGCATCGGCTTCCAGTGGCTCTCTTGGCCACT 203
QY 21 LeuValLeuIleCysAlaGlyGlnGlyAlaArgGluAspGlyGlyProAlaCysTyr 40
DB 204 CTGGTGTCTATCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 263
QY 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60

DB 264 GCGGATTTGACCTGATCTTATTTTGGACAAATTCAGAAAGTGTGTCACCACTGGAAAT 323
QY 61 GluIleTyrThrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
DB 324 GAATCTATTACTTTGTGAAAGGTTGCTCAAAATTCATCCAGCCCACTGGAGAAATG 383
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
DB 384 TCCCTTATTGTTTCTTCCACCGGAGAACACTTAAATGAACTGACAGAAAGCAGAGAA 443
QY 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
DB 444 CAATCCGTCACAGCCCTAGAAAGACTCCAGAAAGTTCTGCGCAGAGAGACACTTACATG 503
QY 121 HisGlnGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
DB 504 CATGAAGGATTGAAAGGCGCAGTGAAGCATTTATTAAGAAACAGAACAGAGGTCAGG 563
QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlyLeuHisGluAspLeuPhePheTyr 160
DB 564 ACAGCCAGCGCTATCTTGTGCTTGTGATGATGAGAACTCCATGAAATCTCTTTTCTAT 623
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
DB 624 TCAGAGAGGAGGCTAATAGGTCTCGAGATCTTGTCATTTGTTACTGTGTGTGTGTG 683
QY 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValIlePro 200
DB 684 AAAGATTTCAATGAGACACAGCTGCGCCGAGATTGCGAGACGTAAAGATCATGTGTTCC 743
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
DB 744 GTGAATGACGGCTTTTCAAGCTCTGCAAGGATATATCATCTCAATTTTGAAGAGCTCTG 803
QY 221 IleGluIleLeuAlaIleAlaProSerThrIleCysAlaGlyGluSerPheGlnVal 240
DB 804 ATGGAATCTTACACACTGAAACCATCCATATGTGAGAGATGATCATTTCAAGTTGTC 863
QY 241 ValArgGlyAseNGlyPheArgHisAlaArgAsnValAspArgValLeuCySerPheLys 260
DB 864 GTGAGAGGAAACGGCTTCCGACATGCGCCGCACTGAGCAGGCTCTTGCAGCTTCAAG 923
QY 261 IleAsnAspSerValThrLeuAsnGlyLeuProPheSerValGluAspThrTyrLeuLeu 280
DB 924 ATCAATGACTCGGTCACACTCAATGAGAGCCCTTTCTGTGGAAGATCTTATTACTG 983
QY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaLeuGlnValSerMetAsn 300
DB 984 TGTCACAGCGCTATCTTAAAGAGTTGGATGAACTGACCTCCAGGTGAGATTAAC 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
DB 1044 GATGGCTCTCTTATCTTCAAGTTCTGTATCTATCCACACACTGTTCTGACGGT 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTyr 340
DB 1104 TCCATCTGCGCATCGCCCTGCTGATCTCTGCTCTGCTGCTGCTGCTGCTGCTG 1163
QY 341 TrpPheTrpProLeuCySerThrValIleIleIleGluValProProProAlaGlu 360
DB 1164 TGGTTCTGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1223
QY 361 GluSerGluGlu 364
DB 1224 GAGAGTGAGGAA 1235

RESULT 9

US-10-979-159-176
; Sequence 176, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein

APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/10/979,159
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US/09/918,715
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 176
LENGTH: 5540
TYPE: DNA
ORGANISM: Homo sapiens
US-10-979-159-176

Alignment Scores:

Pred. No.: 1,48e-225 Length: 5540
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.96% Indels: 0
DB: 9 Gaps: 0

US-09-970-076-2 (1-368) x US-10-979-159-176 (1-5540)

QY 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
DB 144 ATGGCCAGCGCGGAGGAGGAGCGCTCGGCATCGGCTCCAGTGGCTCTTTGGCCACT 203
QY 21 LeuValLeuIleCysAlaGlyGlnGlyValArgGluAspGlyGlyProAlaCysTrp 40
DB 204 CTGGTCTCATCTGCGCGCGGAGGAGGAGGAGGAGGATGGGCTCCAGCTCTCTAC 263
QY 41 GlyGlyPheAspLeuTrpPheIleLeuAspLeuSerGlySerValLeuHisIleTrpPan 60
DB 264 GGGGAGATTGACCTGATCTTCATTTTGGACAAATCAGAAAGTGTGTCACACCTGAAAT 323
QY 61 GluIleTyTrpPheValGlnGlnLeuAlaHisLeuPheIleSerProGlnLeuAspMet 80
DB 324 GAATCTATTAATCTTGTGGAAAGCTTGGCTCACAATTCATCAGCCCAAGCTTGAAATG 383
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLeuLeuThrGluAspArgGlu 100
DB 384 TCCTTATTTGTTTCTCCACCCGAGGAACTTAATGAACCTGAACCTGACAGAAAGAA 443
QY 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnValLeuProGlyGlyAspTrpMet 120
DB 444 CAATCCGTCAGAGCCCTGAGAAAGCTCCAGAAAGTCTGCGAGAGAGACACTTACATG 503
QY 121 HisGlyGlyPheGluArgAlaSerGlnGlnIleTyTrpGluAsnArgGlnGlyTrpArg 140
DB 504 CATGAAGATTGTAAGAGGCGCACTGAGCAATTTATTAATAACAGACAAAGGTTACAG 563
QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTrp 160
DB 564 ACAGCCAGCGCTCATCATCTTGTGATGATGAGAACTCATGAAGATCTCTTTCTAT 623
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyValIleValTrpCysValGlyVal 180
DB 624 TCAGAGAGGAGGCTTAATAGTCTTCGAGATCTTGTCGCAATTTTACTGTGTGGTGG 663
QY 181 LysAspPheAsnGluTrpGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
DB 684 AAAGATTTCAATAGACACAGCTGGCCCGAATGGCGACAGTAAGATCATGTGTTCC 743
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220

DB 744 GTGAATGACGGCTTTCAAGCTCTGCAAGGCATCATCTCAATTTTGAAGAAGTCTGCC 803
QY 221 IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
DB 804 ATCGAATTTCTGACAGCTGAAACCATCCACCAATGTGACAGAGATCATTTCAAGTTC 863
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
DB 864 GTGAGAGGAAAGCGCTCCGACATGCCGCAACGTGACAGGAGTCTTGACAGTTCAAG 923
QY 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTrpLeuLeu 280
DB 924 ATCAATGACTCGGTCACTCATATAGAGCCCTTTCTGTGGAAGATTCATTAATTAACG 983
QY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
DB 984 TGTCAGCGCCCTATCTTAATAAAGATTGGCATGAAGCTGCATCCAGGTCAAGATGAAC 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThiAsCysSerAspGly 320
DB 1044 GATGGCTCTCTTTATCTCCAGTTCGTGCATCATCACCAACACACTGTTCTGACGGT 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340
DB 1104 TCCATCTGGCCATGCGCTGCTGATCCGTTCCTGCTCTGAGCCCTGCTCTCTG 1163
QY 341 TrpPheTrpProLeuCysCysThrValIleIleLysGluValProProProAlaGlu 360
DB 1164 TGCTTGGCCCTCTGCTGCTGCTGATTAACAGAGGTCCCTCCACCCCTGCCGAG 1223
QY 361 GluSerGluGlu 364
DB 1224 GAGAGTGAGGAA 1235

RESULT 10

US-10-979-159-231
Sequence 231, Application US/10979159
Publication No. US20050142138A1
GENERAL INFORMATION:

APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/10/979,159
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US/09/918,715
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 231
LENGTH: 5540
TYPE: DNA
ORGANISM: Homo sapiens
US-10-979-159-231

Alignment Scores:

Pred. No.: 1,48e-225 Length: 5540
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.96% Indels: 0
DB: 9 Gaps: 0

US-09-970-076-2 (1-368) x US-10-979-159-231 (1-5540)

QY 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20


```
|||||
Db TCAGAGAGGAGGCTAATAGTCTCGAGATCTTGAGCAATGTTACTGTGTGTG 683
QY 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerIleAspHisValPhePro 200
Db 684 AAAGATTTCAATGAGACACAGCTGGCCGGATTGGGACAGTAAGATCATGTGTTCC 743
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIleValSerCys 220
Db 744 GTGAAATGAGCGCTTTCAGGCTCTGCAAGGATCATCATCATCTTGAAGAAGTCTTC 803
QY 221 IleguIleLeuAlaIleGluProSerThrIleCysAlaGlyIleValSerPheGlnVal 240
Db 804 ATCGAATTTCTAGCACCTGAAACCATCCACATATGTGACAGAGATCATTTCAAGTTGTC 863
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheIys 260
Db 864 GTGAGAGGAAACGGCTTCGACATGCCGCAACGTGACAGGGTCTCTGACGCTTCAG 923
QY 261 IleAsnAspSerValThrLeuAsnGluIysProPheSerValGluAspThrTyrlLeu 280
Db 924 ATCAATGATCTCGGTACACCTCATGAGAACCTTTTCTGTGSAAGATCTTATTACTG 983
QY 281 CysProAlaProIleLeuIysGluValGlyMetIysAlaAlaLeuGlnValSerMetAsn 300
Db 984 TGTCACAGCGCTATCTTAAAGAAGTTGGCATGAAAGCTGCACTCCAGGTCACATGAAAC 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
Db 1044 GATGGGCTCTCTTTATCTTCAGATTCGTATCATACACCAACACATGTTCTGACGGT 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuTyr 340
Db 1104 TCCATCTGCGCCATCCGCCCTCGATGATCTCTCTCTCTTACCTGCTCTCTCTG 1163
QY 341 TrpPheTrpProLeuCysCysThrValIleIleIysGluValProProProAlaGlu 360
Db 1164 TGGTTCTGGCCCTCTGCTGACATGATATATCAAGAGGTCCTCCACCCCTGCGGAG 1223
QY 361 GluSerGluGlu 364
Db 1224 GAGAGTGAGGAA 1235

RESULT 12
US-09-918-715-186
; Sequence 186, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918.715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 186
; LENGTH: 5220
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-918-715-186

Alignment Scores:
Pred. No.: 6,5e-213 Length: 5220
Score: 1793.00 Matches: 342
Percent Similarity: 97.75% Conservative: 6
```

```
Best Local Similarity: 96.07% Mismatches: 8
Query Match: 93.68% Indels: 0
DB: 3 Gaps: 0
US-09-970-076-2 (1-368) x US-09-918-715-186 (1-5220)
QY 9 IleguIleGlyPheGlnTrpLeuSerLeuAlaThrLeuValLeuIleCysAlaGlyGln 28
Db 292 CTGGGTGGCGGCTCGCGGGACTTGCGGTCTGCACTGCTGCTGCTGCGCCCGGACAC 351
QY 29 GlyIleAspArgGluAspGlyGlyProAlaCysTyrlGlyGlyPheAspLeuTyrlPheIle 48
Db 352 GGGGGCCCGGGAGAGATGGGGACAGCTTCTACGGAGATTCAGCTTCACTTCATC 411
QY 49 LeuAspIysSerGlySerValLeuHisIleIleIleIleIleIleIleIleIleIleIle 68
Db 412 CTGACACAGTCAGAAAGTGTCTGACACCTGGAATGAATATCTACTCTTCTGAGCAG 471
QY 69 LeuAlaHisIysPheIleSerProGlnLeuArgMetSerPheIleValPheSerThrArg 88
Db 472 TTGGGTCAATAGATTCATCAGCCACAGCTAAGATGCTCTTCAATGCTTCTTCTACTCGA 531
QY 89 GlyThrThrLeuMetIysLeuThrGluAspArgGluGlnIleArgGlnIleLeuGluGlu 108
Db 532 GGGACAACTTTAATGAATTAATGAGTGAAGACAGGAAACATCTCGACAAAGCTTCAAGAGAG 591
QY 109 LeuGlnIysValIleuProGlyIleAspThrTyrlMetHisGlyGlyPheGluArgAlaSer 128
Db 592 CTCGAAAGATCTTCCGACGAGAGACACTTTCATGACAGAAAGATTCAGAGGGCCAT 651
QY 129 GluGlnIleTyrlTyrlGluAsnArgGlnGlyTyrlArgThrAlaSerValIleIleAlaLeu 148
Db 652 GAGCAGATTTAATAAGAAACAGTCAAGATTCAGGACGGGACGCTCATCTCCGCTG 711
QY 149 ThrAspGlyGluLeuHisGluAspLeuPhePheTyrlSerGluAsnGluAlaAsnArgSer 168
Db 712 ACGGATGGGACCTGACAGAGACCTTCTTCTACTGAGAGGGAGGCTTAACGATCC 771
QY 169 ArgAspLeuGlyAlaIleValTyrlCysValGlyValIleAspPheAsnGluThrGlnLeu 188
Db 772 CGAGACCTTGGTGCATTTGTTTACTGCGCTTGGCGTGAAGATTTCAATGAATCTCAAGTTG 831
QY 189 AlaArgIleAlaAspSerIysAspHisValPheProValAsnAspGlyPheGlnAlaLeu 208
Db 832 GCTCGGATTCAGACAGTAAGACCAACGTTTCTGTAAGACGAGCTTCCAGGCTCTC 891
QY 209 GlnGlyIleIleHisSerIleLeuIysCysIleGluIleLeuAlaIleGluPro 228
Db 892 CAAGCATTAATCCACTCAATTTTAAAGAAATCTGATCGAAATTTGCGGCTGAACCA 951
QY 229 SerThrIleCysAlaGlyIleSerPheGlnValIleValArgGlyAsnGlyPheArgHis 248
Db 952 TCCACCATTTGCGCGGGAAGTCTTTCAAGTGTGTGAAGGAATGGCTTCCGACAT 1011
QY 249 AlaArgAsnValAspArgValLeuCysSerPheIysIleAsnAspSerValThrLeuAsn 268
Db 1012 GCCCGAATGTGACAGGGTCTCTGACACTTCAAAATCAATGATCACTGACGCTCAAT 1071
QY 269 GluIysProPheSerValGluAspThrTyrlLeuLeuCysProAlaProIleLeuIysGlu 288
Db 1072 GAGAAACCTTGTCTGTGGAAGACATTTATTTGCTGTGCGGACCAATCTTGAAGAAGAA 1131
QY 289 ValGlyMetIysAlaAlaLeuGlnValIleSerMetAsnAspGlyLeuSerPheIleSerSer 308
Db 1132 GTTGGCATTAAGCTCACTGCAAGTCAAGTCAAGAGAGGCTGTCTTCACTCAAGT 1191
QY 309 SerValIleIleThrThrHisCysSerAspGlySerIleLeuAlaIleAlaLeu 328
Db 1192 TGTGATCATCATCAACCAACACATCTTTCAGAGGCTCCATCTGCGATGCTGCTGCTG 1251
QY 329 IleuPheLeuLeuLeuAlaLeuAlaLeuLeuTyrTrpPheTrpProLeuCysCysThr 348
Db 1252 GTCTCTTCTGCTGCTGCGCCCTGCGGCTGCTGTGTGTGCTGCGCCCTGCTGCGACA 1311
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US-09-970-076-2 (1-368) x US-10-474-794-186 (1-5220)

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QY      9 LeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThrLeuValIleuIleCysAlaGlyGln 28
Db      292 CTGGGTCGGGGCTCGGGGACTCTGCGTGGCTGCATCTGCTGCTGCTGCGCGGACAC 351
QY      29 GlyIlyAArgGlyLeuArgIlyGlyProAlaCysTyrgIlyGlyPheAspLeuTyrrPheIle 48
Db      352 GGGGGCGCGCGGAGAGATGGGGGACCAAGCTTGTCTACGAGAGATTCGACCTTCACTTCATC 411
QY      49 LeuAspIlySerGlySerValLeuHisIleTPAsnGlnIleTyrrTyrrPheValIleuGln 68
Db      412 CTGGACAAGTCAGAGAAGTGTGCTGCACCTGGAAGAATCTCACTTCCTCGAGGACAG 471
QY      69 LeuAlaHisIlyAspPheIleSerProGlnLeuArgMetSerPheIleValPheSerThrArg 88
Db      472 TTGGCTCATAGATTCTACGCCACAGCTTAGAGATGCTTCTTCTTCTTCTTCTTCTTCTCA 531
QY      89 GlyThrThrLeuMetIlySerLeuThrGlyAspArgGlyGlnIleArgGlnIlyLeuGlnIle 108
Db      532 GGGACAACCTTTAATGAACCTTAACAGAGACAGGAAACAGATCCGACAGGCGCTAGAAAG 591
QY      109 LeuGlnIlyValLeuProGlyIlyAspThrTyrrMetHisGlyGlyPheGlyIleAlaSer 128
Db      592 CTCACAAAGATTCTGCGCAGAGAGACACTTACATCAGCAAGAGATTCCAGAGGCGCAGT 651
QY      129 GluGlnIleTyrrTyrrGlyLeuAspArgGlyGlnIlyTyrrArgThrAlaSerValIleIleAlaLeu 148
Db      652 GACCAAGATTTACTATAGAACAGCTCAAGATACAGAGCGGCGGCTCATCTCGCGTTG 711
QY      149 ThrAspGlyGlyLeuHisIleGlyAspLeuPhePheTyrrSerGlyLeuArgIlyAlaAspArgSer 168
Db      712 ACGGATGGGAGCTGCACGAGGACCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 771
QY      169 ArgAspLeuGlyAlaIleValTyrrCysValIlyValIlyAspPheAsnGlnIlyTrpGlnLeu 188
Db      772 CGAGACCTTGTGTCGATGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 831
QY      189 AlaArgIleAlaAspSerIlyAspHisIleValPheProValAspAspGlyPheGlnAlaLeu 208
Db      832 GCTCGGATTTGCAACAGTAAAGACAGCTGTTCTGTTGAAACAGGCTTCCAGGCTCTC 891
QY      209 GlnGlyIleIleHisSerIleLeuTyrrIlySerCysIleGlyIleLeuAlaIleGlyPro 228
Db      892 CAAGGATTTATCCACCTCAATTTTAAAGAAATCTGCATGAAATTCGCGCGCTGACCA 951
QY      229 SerThrIleCysAlaGlyIlySerPheGlnValValIlyArgIlyAsnGlyPheArgHis 248
Db      952 TTCACCATCTGCGCGGAGAGTCTTTCAGTGTGCTAAGAGAAATGGCTTCCACAT 1011
QY      249 AlaArgAspValIleAspArgValIleuCysSerPheIlyIleAspAspSerValIleuAsn 268
Db      1012 GCCCGCAATGTGACAGGCTCTCTGCAAGCTTCAAAATCATATCATCATCATCATCATCATCAT 1071
QY      269 GlyIlySerPheSerValGlyAspThrTyrrLeuLeuCysProAlaProIleLeuTyrrGly 288
Db      1072 GAGAACCCCTTGTCTGAGAAACACTTATTTGCTGAGCCCAACCAATCTTGAAAGAA 1131
QY      289 ValIlyMetIlyValIleuGlnValSerMetAspAspGlyLeuSerPheIleSerSer 308
Db      1132 GTTGGCATGAACCTGACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1191
QY      309 SerValIleIleThrThrThrHisCysSerAspGlySerIleLeuAlaIleIleAlaLeu 328
Db      1192 TCTGTATCATCAACCAACACACTGTTCAAGCGGCTCCATCTGCGGATTTGCTGCGTG 1251
QY      329 IleLeuPheLeuLeuAlaLeuAlaLeuLeuTrpIlePheTrpProLeuCysCysThr 348
Db      1252 GTCTCTTCTGCTGCTGCGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1311
QY      349 ValIleIleIlyGlyValIleProProProAlaGlyIlySerGlyIly 364
Db      1312 GTGATCATCAAGAGGTCCTCCACCCCTGTTGAGAGAGAGTGAAGAA 1359
```

RESULT 15

```
US-10-474-794-300
; Sequence 300, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 300
; LENGTH: 5220
; TYPE: DNA
; ORGANISM: Mouse
; US-10-474-794-300
```

Alignment Scores:

Pred. No.:	6,5e-213	Length:	5220
Score:	1793.00	Matches:	342
Percent Similarity:	97.75%	Conservative:	6
Best Local Similarity:	96.07%	Mismatches:	8
Query Match:	93.68%	Indels:	0
DB:	8	Gaps:	0

US-09-970-076-2 (1-368) x US-10-474-794-300 (1-5220)

```
QY      9 LeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThrLeuValIleuIleCysAlaGlyGln 28
Db      292 CTGGGTCGGGGCTCGGGGACTCTGCGTGGCTGCATCTGCTGCTGCTGCGCGGACAC 351
QY      29 GlyIlyAArgGlyLeuArgIlyGlyProAlaCysTyrgIlyGlyPheAspLeuTyrrPheIle 48
Db      352 GGGGGCGCGCGGAGAGATGGGGGACCAAGCTTGTCTACGAGAGATTCGACCTTCACTTCATC 411
QY      49 LeuAspIlySerGlySerValLeuHisIleTPAsnGlnIleTyrrTyrrPheValIleuGln 68
Db      412 CTGGACAAGTCAGAGAAGTGTGCTGCACCTGGAATGAATCTTACTTCTTCTGAGCAG 471
QY      69 LeuAlaHisIlyAspPheIleSerProGlnLeuArgMetSerPheIleValPheSerThrArg 88
Db      472 TTGGCTCATAGATTCTACGCCACAGCTTAGAGATGCTTCAATGCTTCTTCTTCTTCTTCTCA 531
QY      89 GlyThrThrLeuMetIlySerLeuThrGlyAspArgGlyGlnIleArgGlnIlyLeuGlnIle 108
Db      532 GGGACAACCTTTAATGAACCTTAACAGAGACAGGAAACAGATCCGACAGGCGCTAGAAAG 591
QY      109 LeuGlnIlyValLeuProGlyIlyAspThrTyrrMetHisIleGlyIlyPheGlyIlyAlaSer 128
Db      592 CTCGAAAGATTCTGCGCAGAGAGACACTTTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 651
QY      129 GluGlnIleTyrrTyrrGlyLeuAspArgGlyGlnIlyTyrrArgThrAlaSerValIleIleAlaLeu 148
Db      652 GACCAAGATTTACTATAGAACAGCTCAAGATACAGAGCGGCGGCTCATCTCGCGTTG 711
QY      149 ThrAspGlyGlyLeuHisIleGlyAspLeuPhePheTyrrSerGlyLeuArgIlyAlaAspArgSer 168
Db      712 ACGGATGGGAGACTGCACAGAGACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 771
QY      169 ArgAspLeuGlyAlaIleValTyrrCysValIlyValIlyAspPheAsnGlnIlyTrpGlnLeu 188
Db      772 CGAGACCTTGTGTCGATGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 831
QY      189 AlaArgIleAlaAspSerIlyAspHisIleValPheProValAspAspGlyPheGlnAlaLeu 208
```

Db	832	GCTGGAGTTGCAGACAGTBAAGGACCA	CCTGTTTCTCTGGAAACGACGCGCTTC	891
Qy	209	GlnglyIleIleHkHsSerIleuLylalysSerCy	IleGulIleuAlaIleGluPro	228
Db	892	CAGGCAATTATTCATCAATTTTAAAGAAAT	CTCGATCGAAATTCCTGGCGGCTGACCA	951
Qy	229	SerThrIleCyAlaIleGlyGluSerPheGlnVal	ValValArgGlyAsnGlyPheArgHis	248
Db	952	TTCACCAATCTGGCGCGGAGAGTCC	TTTCAAGGTCGTAAGAGGAAAGGCTTCGCAAT	1011
Qy	249	AlaArgAsnValAspArgValIleuCySerPhe	ValIleAsnAspSerValThrIleuAsn	268
Db	1012	GCCGCAATGTGACAGAGGTCCTCTGCGACG	TTCCAAATCATGACTCAGTCACGTCAT	1071
Qy	269	GluIysProPheSerValGluAspThrTyrl	IleuIleuCyProIaIleuIysGlu	288
Db	1072	GAGAAAGCCCTTGTGCTGGAAAGAC	CTTATTGTCGTGCTGCCAGCACCAATCTTGAAAGAA	1131
Qy	289	ValGlyMetIysAlaIleAlaLeuGlnVal	SerMetAsnAspGlyIleuSerPheIleSer	308
Db	1132	GTTGGCAATGAAGCGACGCTGAGAGT	CGACATGAAGACAGCGCGCTCTTCATCTCCAGT	1191
Qy	309	SerValIleIleIleThrThrHisCySer	AspGlySerIleIleuAlaIleAlaIleu	328
Db	1192	TCTGTCATCATACCAACACACACTG	TTCAGCGGCTCATCTCGGCATTCCTGCTG	1251
Qy	339	IleIeuPheLeuLeuLeuAlaLeuAlaLeu	IleuTyrrPheTyrrProIeuCySerThr	348
Db	1252	GTCCTCTTCCTGCTGCTGGCCCTG	CGCGCTCTGCTGCTGGCCCTCTGCTGACACA	1311
Qy	349	ValIleIleIleGlyValProProProPro	IaIleGluIysGlnGlu	364
Db	1312	GGATCATCATAGAGAGTCCCTTCAC	CCCCCTGTTGAGAGAGTGAAGAA	1359

Search completed: December 19, 2005, 02:09:34
Job time : 1230.98 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 18, 2005, 07:41:36 ; Search time 296.957 Seconds
(without alignments)
607,449 Million cell updates/sec

Title: US-09-970-076-2

Perfect score: 1914

Sequence: 1 MATERRAALGIGFQWLAT.....VILKEVPPPESEENKIK 368

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ .p2n.model -DEV=xlh
-Q/cgnt2_1/USPTO.spool/US09970076/runac_14122005_111853_21065/app_query.fasta_1_2410
-DB=Published Applications NA New -QMT=fastcap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62
-TRANS=human0.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076 @CGN_1_1_675 @runac_14122005_111853_21065
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New.*

1: /cgnt2_6/prodata/1/pubpna/US09_NEW_PUB.seq.*
2: /cgnt2_6/prodata/1/pubpna/US06_NEW_PUB.seq.*
3: /cgnt2_6/prodata/1/pubpna/US07_NEW_PUB.seq.*
4: /cgnt2_6/prodata/1/pubpna/US08_NEW_PUB.seq.*
5: /cgnt2_6/prodata/1/pubpna/PCT_NEW_PUB.seq.*
6: /cgnt2_6/prodata/1/pubpna/US10_NEW_PUB.seq.*
7: /cgnt2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
8: /cgnt2_6/prodata/1/pubpna/US11_NEW_PUB.seq2.*
9: /cgnt2_6/prodata/1/pubpna/US11_NEW_PUB.seq3.*
10: /cgnt2_6/prodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1894	99.0	5540	7	US-11-186-284-198
2	145.5	7.6	4740	7	US-11-080-026-3
3	131	6.8	11447	7	US-11-186-284-25
4	122	6.4	2834	6	US-10-750-185-39040
5	113.5	5.9	1325	6	US-10-750-185-56394
6	113.5	5.9	2501	6	US-10-821-234-182
7	113.5	5.9	3449	6	US-10-131-826A-293
8	111	5.8	3564	6	US-10-601-368-20

9	111	5.8	4858	6	US-10-601-368-19	Sequence 19, Appl
10	107.5	5.6	3175	6	US-10-995-561-465	Sequence 464, App
11	107.5	5.6	3464	6	US-10-995-561-465	Sequence 465, App
12	107.5	5.6	3468	6	US-10-995-561-466	Sequence 466, App
13	107	5.6	3564	6	US-10-601-368-2	Sequence 2, Appl1
14	107	5.6	3967	7	US-11-000-463-574	Sequence 574, App
15	107	5.6	3969	7	US-11-000-463-102	Sequence 102, App
16	107	5.6	5042	6	US-10-601-368-1	Sequence 1, Appl1
17	105.5	5.5	3868	6	US-10-995-561-404	Sequence 404, App
18	103.5	5.4	2765	6	US-10-750-185-25275	Sequence 25275, A
19	101.5	5.3	47572	6	US-10-995-561-13356	Sequence 13356, A
20	100	5.2	2773	7	US-11-102-240-33	Sequence 33, Appl
21	96	5.0	3884	6	US-10-601-368-17	Sequence 17, Appl
22	94	4.9	1062	7	US-11-137-465-12	Sequence 11, Appl
23	94	4.9	1347	7	US-11-137-465-12	Sequence 12, Appl
24	91.5	4.8	1881	6	US-10-467-657-5431	Sequence 5431, Ap
25	90.5	4.7	3144	6	US-10-392-234A-17	Sequence 17, Appl
26	88	4.6	3189	7	US-11-137-465-10	Sequence 10, Appl
27	87	4.5	2715	6	US-10-507-725-4	Sequence 4, Appl1
28	86	4.5	1705	6	US-10-750-185-50386	Sequence 50386, A
29	85.5	4.5	1278	6	US-10-467-657-2551	Sequence 2551, Ap
30	85.5	4.5	2538	7	US-11-147-047-20	Sequence 20, Appl
31	82	4.3	3989	6	US-10-750-185-47454	Sequence 47454, A
32	81.5	4.3	1688	6	US-10-510-386-157	Sequence 157, App
33	81	4.2	11115	6	US-10-513-786-6	Sequence 6, Appl1
34	81	4.2	11115	6	US-10-513-786-6	Sequence 8, Appl1
35	80.5	4.2	3586	7	US-11-080-991-51	Sequence 51, Appl
36	80	4.2	1413	7	US-11-055-822-411	Sequence 41, Appl
37	79.5	4.2	2317	6	US-10-793-626-4357	Sequence 4357, Ap
38	79.5	4.2	2987	6	US-10-793-626-3398	Sequence 3398, Ap
39	79.5	4.2	3366	6	US-10-467-657-6111	Sequence 6111, Ap
40	79.5	4.2	5576	6	US-10-995-561-517	Sequence 517, App
41	79.5	4.2	5808	6	US-10-995-561-517	Sequence 517, App
42	78.5	4.1	1895	6	US-10-750-185-42451	Sequence 42451, A
43	78.5	4.1	118996	7	US-11-121-086-84	Sequence 84, Appl
44	78	4.1	1339	6	US-10-467-657-3293	Sequence 3293, Ap
45	78	4.1	1443	6	US-10-467-657-3291	Sequence 3291, Ap

ALIGNMENTS

RESULT 1
US-11-186-284-198
; Sequence 198, Application US/11186284
; Publication No. US2005026493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John B.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITILE OF INVENTION: THERAPY FOR COLON CANCER
; FILE REFERENCE: MP001-029P2RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 5540
; TYPE: DNA

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; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144)...(1838)
US-11-186-284-198

Alignment Scores:
Pred. No.: 3, 276-218 Length: 5540
Score: 1894.00 Matches: 364
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.96% Indels: 0
DB: 7 Gaps: 0

US-09-970-076-2 (1-368) x US-11-186-284-198 (1-5540)

QY 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
DB 144 ATGGCCAGCGCGGAGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTGGCCACT 203
QY 21 LeuValLeuIleCyAlaGluGlnGlyValArgArgGluAspGlyValProAlaCysTyr 40
DB 204 CTGGCTCTACTGCGCGGCGGAGGAGCGAGGAGGATGGGGTCCAGCTTCTC 263
QY 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIstPasn 60
DB 264 GGGGATTTGACCTGTACTTCACTTTTGGACAATCAGGAAGTGTGTGCACTCGAAT 323
QY 61 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
DB 324 GAATCTAATTAATCTTGTGGAAAGTTGGCTCACAAATTCATCGCCCAAGTTCGAGAATG 383
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
DB 384 TCCCTTATTTGTTTCTCCACCCAGAGAACCTTAAATGAACTGACAGAGACAGAA 443
QY 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
DB 444 CAATCCGTCAAGGCGCTAGAAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATG 503
QY 121 HisGlnGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
DB 504 CATGAAGGATTTGAAAAGGGCGACGTGAGCAGATTATTAATAAACAAGACAGAGGTCACAG 563
QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPheTyr 160
DB 564 ACAGCCAGCGCTCATCTGCTTGTGACTGATGAGAACTCCATAGAAGTCTCTTTTCTAT 623
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
DB 624 TCAGAGAGGGAGGCTAATAGTCTCGAGATCTTGTCATTTGTTTACGTGTGGTGTG 683
QY 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
DB 684 AAAGATTTCAATAGACACACGCTGCGCCGATGGCGACAGTAAGATCATGTGTTTCCC 743
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
DB 744 GTAAATGACGGGCTTTCAGGCTCTGCAAGGCACTCATCTCACTCAATTTTGAAGAAGTCTGC 803
QY 221 IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 240
DB 804 ATGGAATTTCTAGCAGCTGAACCATCCACATATGTGCAGAGAGTCAATTTCAAGTTGTC 863
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
DB 864 GTAGAGGAAACGGCTTCCACATGCCCCGCAACGTGACAGGGGCTCTGCACTTCAAG 923
QY 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu 280
DB 924 ATCAATGACTCGGTCACTCAATGAGAGCCCTTTTCTGTGAGAGTACTTATTTTACTG 983
QY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaIleLeuGlnValSerMetAsn 300
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DB 984 TGTCCAGCGCTTATCTTAAAGATGTGCATGAAGCTGCATCCAGTCCAGCATGAAC 1043
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
DB 1044 GATGGCTCTCTTATCTTCAATGTTCTGTGATCATCATCACACACACACTGTTTACGGT 1103
QY 321 SerIleLeuAlaIleAlaLeuLeuIleuPheLeuLeuAlaLeuAlaLeuLeuTrp 340
DB 1104 TCCATCTCGGCATGGCCCTGCTGATCCGTTCCTGCTCTTACGCCCTGCTCTCTG 1163
QY 341 TrpPheTrpProLeuCysCysThrValIleIleLysGluValProProProAlaGlu 360
DB 1164 TGGTCTGGCCCTCTGCTGCTGCACTGATTAACAAGAGAGTCCCTCCACCCCTGCCAG 1223
QY 361 GluSerGluGlu 364
DB 1224 GAGAGTGAAGAA 1235

RESULT 2
US-11-080-026-3
; Sequence 3, Application US/11080026
; Publication No. US20050260192A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Shimooka, Motomu
; APPLICANT: Lu, Chafan
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; FILE REFERENCE: CFEF-P02-021
; CURRENT APPLICATION NUMBER: US/11/080,026
; PRIOR FILING DATE: 2005-03-15
; PRIOR APPLICATION NUMBER: 09/945,265
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,700
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-080-026-3

Alignment Scores:
Pred. No.: 5, 698-06 Length: 4740
Score: 145.50 Matches: 60
Percent Similarity: 45.85% Conservative: 45
Best Local Similarity: 26.20% Mismatches: 81
Query Match: 7.60% Indels: 43
DB: 7 Gaps: 12

US-09-970-076-2 (1-368) x US-11-080-026-3 (1-4740)

QY 44 AspLeuTyrPheIleLeuAspLysSerGlySerValLeu---HisIstPasnGluIle 62
DB 520 GACATGCGCTTCTTGAATGATGCGCTGTGATGATCATCCACATGACTTCCGCGGAGT 579
QY 63 TyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSerPne 82
DB 580 AAGAGCTGTGTCAACT-----GTATGAGAGCAATTTAAAGATCCAA 624
QY 83 IleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAsp----- 98
DB 625 ACCTTGTCTCT-----TTGATGCACTACTCTGAAGAAATTCGCGATTCC 669
QY 99 -----ArgGluGlnIleArgGlnGlyLeuGlnGluGln 110
DB 670 TTACTTCAAGAGTTCAGAAACACCTTAACCAAGATCACTGTGAAGCCAATPACG 729
QY 111 LysValLeuProGlyLysAspThrTyrTrpMetHisGlnGlyPheGluArgAlaSerGluGln 130
DB 730 CAGCTGCTT-----GGGGGACACACACGGCCACGGGATTCGCAAGTGTGACGAG 783
```

QY 131 IletyTyrGluaenArgInglyTyrArgThrAla---SerValIleIleAlaLeuThr 149
Db 784 CTGTTTAACTACATCCACCAAGAGCCGGAAGAAATGCTTTAAAGATCCTAGTGTGATCAGG 843
QY 150 AspGlyLeuLeuHsiGluAepLeuPhePheTyrSerGlu-----ArgGluAlaAsnArg 167
Db 844 GATGGAGAAAAGTTTGGCGATCCCTTGGGATATGAGATGATGATCCCTGAGGCGACAGAGA 903
QY 168 SerArgAspLeuGlyAlaIleValTyrCysValGlyValIlyAspPheAsnGluThrGln 187
Db 904 GAG-----GGAGTCATTCGCTACGTATGGGGAGATGCGCTCCGACGTAGG 954
QY 188 LeuAlaArg-----IleAlaAspSer-----LysAspHisValPhePro 200
Db 955 AAATCCGCGCAAGAGCTTAAATACCATGTCATCCAGCCGCTCGTATCAAGTGTTCAG 1014
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
Db 1015 GTGAATTAAC---TTTGAGGCTCTGAAAGACATTCAGAAACAGCTTCGGGAGAG--- 1065
QY 221 IleGluIleLeuAlaLeuGluProSerThrIleCysValGlyGluSerPheGlnVal 240
Db 1066 -----ATCTTGGCATCGAGGGGTACTCAGACAGAGAGTAGACGCTCTTGACATGAG 1119
QY 241 ValArgGlyAsnGlyPheArgHisAla 249
Db 1120 ATGCTCAGAGAGGCTTCAGCGCTGCC 1146

RESULT 3
US-11-186-284-25
Sequence 25. Application US/11186284
Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kametkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Ribodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MEMO1-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186, 284
PRIOR FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301, 822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339, 971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361, 978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381, 988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 11447
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1) ... (9192)
US-11-186-284-25

Alignment Scores:
Pred. No.: 0.00135 Length: 11447
Score: 131.00 Matches: 72
Percent Similarity: 43.11% Conservative: 72
Best Local Similarity: 21.56% Mismatches: 118
Query Match: 6.84% Indels: 72

DB: 7 Gaps: 17
US-09-970-076-2 (1-368) x US-11-186-284-25 (1-11447)
QY 44 AspLeuTyrPheIleLeuAepLysSerGlySerVal---LeuHisThrAsnGluIle 62
Db 418 GATTTGGTTTCTCTCGATGAGTGGCTCTTGAGAGTGGAGAAATATTTCAATGATCATTT 477
QY 63 TyrTyrPheValGluGlnLeuAlaHisLysPheIle-----SerProGlnLeuArgMet 80
Db 478 TTAGACTTCAATTCCTGCTCTTGTGTCTCTTTTGACATTTGGGAGAGAGAGAAAGAGTT 537
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysSerThrGlu-----Asp 98
Db 538 GAGTTGTTTAAATACAGCTTGTACACAGAGATCGAATTTTAACTTAATCACTGATCA 597
QY 99 ArgGluGlnIleArgInglyLeuGlnGluLeuGlnLysValLeuProGlyIlyAspThr 118
Db 598 AGGATGAATCTTCTGTCGCAATTAATAAAATTCGA-----TATAAAGTGGCAACACA 651
QY 119 TyrMetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsn----- 135
Db 652 ATGACAGGGGATGCCATTTGATTATTAAATAATCTTACGGAATCTGCTGGGCA 711
QY 136 ArgGlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHsiGlu 155
Db 712 AGAGTTGGCTTTCTTAAAGTGGCAATTTATT-----ACGATGAAATCCAGAT 765
QY 156 AspLeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleVal 175
Db 766 GAAGTG-----GAAATTCAGCAAGAGAGAGCTGTGATGTGAGTTGAAGTT 813
QY 176 TyrCysValGlyValIlyAspPheAsnGluThrGlnLeuAlaArgIleAlaAsp----- 193
Db 814 TTCTCTTGGCGATTAAAGCTGCAATGCAAAAGAACTCAAAAGATGCTTCACACCT 873
QY 194 SerLysAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGlyIleHis 213
Db 874 TCACGTGAACCATTTTTCATATGCGCCAC---TTTGATGCAATTTGGATTTACAGAT 930
QY 214 SerIleLeuLysLysSerCysIle-----GluIleLeuAlaAla 226
Db 931 GAGATCATCTCCAGAGTGTCTCAGAGTTGATGAGAGCTGTGTGAAATGTTAGTGA 990
QY 227 Glu-----ProSerThrIleCysValGlyIlySerPheGlnValVal 241
Db 991 GAAAGAGTTGTGAGCTCTCTCAAAATTTGATTCATGAGAGTCTTCAAAATATGTT 1050
QY 242 ArgGlyAsn-----GlyPheArg----- 247
Db 1051 AAGCTTAATTTGAATCATCTCTTACATGATCCAGTACGTAGCTACAAAGTCACTCCACACA 1110
QY 248 -----HisAlaArgAsnValAspArgValLeuCysSerPheLys 260
Db 1111 ATGACTGCAGAGAGCGAGACGACGCTCGAGTGGCG----- 1149
QY 261 IleAsnAspSerValThrLeuAsnGlyLysProPheSerValIlyAspThrTyrLeuLeu 280
Db 1150 ---CCTCAGACAAACGCTCAGTGTTCGCGACCTCTCAGACACGAGATAC----- 1200
QY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
Db 1201 -----CAGATCAGTGTTCGCGCATGTGAAGGAAATGATCATCCAGT 1239
QY 301 AspGlyLeuSerPheIle---SerSerSerValIleIleThrThrHisCysSerAsp 319
Db 1240 GAACCATTTCAATATGAGAGAGACCTCAGCCATGAAATGTTCAAGTGAATGTTACGTT 1299
QY 320 GlySerIleLeuAlaIleAlaLeuLysIleLeuPheLeuLeu 333
Db 1300 GGT-----GTGATATATAAAGCCGATATTGTGTTTGGTT 1335

RESULT 4

Oy	200	ProValiaAaerGlyPheGlnAlaLeuInglyIleIleHLeSerIleLeuLysSer	219
Db	966	CTGTGGCGCAAC---TTTCAAGCCAAATTGAAGCCTGACTCAAGTCTTCCAAAGAAGTTG	10222
Oy	220	Cys-----LleGluIleLeuAlaIaIa-----Glu	227
Db	1023	TGCATTAAGTCTGCTCTCTCTGTGTGGCTCTTTCGGGGCATGCTGGAGTAGAGTATTCA	10822
Oy	228	ProSerThrIle-----CysAlaGlyLysSerPheGln	238
Db	1083	CCTTCCCGGGTTCATTCTGTGTCTTACTGTGTCCTCCAAAGTACTGTGCTGGAAAGGGGCTTTTA	11422
Oy	239	ValValIaIaArgGlyAaGlyPheArgHIsala	249
Db	1143	GCAAAAGTCCAG-----ATAAGACACAGT	1166
RESULT 6			
US-10-821-234-182/c			
; Sequence 182, Application US/10821234			
; Publication No. US2005025511A1			
GENERAL INFORMATION:			
; APPLICANT: Labat, Ivan			
; APPLICANT: Stache-Crain, Blrgit			
; APPLICANT: Andarmani, Susan			
; APPLICANT: Tang, Y. Tom			
; TITLE OF INVENTION: Methode for Diagnosis and Treatment of Preeclampsia			
; FILE REFERENCE: 821A			
; CURRENT APPLICATION NUMBER: US/10/821,234			
; CURRENT FILING DATE: 2004-04-07			
; PRIOR APPLICATION NUMBER: US 60/462,047			
; PRIOR FILING DATE: 2003-04-07			
; NUMBER OF SEQ ID NOS: 1704			
; SOFTWARE: pc_seq_version 1.0			
; SEQ ID NO 182			
; LENGTH: 2501			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-821-234-182			
Alignment Scores:			
Pred. No.:			
Score: 0.0157 Length: 2501			
Percent Similarity: 113.50 Matches: 66			
Best Local Similarity: 38.28% Conservative: 63			
Query Match: 19.58% Mismatches: 109			
Query Match: 5.93% Indels: 99			
Gaps: 17			
US-09-970-076-2 (1-368) x US-10-821-234-182 (1-2501)			
Oy	28	GInGIyGlyAaArgGlyLysArgGly---GlyProIaIa-----	38
Db	1631	GAAGAGTCGATGCTGAGGATGGGCAAGCGGCGGGAACAACAGAGCGAAGATCTC	1572
Oy	39	-----CysTyArgIyGlyPheAaerLeuTyrrPheIleLeuAaerLysSerGlySerVal---	55
Db	1571	CTGAGACCTTGAGGCTCATGAAACATCACTACCTGCTAGATGATGATCAGACAGCATGGG	1512
Oy	56	-----LeuHieHieTrpAaerGluIleTyrrTyrrPheValGluGlnLeuAlaHis	71
Db	1511	GCCAGCAACTTCACAGAGCCAAAGTGTCTAATCAATTATTAAGAAAGGTGCAAGT	1452
Oy	72	LysPheIleSerProGlnLeuTyrrMetSerPheIleValIlePheSerThrArgGlyThrThr	91
Db	1451	TATGTGTGAAGCCA-----AGATATGCTCAAGTACATATGCAACATACCCCAAAATT	1398
Oy	92	LeuMetLysLeuThrGlu-----AaerArgGlnGlnIleArgGlnIyLeuGlu	107
Db	1397	TGGGTCAAAAGTGTCTGAAGACAGACAGCATATGACAGCTGGGTCAAGACAGCTCAAT	1338
Oy	108	GluLeu-----GlnLysValLeuProGlyGlyAaerThrTyrrMetHieGluIy	123
Db	1337	GAATATCATTTATGAAGACCAACCAAGTTGAATGAGGAACTAATACC-----	1293

Oy	124	PheGluValArgAlaSerGluGlnIleTyrTyrCysValuAsnArg	-----	136
Db	1292	---AAGAAGGCGCTCCAGCAGGTATACAGCATATGAGCTGGCAGATGAGCTCCCTCT	-----	1236
Oy	137	GlnGlyTyr---ArgThrAlaSerValIleIleAlaLeuThrAspGly	-----	151
		:::		
Db	1235	GAAGGCTGGAACCCGACCCGCGCATGTATCATCTCTCATGCTGATGGATTCACAAACATG	-----	1176
Oy	152	-----GlnLeuIleGluAspLeuPhePheTyrSerGlu	-----	162
Db	1175	GCGCGGGAACCAATTACTGTCATTGATGAGATGCCGAGCTTGCTATACATTGGCAGAGAT	-----	1116
Oy	163	ArgGluIleAsnArgSerArgAspLeuGlyValaIleValTyrCysValaGly	-----	180
Db	1115	CGCAAAACCCAGACGAGAGATTAATCTGGATGTCTATGTATGTTGGGGGTCCGGGCTTGGTG	-----	1056
Oy	181	LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro	-----	200
Db	1055	AACCAAGTGAACATCAATGCTTGGCTTCCAAAGAAATAGCAATGATGTTGTTCAA	-----	996
Oy	201	ValAsnAspArgLysPheGlnAlaLeuGlnGlyTyrIleHisSerIleLeuLysSerCys	-----	220
Db	995	GTCAGAGAT---ATGGAACCTCGAAGATGTTTCTTACAAATGATGATGAAGAAGC---	-----	942
Oy	221	IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVala	-----	240
		:::		
Db	941	-----CAGTCTCTGAGTCTCTGT-----	-----	924
Oy	241	ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys	-----	260
Db	923	-----GGCATGTTGTGGAAACACAGAGAGGGTACCAT-----	-----	891
Oy	261	IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu	-----	280
Db	890	-----TACCACAGAGACATGAGCGCCAGATCTCAGTC-----	-----	855
Oy	281	CysProAlaProIleLeuLysGluValaGlyMetLysAlaAlaLeuGlnValaSerMetAsn	-----	300
Db	854	-----ATTGCGCCTTCAAAGGAGCAGCAGAGCTGTATGGGG-----	-----	819
Oy	301	AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThrAspCys	-----	317
		:::		
Db	818	-----GCTGTGTCTCTGAGTACTTGTGCTGACAGCAGCACATTTG	-----	777
RESULT 7				
US-10-131-826A-293				
Sequence 293, Application US/10131826A				
Publication No. US20050245730A1				
GENERAL INFORMATION:				
APPLICANT: Baker, Kevin P.				
APPLICANT: Beresini, Maureen				
APPLICANT: Deforge, Laura				
APPLICANT: Desnoyers, Luc				
APPLICANT: Filvaroff, Ellen				
APPLICANT: Gao, Wei-Qiang				
APPLICANT: Gerritsen, Mary E.				
APPLICANT: Goddard, Audrey				
APPLICANT: Godowski, Paul J.				
APPLICANT: Gurney, Austin L.				
APPLICANT: Sherwood, Steven				
APPLICANT: Smith, Victoria				
APPLICANT: Stewart, Timothy A.				
APPLICANT: Tumas, Daniel				
APPLICANT: Watanabe, Colin K				
APPLICANT: Wood, William				
APPLICANT: Zhang, Zemin				
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC				
FILE REFERENCE: P33081C128				
CURRENT APPLICATION NUMBER: US/10/131,826A				
CURRENT FILING DATE: 2002-04-24				
PRIOR APPLICATION NUMBER: 60/049911				

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/ PRIOR FILING DATE: 1997-06-18
/ PRIOR APPLICATION NUMBER: 60/056974
/ PRIOR FILING DATE: 1997-08-26
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059115
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059117
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059122
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059184
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059352
/ PRIOR FILING DATE: 1997-09-19
/ PRIOR APPLICATION NUMBER: 60/059588
/ PRIOR FILING DATE: 1997-09-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO: 293
/ LENGTH: 3449
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-131-826A-293

Alignment Scores:
Pred. No.: 0.0263 Length: 3449
Score: 113.50 Matches: 55
Percent Similarity: 43.90% Conservative: 53
Best Local Similarity: 22.36% Mismatches: 103
Query Match: 5.93% Indels: 35
DB: 6 Gaps: 13

US-09-970-076-2 (1-368) x US-10-131-826A-293 (1-3449)
QY 44 AapLeuTyRheIleuAerLySerGlySerVal---LeuHisIstPraengIuile 62
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 372 GACCTGGTTTCAATGCACTGCACTGCGAGTGTCAACACCCATGACTGCAAGAGT 431
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 63 TyTyTyRhe---ValGluIleuAlaHisLeuRheIleSerProGluLeu---ArgMet 80
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 432 AACGAGTTCACTGGGACATCTTGCATCTTGGACATCTGCTGATGACCCGAGT 491
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 81 SerRheIleValRheserThrArgGlyThrThleu-----MetLysLeu 95
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 492 GGCCTGCTCCAAATAT-----GGCAGCACTGTCAAGATGATGTTCCCTCAAGACC 542
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 96 ThrGluAerArgGluGluIleArgGluIleuGluIleuGluIleuValLeuProGly 115
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 543 TTCAGAGAGAACGTCGAGGTGAGCGGTGCTGCAAGAGATGGCGCATCTGTCACGGGC 602
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 116 GluAerThrTyRheHisGluGlyRheGluArgAlaSerGluIleTyTyGluAer 135
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 603 ACCATGACTGGCTGGCCATCCAGATAT-----GCCCTGAACATCGCATCTCGAAG 653
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 136 ArgGluIleTyTyRg-----ThraLaserValIleIleAlaLeuThrAer 150
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 654 GCAGAGGGGGCCGGCCCTGAGGAGAGATGTGCCAGGGGTCAATGATGTGACAGAT 713
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 151 GluIleuHisGluAerLeuRheRheTySerGlyuArgGluIleAerAerAerAer 170
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 714 GGGAGACCTCAGACTCCGTC-----GCCAGGTGGCTGTAAAGCAGCGGAC 761
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 171 LeuGlyAlaIleValTyTyValGlyVal-----LysAerPheAerGluThrGluLeu 188
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 762 ACCGGCATCTTAATCTTGCAATGATGTGGGCGAGGTAACTTCAACACCTTGAGATCC 821
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 189 AlaArgIleAlaAerSerTyAerRheValRheProValAerAerGlyRheGluIleu 208
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 822 ATTGGAGTAGCCCGCCATGAGAGCAATGATCTTCTTGTCGCAAT---TTCACGCAAGATT 878
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
QY 209 GInGlyIleIleHisSerIleuLySerGlyIleGluIleuAlaAerPro 228
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 879 GAGACGTCGACTCCGTTGTCAGAAAGTTGTACAGCGCCACATGTGCGACGCCCTG 938
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 229 SerThrIleCyAlaGlyGluSerPheGluValValArgGlyAerGlyRheArgHis 248
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 939 GAGCATTACTGTGCC-----CACTTGTGCATCAACATCTCGGCTCATAGCTTGCAGG 992
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 249 AlaArg-----AerValAerArgValLeuCySerPheLyIleAerAer 263
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 993 TGCAGAACAGGCTACATTTCTCACTCGGATCGAGTCAAGAGACTTGC-----AGAAATCCAGAT 1046
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 264 SerValThrLeuAerGlu 269
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1047 CTGTGTGCATGAGAGAC 1064
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
US-10-601-368-20
/ Sequence 20, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lots, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ PRIOR FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 20
/ LENGTH: 3564
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(3564)
US-10-601-368-20

Alignment Scores:
Pred. No.: 0.0558 Length: 3564
Score: 111.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 5.80% Indels: 38
DB: 6 Gaps: 9

US-09-970-076-2 (1-368) x US-10-601-368-20 (1-3564)
QY 39 CyTyTyGlyValRheAerLeuTyRheIleuAerLySerGlySerValLeuHis 58
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 475 TGCAGACTTAATGACATCTGCTATTTGTAGATGGCTCCAAACAGATC---TACCCC 531
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 59 TrAengIuIleTyTyRheValGluIleuAlaHisLeuRhe---IleSerPro--- 76
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 532 TGGGTGAGGTCCAAACATCTTCTCATCATATCTGCAAAAAGTTCACTTGGCCCGGC 591
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 77 GInLeuAerMetSerRheIleValRheserThrArgGlyThrThleuMetLyAer 96
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 592 CAGATCCAGTGCAGAAATAGTCCAGTATGAGAAAGATCCGTCATGATGATCCACTT--- 648
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 97 GluAerArgGluIleArgGluIleuGluIleuGluIleuValLeuProGlyGly 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 649 AATGATACAGCTCTGTAAAGATGTGTGGAAGCCGCCAGCCACATTAAGCAGAGGA 708
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 117 AepThrTyRheHisGluGlyRheGlu-----ArgAlaSerGluIleTyTy 133
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 709 GGGACAGAAACCCGACGCGCATTTGGCATTTGAATTTGACAGCGCTTCCAGAG 768
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 134 GluAerArgGluIleTyTyRgThrAlaSerValIleIleAlaLeuThrAerGlyLeu 153
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 769 GGTGAAGAAAGGGCCAG-----AAAGTATGATTGTATCATCAGACGGGAAATCC 822
Qy 154 Hiegluasp----- 156
Db 823 CACGACAGCCCGACCTGAGAAAGTATCCGGCAGACGAGAAAGCAACGTGACCAGA 882
Qy 157 -----Leuphepetyrsergluarglu1aasnargserargapleu 171
Db 883 TACGCTGTGGCCGTTTGGGCTACTACACCGCAGGGGAGTCAATCCAGACATTTTCTA 942
Qy 172 G1YAla1leValTYrCyval1glYval1lyasp-----PheangluThrln 187
Db 943 AATGAATCAAAATACATGCGCAGACCGCTGAGACAAAGACATTTCTCAACGTACAGAT 1002
Qy 188 Leu1aArg1leal1aasper1yAspH1sval1PheProVal1asnarg1yPheGlnAla 207
Db 1003 GAGCGCGCCCTG-----MAGGACATTGTGATGCCCTTGGGACAGAGATCTTCAGC 1053
Qy 208 leuGlnGly 210
Db 1054 TTGGAAGGC 1062

RESULT 9
US-10-601-368-19
/ Sequence 19, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yong
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ PRIOR FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 19
/ LENGTH: 4858
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (28)...(3591)
US-10-601-368-19

Alignment Scores:
Pred. No.: 0.0916 Length: 4858
Score: 111.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 5.80% Indels: 38
Gaps: 9
DB: 6

US-09-970-076-2 (1-368) x US-10-601-368-19 (1-4858)
Qy 39 CyetYc1yglYpHeapleuTYrPhe1leleuasp1ySerGlySerVal1leuH1sH1s 58
Db 502 TGGCAAGACTTACATGACATGCTCATTTGTCTTAGATGGCTCCAAAGCATC---TACCC 558
Qy 59 TTPAanglu1leTYrTYrPheVal1gluGlnLeuAlaH1s1yasphe---1leSerPro--- 76
Db 559 TGGGTGGAGGCTCCAAACACTTCTCATCATATATCCTCAAAAGTTTCTTATGGCCCGGC 618
Qy 77 GlnLeuArgMetSerPhe1leVal1PheSerThrArgGlyThr1leuMet1y1leuThr 96
Db 619 CAGATCCAGGTGGAAATAGTCCAGTATGAGAAAGATGCCCTCATGATTCACACTT--- 675
Qy 97 GluAspArgGluGln1leArgGln1yLeuGluGluLeuGln1yVal1leuProGlyGly 116
```

```
Db 676 AATGACTACAGCTGTGTAAAGATGTGTGTGAAGCCGCCACATTCAGACAGAGA 735
Qy 117 AsPTThrTYrMetH1seglu1yPheGlu-----ArgAlaSerGluGln1leTYrTYr 133
Db 736 GGGACAGAGACCCGCAACGGCATTTGGCATTTGAATTTGCACGCTCGAGGCTTTCAGAG 795
Qy 134 GluAsnArgGln1yTYrArgThrAlaSerVal1le1leAlaLeuThrAspGlyGluLeu 153
Db 796 GGTGAAGAAAGGGCCAG-----AAAGTATGATTGTCTATCAGACGGGAAATCC 849
Qy 154 Hiegluasp----- 156
Db 850 CACGACAGCCCGACCTGAGAAAGTATCCGGCAGACGAGAAAGCAACGTGACCAGA 909
Qy 157 -----Leuphepetyrsergluarglu1aasnargserargapleu 171
Db 910 TACGCTGTGGCCGTTTGGGCTACTACACCGCAGGGGAGTCAATCCAGACTTTTCTA 969
Qy 172 G1YAla1leValTYrCyval1glYval1lyasp-----PheangluThrln 187
Db 970 AATGAATCAAAATACATGCGCAGACCGCTGAGACAAAGACATTTCTCAACGTACAGAT 1029
Qy 188 Leu1aArg1leal1aasper1yAspH1sval1PheProVal1asnarg1yPheGlnAla 207
Db 1030 GAGCGCGCCCTG-----MAGGACATTGTGATGCCCTTGGGACAGAGATCTTCAGC 1080
Qy 208 leuGlnGly 210
Db 1081 TTGGAAGGC 1089

RESULT 10
US-10-995-561-464
/ Sequence 464, Application US/10995561
/ Publication No. US2005027054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ TITLE OF INVENTION: DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ PRIOR FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 464
/ LENGTH: 3175
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-464

Alignment Scores:
Pred. No.: 0.123 Length: 3175
Score: 107.50 Matches: 50
Percent Similarity: 40.28% Conservative: 37
Best Local Similarity: 23.15% Mismatches: 84
Query Match: 5.62% Indels: 45
Gaps: 9
DB: 6

US-09-970-076-2 (1-368) x US-10-995-561-464 (1-3175)
Qy 45 leuTYrPhe1leleuasp1ySerGlySerVal1----- 55
Db 243 GTGTACTGTGTGTGGACACCTGGAGAGCGTACCATGCAATGCCCAACGACATCTTG 302
Qy 56 LeuH1sH1s1eTPAanglu---1leTYrTYrPheVal1gluGlnLeuAlaH1s1yPhe1le 74
Db 303 CTCCTTCCACATGAGAGAGTTGCGCGCAGTTTATAGCCAGGTGAGAAACAGATTCTAC 362
Qy 75 SerProGlnLeuArgMetSerPhe-----1leVal1PheSerThrArgGlyThr 90
Db 363 CTGACACAGGTGCGCTGAGCTGGCGCTATGCGGCTCATCTTCTACACGAGTGGAG 422
Qy 91 ThrLeuMet1y1leuThrGlnAspArgGluGln1leArgGln1yLeuGluGluLeuGln 110
```



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Db      423 GGTTCAGCCACCGGCGACGACCGGCTCTTCATCAAGAACCTGCAGGCGCATCACG 482
Qy      111 LysValLeuProGlyIAspThrTyrmethIAsgluGlyPheGluArgAlaSerGluGln 130
Db      483 TCCTTCGCGCGGCGC-----ACCTTCACCGACTGCGCGCTGGCCAACTAGACGAGACG 536
Qy      131 IleTyTrGluAsnArgGlnGlyTyArgThrAlaSerValIleIleAlaLeuThrAsp 150
Db      537 ATCCGCGAGACCGGACGACGAGGCG-----ACGTCACACTTCGCGCGTGCATCACCGAC 590
Qy      151 GlyGluLeuHisGluAspLeuPhePheTySerGluArgGluAlaAsnArgSerArgAsp 170
Db      591 GGCACAGTCACCGGCGACCGCCCTCGGCGGCGATCAAGCTGACGCGCGCGCGCGAG 650
Qy      171 LeuGlyAlaIleValTyCysVal-----GlyValLys 181
Db      651 GAGGCGATCCGGCTCTTCGCGCGTGGCCCCCAACCAAGACTGAAAGACGAGCGCTGGCG 710
Qy      182 AspPheAsnGluThr-----GlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 199
Db      711 GACATCGCGACGACCGCGCGACGAGCTTACCGC-----AACGACTACGCGCACG 758
Qy      200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu----- 216
Db      759 ATGCTCCYGACTCCACCGAGATCRAACAGACACCATCAACCGCATCATCAAGTCATG 818
Qy      217 -----LysLysSerCysIleGluIle 223
Db      819 AAACAGAAAGCTTACGAGAGAGTCTACAAAGTAGAGTGCCTGGAATTC 866

```

RESULT 11

```

US-10-995-561-465
; Sequence 465, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 3464
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-465

```

Alignment Scores:

```

Pred. No.: 0.142 Length: 3464
Score: 107.50 Matches: 50
Percent Similarity: 40.28% Conservative: 37
Best Local Similarity: 23.15% Mismatches: 84
Query Match: 5.62% Indels: 45
DB: Gaps: 9

```

US-09-970-076-2 (1-368) x US-10-995-561-465 (1-3464)

```

Qy      45 LeuTyPheIleLeuAspLysSerGlySerVal----- 55
Db      243 GTGTACTTGTGCTGTGACACCTCGAGAGAGCTGACCATGACAGTCCCGCCAGCATCTCG 302
Qy      56 LeuHisIleTrpAsnGlu---IleTyTrPheValGlnGlnLeuAlaHisLysPheIle 74
Db      303 CTCCTCCACATGAAGAGATTGCGCGCAGTTCATGACGACGAGAAAGATTCTAC 362
Qy      75 SerProGlnLeuArgMetSerPhe-----IleValPheSerThrArgGlyThr 90
Db      363 CTGACACAGGTGCGCTGAGAGTGGCGCTTAYGCGCGCTGCACATTCTTGAACAGGTGAG 422

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Qy      91 ThrLeuMetLysLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGlnGluLeuGln 110
Db      423 GGTTCAGCCACCGGCGACGACCGGCTCTTCATCAAGAACCTGCAGGCGCATCACG 482
Qy      111 LysValLeuProGlyIAspThrTyrmethIAsgluGlyPheGluArgAlaSerGluGln 130
Db      483 TCCTTCGCGCGGCGC-----ACCTTCACCGACTGCGCGCTGGCCAACTAGACGAGACG 536
Qy      131 IleTyTrGluAsnArgGlnGlyTyArgThrAlaSerValIleIleAlaLeuThrAsp 150
Db      537 ATCCGCGAGACCGGACGACGAGGCG-----ACGTCACACTTCGCGCGTGCATCACCGAC 590
Qy      151 GlyGluLeuHisGluAspLeuPhePheTySerGluArgGluAlaAsnArgSerArgAsp 170
Db      591 GGCACAGTCACCGGCGACCGCCCTCGGCGGCGATCAAGCTGACGCGCGCGCGCGAG 650
Qy      171 LeuGlyAlaIleValTyCysVal-----GlyValLys 181
Db      651 GAGGCGATCCGGCTCTTCGCGCGTGGCCCCCAACCAAGACTGAAAGACGAGCGCTGGCG 710
Qy      182 AspPheAsnGluThr-----GlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 199
Db      711 GACATCGCGACGACCGCGCGACGAGCTTACCGC-----AACGACTACGCGCACG 758
Qy      200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu----- 216
Db      759 ATGCTCCYGACTCCACCGAGATCRAACAGACACCATCAACCGCATCATCAAGTCATG 818
Qy      217 -----LysLysSerCysIleGluIle 223
Db      819 AAACAGAAAGCTTACGAGAGAGTCTACAAAGTAGAGTGCCTGGAATTC 866

```

RESULT 12

```

US-10-995-561-466
; Sequence 466, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 3468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-466

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Alignment Scores:

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Pred. No.: 0.142 Length: 3468
Score: 107.50 Matches: 50
Percent Similarity: 40.28% Conservative: 37
Best Local Similarity: 23.15% Mismatches: 84
Query Match: 5.62% Indels: 45
DB: Gaps: 9

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US-09-970-076-2 (1-368) x US-10-995-561-466 (1-3468)

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Qy      45 LeuTyPheIleLeuAspLysSerGlySerVal----- 55
Db      243 GTGTACTTGTGCTGTGACACCTCGAGAGAGCTGACCATGACAGTCCCGCCAGCATCTCG 302
Qy      56 LeuHisIleTrpAsnGlu---IleTyTrPheValGlnGlnLeuAlaHisLysPheIle 74
Db      303 CTCCTCCACATGAAGAGATTGCGCGCAGTTCATGACGACGACGAGAAAGATTCTAC 362
Qy      75 SerProGlnLeuArgMetSerPhe-----IleValPheSerThrArgGlyThr 90
Db      363 CTGACACAGGTGCGCTGAGAGTGGCGCTTAYGCGCGCTGCACATTCTTGAACAGGTGAG 422

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Qy 91 ThrleuWetLysleuThrgluAerArgGluGlnleArgGlnGlyleuGln 110
|||
Db 423 GTGTTACAGCCACCGGCGACGCGGCTTCCTTCAAGAACTCGAGGGCATACG 482
Qy 111 LysValLeuProGlyArgPheThrTyMetHleGluGlyPheGluArgAlaSerGluGln 130
|||
Db 483 TCCTTCGCGCGGCGC-----ACCTTACCGAGCTGGCGGCTGGCAATGACGAGACAG 536
Qy 131 IleTyTrgGluLeuArgGlnGlyTyArgThrAlaSerValIleleAlaLeuThrAsp 150
|||
Db 537 ATCCGGACGACCGCGACAGAGGCG-----ACCTGCACCTTCGCGCTGATCACCAGAC 590
Qy 151 GluGluLeuHleGluAerLeuPhePheTySerGluArgGluAlaAerArgSerArgAsp 170
|||
Db 591 GGGCAGCTCACCGGCGACCGCTTCGGGGGATCAAGTCAAGCGCGAGCGCGGAG 650
Qy 171 LeuGlyAlaIleValTyTrGlyVal-----GlyValLys 181
|||
Db 651 GAGGGCATCGCGCTTCGCGCTGGCCCCCAACCAAGAACTGAAGAGAGCGGCTTCGG 710
Qy 182 AepPheArgGluThr-----GlnLeuAlaArgIleAlaAerSerLysAerPheValPhe 199
|||
Db 711 GACATCGCGACGACGCGCGACGAGCTTACCGC-----AACGACTACGCGACCC 758
Qy 200 ProValAsnAerGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu----- 216
|||
Db 759 ATGCTGCGCTCACTCCACGAGATCCACAGACACCACTCAACGCGATCATCAAGTCAAG 818
Qy 217 -----LysLysSerCysIleGluIle 223
|||
Db 819 AAACACGAAAGCTTACGAGAGTCTTACAGAGTGAAGTCTGCTCGGAATC 866
RESULT 13
US-10-601-368-2
; Sequence 2, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ. ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3564
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3564)
US-10-601-368-2
Alignment Scores:
Pred. No.: 0.171 length: 3564
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 5.59% Indels: 38
DB: Gaps: 9
US-09-970-076-2 (1-368) x US-10-601-368-2 (1-3564)
Qy 39 CysTyTrgIleGlyPheAerPheIleLeuAerLysSerGlySerValLeuHleHis 58
|||
Db 475 TGGCAGACCTACATGACATCGATCTGTCTCGATGCGTCCAAAGACATC--TACCC 531

Qy 59 TrpAsnGluIleTyTrgPheValGluGlnLeuAlaHisLysPhe---IleSerPro--- 76
|||
Db 532 TGGGTGAGGTTACAGACCTTCTCATCAATCATCTGTAAGAAAGTTTATCATTTGCGCAGG 591
Qy 77 GlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrleuWetLysLeuThr 96
|||
Db 592 CAGATCCAGGTGTGAGTGTGACATGAGTGAAGATGTGTGATGATGATTTACCTC--- 648
Qy 97 GluAerArgGluGlnIleArgGlnGlyleuGlnGluGlnLysValLeuProGlyGly 116
|||
Db 649 AACGACTACAGCTCTGTAAAGATGTGTGAAGCTGCCAGCCATTTGACAGAGAGA 708
Qy 117 AepThrTyMetHleGluGlyPheGlu-----ArgAlaSerGluGlnIleTyTrg 133
|||
Db 709 GGAACAGACGCCGACGCGATTTGGCATTTGATTCACAGCTTCAAGGCTTCCAGAG 768
Qy 134 GluAsnArgGlnGlyTyTrgThrAlaSerValIleleAlaLeuThrAspGlyGluLeu 153
|||
Db 769 GGTGAAGAGAAAGAGACCAAG-----AAGGTATGATTTGTATCAGATGGGAGATCC 822
Qy 154 HisGluAerPhe----- 156
|||
Db 823 CACGACAGCCGACAGCTCGAAGAGTATCCAGCAAGCGAAAGACAACTGAACAGA 882
Qy 157 -----LeuPhePheTySerGluArgGluAlaAerArgSerArgAerPhe 171
|||
Db 883 TATGCGGTGCGCTCTCGGCTTACTACACCGAGGGGATCAATCCAGAACTTTCTA 942
Qy 172 GlyAlaIleValTyTrGlyValGlyValLysAsp-----PheAsnGluThrGln 187
|||
Db 943 AATGAATCAATATACATCGCGACGATGACCTGATGACAGACATTTCAATGACATGAT 1002
Qy 188 LeuAlaArgIleAlaAerSerLysAerPheValPheProValAsnAerGlyPheGlnAla 207
|||
Db 1003 GAGCTGCGCTG-----AAGGACATTTGTGATGATGCTGGGAGACAGAACTTTCAGC 1053
Qy 208 LeuGlnGly 210
|||
Db 1054 CTGGAAGGC 1062
RESULT 14
US-11-000-463-574
; Sequence 574, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Aendi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: NOVEL Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870


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Qy 157 -----LeuphepheTySerGluArgGluIaenArgSerArgAspLeu 171
Db 934 TATGGCGTGGCCGCTCTGGGCTACTACACCGCAGGGGATCAATCCAGAACTTTCTA 993
Qy 172 GlyAlaIleValTyrCysValGlyValLysAsp-----PheAsnGluThrGln 187
Db 994 AATGAATCAAAATACATCGCCAGTACCTGATGACAAGCACTTCTTCAATGTCACGTGAT 1053
Qy 188 LeuAlaArgIleAlaAspSerLysAspHisValPheProValaenAspGlyPheGlnAla 207
Db 1054 GAGGCTGCCTTG-----AAGGACATTGTGATGCCCTGGGGGACAGAAATCTTCAGC 1104
Qy 208 LeuGlnGly 210
Db 1105 CTGGAAGGC 1113

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Search completed: December 19, 2005, 02:29:25
 Job time : 324.957 secB

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; APPLICANT: Gallatin, W. Mich
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,889
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: P38,659
; REFERENCE/DOCKET NUMBER: 27866/32168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-889-46

Query Match      10.8%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7.4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY      11 PACYG-GPDLVYFILDKSGSV-LHHMNEIYFVFEQLAHKRTSPQLRMSFIVFSTRGTTLMK 68
DB      144 PEPGCGEMDIALFIDSGSIDQSDFTQMKDFYKALMGQLASTSTSLMQYSITLKTHT 203
QY      69 LTEDR-----EQIRGLBELQKVLPGGDTVMHEGFERASEQIYYENRQGYRTA-SVITIAL 122
DB      204 FTEFKSSLSPQSLVDATVOLQ-----GLTYTASGIQKVVKELPHSKNGARKSAKKILIVI 258
QY      123 TGELHEDLFFYSE--REANRSRDGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
DB      259 TGGQKRDPLEVRHVIPEAKA---GIIRYAGVGDAPREPTALQELNLTIGSAPSGDHVF 315
QY      174 PVNDGFQALOGIHTSLKSCIEILAAPEPTICAGESFQVVVYVNGFRHARNVD 227
DB      316 KVGN-FVALRSIQROIQEK-----IFAIEGTESRSSSSFOHEMSQEGFSSALSMD 364

RESULT 3
US-08-485-618-46
; Sequence 46, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
```

```

; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,618
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; APPLICATION NUMBER: US 08/362,652
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32797
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-618-46

Query Match      10.8%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7.4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY      11 PACYG-GPDLVYFILDKSGSV-LHHMNEIYFVFEQLAHKRTSPQLRMSFIVFSTRGTTLMK 68
DB      144 PEPGCGEMDIALFIDSGSIDQSDFTQMKDFYKALMGQLASTSTSLMQYSITLKTHT 203
QY      69 LTEDR-----EQIRGLBELQKVLPGGDTVMHEGFERASEQIYYENRQGYRTA-SVITIAL 122
DB      204 FTEFKSSLSPQSLVDATVOLQ-----GLTYTASGIQKVVKELPHSKNGARKSAKKILIVI 258
QY      123 TGELHEDLFFYSE--REANRSRDGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
DB      259 TGGQKRDPLEVRHVIPEAKA---GIIRYAGVGDAPREPTALQELNLTIGSAPSGDHVF 315
QY      174 PVNDGFQALOGIHTSLKSCIEILAAPEPTICAGESFQVVVYVNGFRHARNVD 227
DB      316 KVGN-FVALRSIQROIQEK-----IFAIEGTESRSSSSFOHEMSQEGFSSALSMD 364

RESULT 4
US-08-362-652-46
; Sequence 46, Application US/08362652
; Patent No. 5766850
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
```

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ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-46
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Query Match 10.8%; Score 166; DB 1; Length 1155;

Best Local Similarity 28.2%; Pred. No. 7.4e-09;

Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

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11 PACYG-GFDLYPFLDKSGSV-LHNMNEYFVEQLAHKFTSPOLRMGFVIFSTRGTTLMK 68
144 PECPGQEMDIAFLIDSGSIDQSFQMKDFVAKLMGQLASTSTSPIMQYSNILKTHFT 203
69 LTEDR-----EQIRQGLEHLOKVLPGDVTYMHGFEFASQIYYENRGYRTA-SVIAL 122
204 FTEFKSLSPQSLVDALVQLQ---GLTYTASGIQKVVVELFHSKNGAKRSKAKILIVI 258
123 TDGELHEDLFFYSE--REANRSRLGAIYVCVKD-FNE-TQLART-----ADSKDHVF 173
259 TDGQKRPDPLEYRHVPEAKA---GIRIYAIGVDAFREPTLQELINTIGSAPSDHVF 315
174 PVNDGFOALOGIHSILKSCIEILAAEPSTICAGSFQVYVVRNGFRHARNVD 227
316 KVGN-FVALRSIQROIQEK---IFAIEGTERSSSSSFQHEMGEQGFSSLSMD 364
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RESULT 5

US-08-605-672-46

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; Sequence 46, Application US/08605672
; Patent No. 5817515
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-46
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Query Match 10.8%; Score 166; DB 1; Length 1155;

Best Local Similarity 28.2%; Pred. No. 7.4e-09;

Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

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11 PACYG-GFDLYPFLDKSGSV-LHNMNEYFVEQLAHKFTSPOLRMGFVIFSTRGTTLMK 68
144 PECPGQEMDIAFLIDSGSIDQSFQMKDFVAKLMGQLASTSTSPIMQYSNILKTHFT 203
69 LTEDR-----EQIRQGLEHLOKVLPGDVTYMHGFEFASQIYYENRGYRTA-SVIAL 122
204 FTEFKSLSPQSLVDALVQLQ---GLTYTASGIQKVVVELFHSKNGAKRSKAKILIVI 258
123 TDGELHEDLFFYSE--REANRSRLGAIYVCVKD-FNE-TQLART-----ADSKDHVF 173
259 TDGQKRPDPLEYRHVPEAKA---GIRIYAIGVDAFREPTLQELINTIGSAPSDHVF 315
174 PVNDGFOALOGIHSILKSCIEILAAEPSTICAGSFQVYVVRNGFRHARNVD 227
316 KVGN-FVALRSIQROIQEK---IFAIEGTERSSSSSFQHEMGEQGFSSLSMD 364
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RESULT 6

US-08-482-293A-46

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; Sequence 46, Application US/08482293A
; Patent No. 5831029
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-46

Query Match 10.8%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7,4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 11 PACYGFGLDYILDKSGSV-LHHMNEYFVEQLAHKFTSPQLRMSFIVSTRGTTLMK 68
DB 144 PCPCGEMDIAPFLIDSGSIDQSDFTQMKDFVAKLMGQLASTSTSLMQYSNLTHTFT 203
QY 69 LTEDR-----EQIRGLBELQKVLPGDITYMHGFERASQIYENRGYRTA-SVITLA 122
DB 204 FTEFSSLSPOSQVLDATVQLQ-----GLTYTAGIQLKVKELPHSKNGARKSKKILIV 258
QY 123 TGBELHEDLFFYSE--REANRSRLGAIYVCVXD-FNE-TQLARI-----ADSKDHYF 173
DB 259 TDCQKFRDPLEYRHVYIPEAKA---GIIFYAIGVDAFEPYALQELNLTGSAPOGDHYF 315
QY 174 PVNDGFQALQGIHSLIKKSCIEILAAPEPTICAGESFOVVVNGCFRRHARNVD 227
DB 316 KVGNFVVALRSIQRIQIEK-----IFAIEGTESRSSSFQHEMSQEGFSALSMD 364

RESULT 7

US-08-943-363-46
Sequence 46, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seair Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:

CLASSIFICATION: 530
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-46

Query Match 10.8%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 7,4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 11 PACYGFGLDYILDKSGSV-LHHMNEYFVEQLAHKFTSPQLRMSFIVSTRGTTLMK 68
DB 144 PCPCGEMDIAPFLIDSGSIDQSDFTQMKDFVAKLMGQLASTSTSLMQYSNLTHTFT 203
QY 69 LTEDR-----EQIRGLBELQKVLPGDITYMHGFERASQIYENRGYRTA-SVITLA 122
DB 204 FTEFSSLSPOSQVLDATVQLQ-----GLTYTAGIQLKVKELPHSKNGARKSKKILIV 258
QY 123 TGBELHEDLFFYSE--REANRSRLGAIYVCVXD-FNE-TQLARI-----ADSKDHYF 173
DB 259 TDCQKFRDPLEYRHVYIPEAKA---GIIFYAIGVDAFEPYALQELNLTGSAPOGDHYF 315
QY 174 PVNDGFQALQGIHSLIKKSCIEILAAPEPTICAGESFOVVVNGCFRRHARNVD 227
DB 316 KVGNFVVALRSIQRIQIEK-----IFAIEGTESRSSSFQHEMSQEGFSALSMD 364

RESULT 8

US-09-193-043-46
Sequence 46, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
LENGTH: 1155
TYPE: PRT
ORGANISM: Mus musculus
US-09-193-043-46

Query Match	10.8%	Score 166	DB 2	Length 1155
Best Local Similarity	28.2%	Pred. No. 7	4e-09	
Matches	66	Conservative	42	Mismatches 96
			Indels 30	Gaps 12
QY	11	PACYG-GFDLYFLDKGSV-LHHNWEIYYPVEOLAHKFISQOLMSFVSTRTCTLMK	68	
Db	144	PECPQEMDI AFLIGSSIDSDPTOMKDFPKALMGCLASTSTSFSLMOYSNLIKTHFT	203	
QY	69	LTEDE-----EQIQRGLELOKVLGCGTYMHGEFRASEQIYENRQGYRA-SVIAL	122	
Db	204	FTFEKSSLSPOSVDALVQL-----GLTYTASGLQKVKELFHSKNGARSAKILLVI	258	
QY	123	TDGELHELDLFYSE--REANRSRDLAGIIVYCVGYND-FNE-TQLARI-----ADSKDHF	173	
Db	259	TDGQRFRRDPLEYRHVYIPEAEKA--GIIRYALGVADFAREPTALDELNTIGSAPQDHVF	315	
QY	174	PVNDGFOALOGIHSILKSKCEILIAAPSTICAGESQVYVVRNGGFRHARVD	227	
Db	316	KVGN-FVALRSTQRIQEK---ITAIQGTBRSSSSQIHEHNSQGFSSALSM	364	

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RESULT 9
US-09-688-307A-46
; Sequence 46, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: NO.6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688.307A
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-688-307A-46

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Query Match	10.8%	Score 166	DB 2	Length 1155
Best Local Similarity	28.2%	Pred. No. 7.4e-09		
Matches	66	Conservative	42	Mismatches 96
			Indels 30	Gaps 12
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QY	69	LTEDE-----EQIRGLELEQVLPGDGYHNEGPERAS	EQGYENRQGYTA-SVIAL	122
Db	204	FTFFSSSLSPQSLVAIVQL-----GLTYTASGIAQV	KVELFPHSKNGARSAKILLVI	258
QY	123	TDGELHEDLFYSE--REANRSRDGAIVYCVGYND-FNE	-TQLARI-----ADSKHVF	173
Db	259	TDGQRFRRDPLERYAHYIPEAEKA--GIIRYAIGVD	ADPREPTALDELNTIGASPQDHVF	315
QY	174	PVNDGFOALQGIHSLIKKSCIEILAAEPSTICAESQ	VYVVRNGCGFHARND	227
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RESULT 10
US-09-350-259-46
; Sequence 46, Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 6620915el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1155
; TYPE: prt
; ORGANISM: Mus musculus
US-09-350-259-46

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Query Match	10.8%	Score 166;	DB 2;	Length 1155;
Best Local Similarity	28.2%	Pred. No. 7,4e-09;		
Matches	66;	Conservative 42;	Mismatches 96;	Indels 30; Gaps 12;

QY	11	PACYG-GPDLVFILDKGSV-LHHMNEIYFVEOLAHKFTSPQLRMSPFIVSTGTTLMK	68
DB	144	PECPGQEMDIATFLIDGSGSIDQSDPTQMKDFVKALMQLASTSTSFSLMOYSNTLIKTHFT	203
QY	69	LTERP-----EQIQGHELOKVLPGGDPTWMBEGFEASBOIYVENNGVYTA-SVIAL	122
DB	204	FTEKSKLSPOSTDAIVQD-----GLTTTASGIQKVKEFLFHSKNGAKSKAKKILVI	258
QY	123	TDEGLHEDLFFYS--REANRSBDLGIIVYCVGVKD-FNE-TQIARI-----ADSKDHF	173
DB	259	TDGQKFPDPLEYRAVIEPAEKA---GIIRVAIGVDAPREPTALQELNTIGSAPSODHVF	315
QY	174	PVNDGPQALGIIHSLIKSCITELLAEPSTICAGEFQVVRNNGRRHARNV	227
DB	316	KVNG-PAAKLSIQROIQEK---FPALEGESRKSSTSFQHEMSQEGSSALSMKD	364

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1      RESULT 11
2      US-08-485-618-53
3      ; Sequence 53, Application US/08485618
4      ; Patent No. 5728533
5      ;
6      ; GENERAL INFORMATION:
7      ;
8      ; APPLICANT: Gallatin, W. Michael
9      ; APPLICANT: Van der Vlieten, Monica
10     ; TITLE OF INVENTION: No. 5728533a1 Human 2 Integrin Alpha Subunit
11     ; NUMBER OF SEQUENCES: 103
12     ;
13     ; CORRESPONDENCE ADDRESS:
14     ;
15     ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
16     ; STREET: 233 South Wacker Drive, 6300 Sear Tower
17     ; CITY: Chicago
18     ;
19     ; STATE: Illinois
20     ;
21     ; COUNTRY: United States
22     ;
23     ; ZIP: 60606-6402
24     ;
25     ; COMPUTER READABLE FORM:
26     ;
27     ; MEDIUM TYPE: Floppy disk
28     ; COMPUTER: IBM PC compatible
29     ; OPERATING SYSTEM: PC-DOS/MS-DOS
30     ; SOFTWARE: Patentln Release #1.0, Version #1.25
31     ;
32     ; CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/08/485,618
/ FILING DATE:
/ CLASSIFICATION: 435
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32797
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 53:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1161 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-485-618-53
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Query Match 10.8%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 7,4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
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QY 11 PACYG-GPDLTYFLDKSGSV-LHHMNEIYFVEQLAHKFTSPQLRMSFIVFSTRTTLMK 68
DB 144 PBCPGQEMDIATFLDSSGSDIDSDFTQMKDFVAKLMGQLASTSTSLMOYSNIILKTHRT 203
QY 69 LTEDR-----EQIROGLEBELQKVLPGGDTYMHGFERASEQIYENRQGYRTA-SVIAL 122
DB 204 FTEFKSSLSQSLVDALIVQLQ-----GLTYTASGIQKVVELFHSKNGARKSAKILIIYI 258
QY 123 TDSGLHEDLFFYSE--REANRSRLGAIYVCVKD-FNE-TQLARI-----ADSCDHYF 173
DB 259 TDQKFRDPLAEYRHVIPLEAKA---GIIRYAIQVGDAFREPRLDELNTIGSAPSDHYF 315
QY 174 PVDGFOALOGIHTSLIKKSCIEILAEPTICAGSFQVVVYRNGNFRHARNVD 227
DB 316 KVGNI-FVALKRSIQRIQEK---IFAIETGTSRSSSFQHEMSQEGFSSALSMD 364
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RESULT 12

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/ Sequence 53, Application US/08362652
/ Patent No. 5766850
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 93
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/362,652
/ FILING DATE:
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/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32391
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 53:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1161 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-362-652-53
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Query Match 10.8%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 7,4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
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QY 11 PACYG-GPDLTYFLDKSGSV-LHHMNEIYFVEQLAHKFTSPQLRMSFIVFSTRTTLMK 68
DB 144 PBCPGQEMDIATFLDSSGSDIDSDFTQMKDFVAKLMGQLASTSTSLMOYSNIILKTHRT 203
QY 69 LTEDR-----EQIROGLEBELQKVLPGGDTYMHGFERASEQIYENRQGYRTA-SVIAL 122
DB 204 FTEFKSSLSQSLVDALIVQLQ-----GLTYTASGIQKVVELFHSKNGARKSAKILIIYI 258
QY 123 TDSGLHEDLFFYSE--REANRSRLGAIYVCVKD-FNE-TQLARI-----ADSCDHYF 173
DB 259 TDQKFRDPLAEYRHVIPLEAKA---GIIRYAIQVGDAFREPRLDELNTIGSAPSDHYF 315
QY 174 PVDGFOALOGIHTSLIKKSCIEILAEPTICAGSFQVVVYRNGNFRHARNVD 227
DB 316 KVGNI-FVALKRSIQRIQEK---IFAIETGTSRSSSFQHEMSQEGFSSALSMD 364
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RESULT 13

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/ Sequence 53, Application US/08605672
/ Patent No. 5817515
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/605,672
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-53

Query Match 10.8%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 7.4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 11 PACYG-GFDLYFLIDKSGSV-LHHMNEIYFVEQLAHKFTSPQLRMSFIVFSTRGTLMK 68
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QY 69 LTEDR-----EQIRQGLEBLQKVLPGDPTMHGFEFASQIYENKGYRTA-SVIAL 122
DB 204 FTEFKSLSPQSLVDAIVQD-----GLTYTASGIQKVVELPHSKNGAKSAKILIVI 258
QY 123 TDGELHEDLFFYSE--REANRSRLGAIYVCVGVK-FNE-TOLARI-----ADSKDHF 173
DB 259 TDQKFRDPLEYHVHVIPEAKA--GIRYAIGVGDAREPTALQELINTIGSAPSDHVF 315
QY 174 PVNDGFOALQGIHSLIKSCIEILAEPTICAGSFQVYVNGNGFRHARNVD 227
DB 316 KVGN-FVALRSIORQIOEK---IFAIEGTESSSSSFQHMGEQSGSALSMD 364

RESULT 14
US-08-482-293A-53
Sequence 53; Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-53

Query Match 10.8%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 7.4e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 11 PACYG-GFDLYFLIDKSGSV-LHHMNEIYFVEQLAHKFTSPQLRMSFIVFSTRGTLMK 68
DB 144 PBCPGQEMDIAFLIDSGSIDQSDPTQMDKDFVAKMGQLASTSTSFSLMYSNLKTHFT 203
QY 69 LTEDR-----EQIRQGLEBLQKVLPGDPTMHGFEFASQIYENKGYRTA-SVIAL 122
DB 204 FTEFKSLSPQSLVDAIVQD-----GLTYTASGIQKVVELPHSKNGAKSAKILIVI 258
QY 123 TDGELHEDLFFYSE--REANRSRLGAIYVCVGVK-FNE-TOLARI-----ADSKDHF 173
DB 259 TDQKFRDPLEYHVHVIPEAKA--GIRYAIGVGDAREPTALQELINTIGSAPSDHVF 315
QY 174 PVNDGFOALQGIHSLIKSCIEILAEPTICAGSFQVYVNGNGFRHARNVD 227
DB 316 KVGN-FVALRSIORQIOEK---IFAIEGTESSSSSFQHMGEQSGSALSMD 364

RESULT 15
US-08-943-363-53
Sequence 53; Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Williams Jr., Joseph A.
 REGISTRATION NUMBER: 38,659
 REFERENCE/DOCKET NUMBER: 27866/32684
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 53:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1161 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-943-363-53

Query Match 10.8%; Score 166; DB 1; Length 1161;
 Best Local Similarity 28.2%; Pred. No. 7.4e-09;
 Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 11 PACYQ-GPDLTYFLDSSGSV-LHNMNIYFVEQLAHKFTSPQLRMSFVFSRGTLMK 68
 DB 144 PECPGQEMDIAFLIDSSGSDPTQMDPVKALMGQLASTSTSPSLMQYSNITLKHFT 203
 QY 69 LTEDR-----EQIROGLELELOKVLPGADTYMHGEPERASEQIYYENRQGYRTA-SVIAL 122
 DB 204 FTEFKSLSPQSLVDALVQLQ-----GLYTTASGIQKVVELFHSKNGARKSAKTLIYI 258
 QY 123 TDGELHEDLFYSE--REANRSRDLGAIYCVGVKD-FNE-TOLARI-----ADSKDHYF 173
 DB 259 TDGQKFRDPLEYRHVIPLEAKA---GIIRYALGVGDAFREPTALQELINTIGSAPSDHYF 315
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 DB 316 KVGN-FVALRSIQRIQEK---IFAIEGTESRSSSSFOHENSQEGFSSALSHMD 364

Search completed: December 14, 2005, 11:21:05
 Job time : 27.6032 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 11:18:07 ; Search time 88.8744 Seconds
(without alignments)
1386.897 Million cell updates/sec

Title: US-09-970-076-2_COPY_27_321

Perfect score: 1536
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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1536	100.0	403	3 US-09-833-245-621	Sequence 621, App
3	1536	100.0	564	3 US-09-918-715-187	Sequence 187, App
4	1536	100.0	564	3 US-09-918-715-232	Sequence 232, App
5	1536	100.0	564	4 US-10-301-822-199	Sequence 199, App
6	1536	100.0	564	4 US-10-408-765A-1823	Sequence 1823, App
7	1536	100.0	564	4 US-10-474-794-187	Sequence 187, App
8	1536	100.0	564	4 US-10-474-794-232	Sequence 232, App
9	1536	100.0	564	5 US-10-979-159-187	Sequence 187, App
10	1536	100.0	564	5 US-10-979-159-232	Sequence 232, App
11	1536	100.0	564	6 US-11-047-278-6	Sequence 6, App
12	1532	99.7	551	4 US-10-038-307-18	Sequence 18, App1
13	1532	99.7	551	4 US-10-201-292-18	Sequence 18, App1
14	1524	99.2	403	3 US-09-833-245-620	Sequence 620, App
15	1520	99.0	333	3 US-09-796-753-12	Sequence 12, App1
16	1520	99.0	333	4 US-10-038-307-2	Sequence 2, App1
17	1520	99.0	333	4 US-10-201-292-2	Sequence 2, App1
18	1520	99.0	333	6 US-11-047-278-8	Sequence 8, App1
19	1520	99.0	345	4 US-10-038-307-24	Sequence 24, App1
20	1520	99.0	345	4 US-10-201-292-24	Sequence 24, App1
21	1520	99.0	564	4 US-10-038-307-20	Sequence 20, App1
22	1520	99.0	564	4 US-10-201-292-20	Sequence 20, App1
23	1519	98.9	562	3 US-09-918-715-194	Sequence 194, App
24	1519	98.9	562	3 US-09-918-715-301	Sequence 301, App
25	1519	98.9	562	4 US-10-474-794-194	Sequence 194, App
26	1519	98.9	562	4 US-10-474-794-301	Sequence 301, App
27	1519	98.9	562	5 US-10-979-159-194	Sequence 194, App

28	1519	98.9	562	5 US-10-979-159-301	Sequence 301, App
29	1507	98.1	328	4 US-10-038-307-26	Sequence 26, App1
30	1507	98.1	328	4 US-10-201-292-26	Sequence 26, App1
31	1505.5	98.0	342	4 US-10-038-307-22	Sequence 22, App1
32	1505.5	98.0	342	4 US-10-201-292-22	Sequence 22, App1
33	1500	97.7	543	4 US-10-038-307-14	Sequence 14, App1
34	1500	97.7	543	4 US-10-038-307-16	Sequence 16, App1
35	1500	97.7	543	4 US-10-201-292-16	Sequence 16, App1
36	1500	97.7	543	4 US-10-201-292-16	Sequence 16, App1
37	1490	97.0	543	4 US-10-038-307-10	Sequence 10, App1
38	1490	97.0	543	4 US-10-201-292-10	Sequence 10, App1
39	1479	96.3	534	4 US-10-038-307-12	Sequence 12, App1
40	1479	96.3	534	4 US-10-201-292-12	Sequence 12, App1
41	1419	92.4	529	4 US-10-201-292-36	Sequence 36, App1
42	1305.5	85.0	504	4 US-10-201-292-32	Sequence 32, App1
43	1178	76.7	479	4 US-10-201-292-32	Sequence 32, App1
44	1064	69.3	460	4 US-10-201-292-28	Sequence 28, App1
45	1054	68.6	460	4 US-10-201-292-30	Sequence 30, App1

ALIGNMENTS

RESULT 1
US-11-047-278-2
; Sequence 2, Application US/11047278
; Publication NO. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mordridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-047-278-2

Query Match 100.0%; Score 1536; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 7e-149;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GCGGREDGDPACVGGFDLYFLIDKSGSVLHNNELIYFVEQLAHKFIISPOLMSPFVFS	60
DB	27	GCGGREDGDPACVGGFDLYFLIDKSGSVLHNNELIYFVEQLAHKFIISPOLMSPFVFS	86
QY	61	TRGTTMLKLTEDREQIRQGLIELOKYLPGSDIYMHGFEFASQIYENRQRTASVIT	120
DB	87	TRGTTMLKLTEDREQIRQGLIELOKYLPGSDIYMHGFEFASQIYENRQRTASVIT	146
QY	121	ALTDGELHEDLFYSEREANRSRDLAGIYVCVGXDFNETQLARIDSKDHPVNDGFO	180
DB	147	ALTDGELHEDLFYSEREANRSRDLAGIYVCVGXDFNETQLARIDSKDHPVNDGFO	206
QY	181	ALGGIHSILKSCIEIILAEPTICAGSEFQVVVNGFRHARNVDRLVCSFKINDSVT	240
DB	207	ALGGIHSILKSCIEIILAEPTICAGSEFQVVVNGFRHARNVDRLVCSFKINDSVT	266
QY	241	LNKPPSVEDVTYLLCPAPILKEVGMKALQVSNMDGLSFSSSVITTTTHCSGDS	295
DB	267	LNKPPSVEDVTYLLCPAPILKEVGMKALQVSNMDGLSFSSSVITTTTHCSGDS	321

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RESULT 2
US-09-833-245-621
; Sequence 621, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS46PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 621
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-621

Query Match          100.0%; Score 1536; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 8e-149;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGRREDGPGACYGFDLYFLIDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFTIVS 60
    |||||||
DB 27 GCGGRREDGPGACYGFDLYFLIDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFTIVS 86
    |||||||

QY 61 TRGTTLMKLTEDREQIRQGLELOKVLPGGDTYMHGFEFRASQIYYENRQGRITASVII 120
    |||||||
DB 87 TRGTTLMKLTEDREQIRQGLELOKVLPGGDTYMHGFEFRASQIYYENRQGRITASVII 146
    |||||||

QY 121 ALTDGELHEDLPFYSEREANRSRDGAIVYCVGKDFNETQLARIADSKDHVPVNDGFRQ 180
    |||||||
DB 147 ALTDGELHEDLPFYSEREANRSRDGAIVYCVGKDFNETQLARIADSKDHVPVNDGFRQ 206
    |||||||

QY 181 ALOGIHSILKSCIEIIAAEPSTICAGESFOVVVNGNFRHARNVDRVLCSPKINDSVT 240
    |||||||
DB 207 ALOGIHSILKSCIEIIAAEPSTICAGESFOVVVNGNFRHARNVDRVLCSPKINDSVT 266
    |||||||

QY 241 LNEKPSVEDTYLLCPAPILKEVGMKALQVSMNDGLSFISSVIITTHCSDGS 295
    |||||||
DB 267 LNEKPSVEDTYLLCPAPILKEVGMKALQVSMNDGLSFISSVIITTHCSDGS 321
    |||||||

RESULT 3
US-09-918-715-187
; Sequence 187, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
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```
US-09-918-715-187

Query Match          100.0%; Score 1536; DB 3; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.3e-148;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGRREDGPGACYGFDLYFLIDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFTIVS 60
    |||||||
DB 27 GCGGRREDGPGACYGFDLYFLIDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFTIVS 86
    |||||||

QY 61 TRGTTLMKLTEDREQIRQGLELOKVLPGGDTYMHGFEFRASQIYYENRQGRITASVII 120
    |||||||
DB 87 TRGTTLMKLTEDREQIRQGLELOKVLPGGDTYMHGFEFRASQIYYENRQGRITASVII 146
    |||||||

QY 121 ALTDGELHEDLPFYSEREANRSRDGAIVYCVGKDFNETQLARIADSKDHVPVNDGFRQ 180
    |||||||
DB 147 ALTDGELHEDLPFYSEREANRSRDGAIVYCVGKDFNETQLARIADSKDHVPVNDGFRQ 206
    |||||||

QY 181 ALOGIHSILKSCIEIIAAEPSTICAGESFOVVVNGNFRHARNVDRVLCSPKINDSVT 240
    |||||||
DB 207 ALOGIHSILKSCIEIIAAEPSTICAGESFOVVVNGNFRHARNVDRVLCSPKINDSVT 266
    |||||||

QY 241 LNEKPSVEDTYLLCPAPILKEVGMKALQVSMNDGLSFISSVIITTHCSDGS 295
    |||||||
DB 267 LNEKPSVEDTYLLCPAPILKEVGMKALQVSMNDGLSFISSVIITTHCSDGS 321
    |||||||

RESULT 4
US-09-918-715-232
; Sequence 232, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 232
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-232

Query Match          100.0%; Score 1536; DB 3; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.3e-148;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGRREDGPGACYGFDLYFLIDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFTIVS 60
    |||||||
DB 27 GCGGRREDGPGACYGFDLYFLIDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFTIVS 86
    |||||||

QY 61 TRGTTLMKLTEDREQIRQGLELOKVLPGGDTYMHGFEFRASQIYYENRQGRITASVII 120
    |||||||
DB 87 TRGTTLMKLTEDREQIRQGLELOKVLPGGDTYMHGFEFRASQIYYENRQGRITASVII 146
    |||||||

QY 121 ALTDGELHEDLPFYSEREANRSRDGAIVYCVGKDFNETQLARIADSKDHVPVNDGFRQ 180
    |||||||
DB 147 ALTDGELHEDLPFYSEREANRSRDGAIVYCVGKDFNETQLARIADSKDHVPVNDGFRQ 206
    |||||||

QY 181 ALOGIHSILKSCIEIIAAEPSTICAGESFOVVVNGNFRHARNVDRVLCSPKINDSVT 240
    |||||||
DB 207 ALOGIHSILKSCIEIIAAEPSTICAGESFOVVVNGNFRHARNVDRVLCSPKINDSVT 266
    |||||||
```

OY 241 LNEKPFVSVDITYLLCPAPILKEVGMMKALQVSNMDGLSFSSSVITTTTHCSDDG 295

D6 267 LNEKPFVSVDITYLLCPAPILKEVGMMKALQVSNMDGLSFSSSVITTTTHCSDDG 321

RESULT 5
US-10-301-822-199

Sequence 199, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF COLON CANCER

```

/ FIDE REFERENCE: WFM01-0225-2AKM
/ CURRENT APPLICATION NUMBER: US/10/301,822
/ CURRENT FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 60/339,971
/ PRIOR FILING DATE: 2001-12-10
/ PRIOR APPLICATION NUMBER: US 60/361,978
/ PRIOR FILING DATE: 2002-03-05
/ PRIOR APPLICATION NUMBER: US 60/381,988
/ PRIOR FILING DATE: 2002-05-20
/ NUMBER OF SEQ ID NOS: 228
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 199
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-10-301-822-199

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```

Query Match      100.0%; Score 1536; DB 4; Length 564;
Best Local Similarity 100.0%; Pred. No. 1,3e-148;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 GCGGRREDGGPACGCGGFDLYFLIDKSGSVLHHMNEIYFVEQLAHKFI$POLRMSFIYES 60
DB      27 GCGGRREDGGGACGCGGFDLYFLIDKSGSVLHHMNEIYFVEQLAHKFI$POLRMSFIYES 86

OY      61 TRGTTMLMTLTDREBRI$ROGLEELQKVLCGDPYHHEGFEERASEQIYYENRRCGYRTASTYII 120
DB      87 TRGTTMLMTLTDREBRI$ROGLEELQKVLCGDPYHHEGFEERASEQIYYENRRCGYRTASTYII 146

OY      121 ALTDGELHEDLFFYYEREERAN$RDLGALIVYCVGVDPFETOLARIAD$KDHVPFVNDGFO 180
DB      147 ALTDGELHEDLFFYYEREERAN$RDLGALIVYCVGVDPFETOLARIAD$KDHVPFVNDGFO 206

OY      181 ALGGIHSILKKS$CIEILAAEPSTICAGESFQVVVGVNGG$FHHRVNDRVLCSFKINDSVT 240
DB      207 ALGGIHSILKKS$CIEILAAEPSTICAGESFQVVVGVNGG$FHHRVNDRVLCSFKINDSVT 266

OY      241 LNEKRF$VEDTYLLCPAPILKEVGK$KALQV$MNDGL$FISSVITITTHCSDSG 295
DB      267 LNEKRF$VEDTYLLCPAPILKEVGK$KALQV$MNDGL$FISSVITITTHCSDSG 321

RESULT 6
US-10-408-765A-1823
; Sequence 1823, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahn, Bojn D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.

```

```

; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1823
;
; LENGTH: 564
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
;
US-10-408-765A-1823

```

	Query Match	100.0%;	Score 1536;	DB 4;	Length 564;	
	Best Local Similarity	100.0%;	Pred. No. 1,3e-148;			
	Matches 295;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	GQGRREDDGPGACGGRFDLYFIIDKSSVLIHNMETIYFVEQLAHKPSIPOLRMSTIVFS	60			
Db	27	GQGRREDDGPGACGGRFDLYFIIDKSSVLIHNMETIYFVEQLAHKPSIPOLRMSTIVFS	86			
Qy	61	TRGTTLMKLITEDRFOIRQGLELOKVLPGGDTYHNGEFPASBOIYYENOGYRTASVII	120			
Db	87	TRGTTLMKLITEDRFOIRQGLELOKVLPGGDTYHNGEFPASBOIYYENOGYRTASVII	146			
Qy	121	ALTDELDHEDLFYSSEREANRSRDGLIIVYCVGKDFENETQLARIADSKDHVPVNDGFO	180			
Db	147	ALTDELDHEDLFYSSEREANRSRDGLIIVYCVGKDFENETQLARIADSKDHVPVNDGFO	206			
Qy	181	ALQGIHSILKKSICIEILAAEPSTTCGSEFQVYVRNGRPHANVRVLCSFKINDSVT	240			
Db	207	ALQGIHSILKKSICIEILAAEPSTTCGSEFQVYVRNGRPHANVRVLCSFKINDSVT	266			
Qy	241	LNKEPFEVEDPYLLCPAPILKEVGMKALQVSMNDGSLFTSSSYIITTHCSDDSS	295			
Db	267	LNKEPFEVEDPYLLCPAPILKEVGMKALQVSMNDGSLFTSSSYIITTHCSDDSS	321			

```

RESULT 7
US-10-474-794-187
: Sequence 187. Application US/10474794
: Publication No. US20040213793A1
: GENERAL INFORMATION:
: APPLICANT: Carson-Walter, Eleanor
: APPLICANT: St. Croix, Brad
: APPLICANT: Vogelstein, Bert
: APPLICANT: Kinzler, Kenneth
: TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
: FILE REFERENCE: 1107.00179
: CURRENT APPLICATION NUMBER: US/10/474,794
: CURRENT FILING DATE: 2003-10-14
: PRIOR APPLICATION NUMBER: 60/282,850
: PRIOR FILING DATE: 2001-04-11
: PRIOR APPLICATION NUMBER: 60/308,829
: PRIOR FILING DATE: 2001-08-01
: NUMBER OF SEQ ID NOS: 359
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 187
: LENGTH: 564
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-474-794-187

```

	Query Match	100.0%	Score 1536;	DB 4;	Length 564;
	Best Local Similarity	100.0%	Pred. No. 1,36-148;		
	Matches 295;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	G G G G R R D D G G A C G G F D L Y F I L D K S S V L H M N E I Y F V E O L A H K T I P O L R N S F I V E S	60		
Db	27	G G G G R R D D G G A C G G F D L Y F I L D K S S V L H M N E I Y F V E O L A H K T I P O L R N S F I V E S	86		

Qy	61	RGTTLMKLTEDREIORGLLEOKVLPGSGDTYMEGFRASQIYYENRQGRKTASV11	120
Db	87	TRGTTLMKLTEDREIORGLLEOKVLPGSGDTYMEGFRASQIYYENRQGRKTASV11	146
Qy	121	ALTQDELHEDLFFYSEERANRSRDGAIYYCVGVKDQFNETOLAR1ADSXDHYEPVNDGQ	180
Db	147	ALTQDELHEDLFFYSEERANRSRDGAIYYCVGVKDQFNETOLAR1ADSXDHYEPVNDGQ	206
Qy	181	ALQGIHSHLKKSCIEIILAEPSTICAGSSFOYVVRGNGFRANRNDRLCSFKINDSVT	240
Db	207	ALQGIHSHLKKSCIEIILAEPSTICAGSSFOYVVRGNGFRANRNDRLCSFKINDSVT	266
Qy	241	LNKEPFSVEDTYLLCPAPILKEVGMKAALQVSNNDGLSFSSSVITTTTHCSGSG	295
Db	267	LNKEPFSVEDTYLLCPAPILKEVGMKAALQVSNNDGLSFSSSVITTTTHCSGSG	321

```

RESULT 8
US-10-474-794-232
Sequence 232, Application US/10474794
Publication No. US20040213793A1
GENERAL INFORMATION:
APPLICANT: Carson-Malter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/282,550
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 232
LENGTH: 564
TYPE: PRT
ORGANISM: Homo sapiens
US-10-474-794-232

```

	Query Match	100.0%	Score 1536;	DB 4;	Length 564;		
	Best Local Similarity	100.0%	Pred. No. 1,3e+148;				
	Matches	295;	Conservative	0;	Mismatches	0;	
				Indels	0;	Gaps	0
QY	1	G G G G R R D D G P A C C G G F D L Y F I L D K G S V L H M N E I Y Y F E O L A H K F I S Q L M S T I V F S	60				
Db	27	G G G G R R D D G P A C C G G F D L Y F I L D K G S V L H M N E I Y Y F E O L A H K F I S Q L M S T I V F S	86				
QY	61	T R G T I L M K L T E R E Q I R Q G L E E L O K V L P G G D T Y M H G F E R A S E Q I Y Y E N P Q Y R T A S V I I	120				
Db	87	T R G T I L M K L T E D R E Q I R Q G L E E L O K V L P G G D T Y M H G F E R A S E Q I Y Y E N P Q Y R T A S V I I	146				
QY	121	A L T D G E L H E D L F F Y S R E A N R S D L G A I Y Y C V G V D P N E F Q L A R I N D S K D H V P P A N D F Q	180				
Db	147	A L T D E L H E D L F F Y S R E A N R S D L G A I Y Y C V G V D P N E F Q L A R I N D S K D H V P P A N D F Q	206				
QY	181	A L O G I I H S I L K K S C I E I I L A A P E T T I C A G E S F Q V V V A N G N G F R H A R N A N D R V L C S F K I N D S V T	240				
Db	207	A L O G I I H S I L K K S C I E I I L A A P E T T I C A G E S F Q V V V A N G N G F R H A R N A N D R V L C S F K I N D S V T	266				
QY	241	I N E K P F S V E D Y T L L C A P I L K E V G M A A Q V S N N D G L S F S S S V I I T T T H C S G S	295				
Db	267	I N E K P F S V E D Y T L L C A P I L K E V G M A A Q V S N N D G L S F S S S V I I T T T H C S G S	321				

RESULT 9
US-10-979-159-187
; Sequence 187, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix

```

? APPLICANT: Bert Vogelstein
? APPLICANT: Kenneth Kinzler
? TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
? FILE REFERENCE: 1107.00134
? CURRENT APPLICATION NUMBER: US/10/979,159
? CURRENT FILING DATE: 2004-11-03
? PRIOR APPLICATION NUMBER: US/09/918,715
? PRIOR FILING DATE: 2001-08-01
? PRIOR APPLICATION NUMBER: 60/222,599
? PRIOR FILING DATE: 2000-08-02
? PRIOR APPLICATION NUMBER: 60/224,360
? PRIOR FILING DATE: 2000-08-11
? PRIOR APPLICATION NUMBER: 60/282,850
? PRIOR FILING DATE: 2000-04-11
? NUMBER OF SEQ ID NOS: 358
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 187
? LENGTH: 564
? TYPE: PR1
? ORGANISM: Homo sapiens
US-10-979-159-187

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	Query Match	Best Local Similarity	100.0%;	Pred. No. 1.3e-148;	Score 1536;	DB 5;	Length 564;	
	Matches	295;	Conservative	0;	Mismatches	0;	Indels	0;
QY	1	GGGRRRDGGPACGCGFDLYFLIDKSGSVLHNNHNYIPLYEQLAHKTSIQOLNMSFVFS	60					
Db	27	GGGRRRDGGPACGCGFDLYFLIDKSGSVLHNNHNYIPLYEQLAHKTSIQOLNMSFVFS	86					
QY	61	TRGTTLAKLTREDREIQIGLEELQKVLPGGDTVMHEGFERASEQIYYENNGQYTAVII	120					
Db	87	TRGTTLAKLTREDREIQIGLEELQKVLPGGDTVMHEGFERASEQIYYENNGQYTAVII	146					
QY	121	ALTDGELHEDLFYTSEREANRSRDGLAIYVCVGKDPNEIQLARIADSKHVPFVNDGFO	180					
Db	147	ALTGEELHEDLFYTSEREANRSRDGLAIYVCVGKDPNEIQLARIADSKHVPFVNDGFO	206					
QY	181	ALGQIHSILKSKSCIEELIAPSPITICGSESFQVYVRNGNGFRHARVNDVLCFSKINDSVT	240					
Db	207	ALGQIHSILKSKSCIEELIAPSPITICGSESFQVYVRNGNGFRHARVNDVLCFSKINDSVT	266					
QY	241	LNKRPSEVEDTYLCPAPILKEGKMALOVSNNDGISFISSSVYITTTTCSDGS	295					
Db	267	LNKRPSEVEDTYLCPAPILKEGKMALOVSNNDGISFISSSVYITTTTCSDGS	321					

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RESULT 10-159-232
; Sequence 232, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Knizler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107 00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/919,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 232
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-979-159-232

Query Match	100.0%;	Score 1536;	DB 5;	Length 564;
Best Local Similarity	100.0%;	Pred. No. 1.3e-148;		
Matches 295;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	GGGGRREDGGPAC	CYGF	FDLY	FINDKGS	VLAHNN	EIYY	FVEQ	LAHK	IS	QOLMS	FVFS	60		
Db	27	GGGGRREDGGPAC	CYGF	FDLY	FINDKGS	VLAHNN	EIYY	FVEQ	LAHK	IS	QOLMS	FVFS	86		
QY	61	TGRTITLMKLT	EDREQ	IRQGL	EELQKYL	PGGDTYMH	BGF	EPAS	EQIYY	ENFQ	YRTASV	II	120		
Db	87	TGRTITLMKLT	EDREQ	IRQGL	EELQKYL	PGGDTYMH	BGF	EPAS	EQIYY	ENFQ	YRTASV	II	146		
QY	121	ALTQDELHEDD	LF	FYSER	EA	NRSH	DGLAIY	CV	YKQ	PN	ERQ	LARI	DS	180	
Db	147	ALTQDELHEDD	LF	FYSER	EA	NRSH	DGLAIY	CV	YKQ	PN	ERQ	LARI	DS	206	
QY	181	ALQGIHHSILKKS	CIEI	LA	EPSTI	CAGBS	FQV	VVR	NGR	GH	RA	NDRV	LC	240	
Db	207	ALQGIHHSILKKS	CIEI	LA	EPSTI	CAGBS	FQV	VVR	NGR	GH	RA	NDRV	LC	266	
QY	241	LNKKEP	SV	SDTYL	LC	PA	PI	LKEV	GM	KA	AL	OV	SN	DS	295
Db	267	LNKKEP	SV	SDTYL	LC	PA	PI	LKEV	GM	KA	AL	OV	SN	DS	321

RESULT 11
US-11-047-278-6

1 APPLICANT: Young, John A. T
 2 APPLICANT: Bradley, Kenneth A.
 3 APPLICANT: Collier, Robert J.
 4 APPLICANT: Mogridge, Jeremy S.
 5 TITLE OF INVENTION: Anthrax Toxin Receptor
 6 FILE REFERENCE: 960296.97745
 7 CURRENT APPLICATION NUMBER: US/11/047,278
 8 CURRENT FILING DATE: 2005-01-31
 9 PRIOR APPLICATION NUMBER: US/09/970,076
 10 PRIOR FILING DATE: 2001-10-03
 11 PRIOR APPLICATION NUMBER: 60/251,461
 12 PRIOR FILING DATE: 2000-12-05
 13 NUMBER OF SEQ ID NOS: 10
 14 SOFTWARE: PatentIn Ver. 2.1
 15 SEQ ID NO 6
 16 LENGTH: 564
 17 TYPE: prt
 18 ORGANISM: Homo sapiens
 19 US-11-047-278-6

Query Match	100.0%;	Score 1536;	DB 6;	Length 564;
Best Local Similarity	100.0%;	Pred. No. 1.3e-148;		
Matches 295;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	GGGGRREDGGPACGCGFDFIYFINDKSGSVLHNNHNIYYFEOJLAHKHISPOLMMSFVFS	60
Db	27	GGGGRREDGGPACGCGFDFIYFINDKSGSVLHNNHNIYYFEOJLAHKHISPOLMMSFVFS	86
QY	61	TRGTTLMKLTEDREQIROGLEELQVLPGGDIYMHGEPFASQIYYENQGYRTASVII	120
Db	87	TRGTTLMKLTEDREQIROGLEELQVLPGGDIYMHGEPFASQIYYENQGYRTASVII	146
QY	121	ALTDEGLHDDLFFYSREANRNSDGLAIYCVGKVPNEPOLARINDSKHVPVYDGFQ	180
Db	147	ALTDEGLHDDLFFYSREANRNSDGLAIYCVGKVPNEPOLARINDSKHVPVYDGFQ	206
QY	181	ALOGIHSILKKSCEIILAAEPSTICAGESFOVVVNGNGRHHARNDRVLCSFKINDSVT	240
Db	207	ALOGIHSILKKSCEIILAAEPSTICAGESFOVVVNGNGRHHARNDRVLCSFKINDSVT	266
QY	241	LNKRPESVEDIYLLCAPRLIKVEGMKALOVSNNDGLSTISSVIIITTHCSDSG	295

Db 267 LNEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFSSVIIITTHCSDGS 321

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RESULT 12
US-10-038-307-18
; Sequence 18, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Eogin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ. ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-18

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Query Match	99.74%	Score 1532;	DB 4;	Length 551;
Best Local Similarity	100.04%	Pred. No. 3.3e-148;		
Matches 294;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	GQGRREDGPRAC	CYGGFDLYFL	LDSSGSLH	HMNEIYFV	EQLAHKFIS	POLRMS	FVFS	60
Db	27	GQGRREDGPRAC	YGGFDLYFL	LDSSGSLH	HMNEIYFV	EQLAHKFIS	POLRMS	FVFS	86
Qy	61	TRGTTLMKLTED	REJOIRQGLE	BLQVLPQ	GDTVMH	EGFERASEO	YYENRQ	GFTASV	120
Db	87	TRGTTLMKLTED	REJOIRQGLE	BLQVLPQ	GDTVMH	EGFERASEO	YYENRQ	GFTASV	146
Qy	121	ALTDGELHBDL	LFYSEREANR	SRDGLVY	CVGVND	FNETOLAI	DSKDHV	FPVNGFO	180
Db	147	ALTDGELHBDL	LFYSEREANR	SRDGLVY	CVGVND	FNETOLAI	DSKDHV	FPVNGFO	206
Qy	181	ALOGIHSILKSC	IEIIAAEPSTI	CAGESFQV	VVRNG	GPHARAVDR	VILCSF	KINDSVT	240
Db	207	ALOGIHSILKSC	IEIIAAEPSTI	CAGESFQV	VVRNG	GPHARAVDR	VILCSF	KINDSVT	266
Qy	241	LNKRPSSVDYIL	CPAPILKEV	GKAAIQV	SNMGIS	FISSSV	YITTH	THCSDG	294
Db	267	LNKRPSSVDYIL	CPAPILKEV	GKAAIQV	SNMGIS	FISSSV	YITTH	THCSDG	320

RESULT 13
US-10-201-292-18
; Sequence 18, Application US/10201292

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Query Match	99.7%;	Score 1532;	DB 4;	Length 551;
Best Local Similarity	100.0%;	Pred. No. 3.3e-148;		

Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGRRDDGGPACGCGDLYFIIDKSGSVLHNNNEIYFVEQOLAHKFIISQLMSPFVFS 60
DB 27 GGGRRDDGGPACGCGDLYFIIDKSGSVLHNNNEIYFVEQOLAHKFIISQLMSPFVFS 86
QY 61 TRGTTLMKLTEDREQIRQGLEELQKVLPGSDTYMHGFEFASQIYENNGYRTASVII 120
DB 87 TRGTTLMKLTEDREQIRQGLEELQKVLPGSDTYMHGFEFASQIYENNGYRTASVII 146
QY 121 ALTDGELHEDLFFYSEERARSRLGAIYVCVGFQNEQTOLARIADSKDHVPVNDGQ 180
DB 147 ALTDGELHEDLFFYSEERARSRLGAIYVCVGFQNEQTOLARIADSKDHVPVNDGQ 206
QY 181 ALGGIHSILKSCIEIIAEPSTICAGESFOVWVGNGFRHARNDRVLCSPKINDSVT 240
DB 207 ALGGIHSILKSCIEIIAEPSTICAGESFOVWVGNGFRHARNDRVLCSPKINDSVT 266
QY 241 LNEKPSVEDTYLLCPAPILKEVGMKALQVSNMDGLSFSSVITTTTCHSDG 294
DB 267 LNEKPSVEDTYLLCPAPILKEVGMKALQVSNMDGLSFSSVITTTTCHSDG 320

RESULT 14
US-09-833-245-620
Sequence 620, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PFS46PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 620
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (175)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (320)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (331)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (368)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-620

Query Match 99.2%; Score 1524; DB 3; Length 403;
Best Local Similarity 99.3%; Pred. No. 1,4e-147;
Matches 293; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGRRDDGGPACGCGDLYFIIDKSGSVLHNNNEIYFVEQOLAHKFIISQLMSPFVFS 60
DB 27 GGGRRDDGGPACGCGDLYFIIDKSGSVLHNNNEIYFVEQOLAHKFIISQLMSPFVFS 86
QY 61 TRGTTLMKLTEDREQIRQGLEELQKVLPGSDTYMHGFEFASQIYENNGYRTASVII 120
DB 87 TRGTTLMKLTEDREQIRQGLEELQKVLPGSDTYMHGFEFASQIYENNGYRTASVII 146
QY 121 ALTDGELHEDLFFYSEERARSRLGAIYVCVGFQNEQTOLARIADSKDHVPVNDGQ 180

DB 147 ALTDGELHEDLFFYSEERARSRLGAIYVCVGFQNEQTOLARIADSKDHVPVNDGQ 206
QY 181 ALGGIHSILKSCIEIIAEPSTICAGESFOVWVGNGFRHARNDRVLCSPKINDSVT 240
DB 207 ALGGIHSILKSCIEIIAEPSTICAGESFOVWVGNGFRHARNDRVLCSPKINDSVT 266
QY 241 LNEKPSVEDTYLLCPAPILKEVGMKALQVSNMDGLSFSSVITTTTCHSDG 295
DB 267 LNEKPSVEDTYLLCPAPILKEVGMKALQVSNMDGLSFSSVITTTTCHSDG 321

RESULT 15
US-09-796-753-12
Sequence 12, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/223,094
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/122,458
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 09/312,359
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/336,536
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 09/345,464
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/365,164
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/399,723
PRIOR FILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: 09/409,634
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 09/471,179
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/474,071
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/474,072
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/514,010
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 09/516,745
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/572,002
PRIOR FILING DATE: 2000-05-14
PRIOR APPLICATION NUMBER: 09/597,993
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/599,596
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/630,334
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 09/606,565
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/606,317
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/665,666
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 09/677,751

; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 12
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-12

Query Match 99.0%; Score 1520; DB 3; Length 333;
Best Local Similarity 100.0%; Pred. No. 2.7e-147;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	G G G R R E D G G P A C Y G F D L Y F I L D K S G S V L H M N E I Y F V E Q L A H K F I S P Q L R M S F I V F S	60
DB	27	G G G R R E D G G P A C Y G F D L Y F I L D K S G S V L H M N E I Y F V E Q L A H K F I S P Q L R M S F I V F S	86
QY	61	T R G T T L M K L T E D R E Q I R Q G L E L O K V L P G G D T Y M H E G F E R A S E Q I Y Y E N R Q G R T A S V I I	120
DB	87	T R G T T L M K L T E D R E Q I R Q G L E L O K V L P G G D T Y M H E G F E R A S E Q I Y Y E N R Q G R T A S V I I	146
QY	121	A L T D G E L H E D L P F Y S E R E A N R S R D L G A I V Y C V G K D F N E T Q L A R I A D S K D H V F P V N D G F Q	180
DB	147	A L T D G E L H E D L P F Y S E R E A N R S R D L G A I V Y C V G K D F N E T Q L A R I A D S K D H V F P V N D G F Q	206
QY	181	A L O G I I H S I L K K S C I E I L A A P S T I C A G E S F Q V V V R N G F R H A N V D R V L C S F K I N D S V T	240
DB	207	A L O G I I H S I L K K S C I E I L A A P S T I C A G E S F Q V V V R N G F R H A N V D R V L C S F K I N D S V T	266
QY	241	L N E K P F S V E D T Y L I C P A P I I K E V G M K A A L Q V S M N D G L S F I S S V I I T T H C S	292
DB	267	L N E K P F S V E D T Y L I C P A P I I K E V G M K A A L Q V S M N D G L S F I S S V I I T T H C S	318

Search completed: December 14, 2005, 11:58:59
Job time : 90.0411 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 11:18:48 ; Search time 4.33534 Seconds
(without alignments)
458.218 Million cell updates/sec

Title: US-09-970-076-2_COPY_27_321

Perfect score: 1536
Sequence: 1 GGGGRREDGGPACYGGFGLY.....GLSPSSSVITTTTCSDGS 295

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51441 seqs, 6734002 residues

Total number of hits satisfying chosen parameters: 51441

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:
1: /cgn2_6/prodata/1/pubppa/US09_NEW_PUB pep.*
2: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB pep.*
3: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB pep.*
4: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB pep.*
5: /cgn2_6/prodata/1/pubppa/PCR_NEW_PUB pep.*
6: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB pep.*
7: /cgn2_6/prodata/1/pubppa/US11_NEW_PUB pep.*
8: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1536	100.0	564	US-11-186-284-199	Sequence 199, App
2	145.5	9.5	1152	US-11-080-026-4	Sequence 4, Appl
3	131	8.5	3063	US-11-186-284-26	Sequence 2, Appl
4	113.5	7.4	739	US-11-057-047-2	Sequence 2, Appl
5	113.5	7.4	764	US-11-057-047-1	Sequence 1, Appl
6	113.5	7.4	738	US-10-821-234-1034	Sequence 1034, App
7	113.5	7.4	915	US-10-131-826A-294	Sequence 294, App
8	113.5	7.4	956	US-11-113-424-39	Sequence 39, Appl
9	111	7.2	1141	US-10-601-368-24	Sequence 24, Appl
10	111	7.2	1166	US-10-601-368-22	Sequence 22, Appl
11	111	7.2	1188	US-10-601-368-21	Sequence 21, Appl
12	110.5	7.2	761	US-11-057-047-6	Sequence 6, Appl
13	107	7.0	1141	US-10-601-368-6	Sequence 6, Appl
14	107	7.0	1166	US-10-601-368-4	Sequence 4, Appl
15	107	7.0	1188	US-10-601-368-3	Sequence 3, Appl
16	107	7.0	1188	US-11-000-463-338	Sequence 338, App
17	107	7.0	1188	US-11-000-463-810	Sequence 810, App
18	104.5	6.8	828	US-10-995-561-983	Sequence 983, App
19	104.5	6.8	918	US-10-995-561-981	Sequence 981, App
20	104.5	6.8	1019	US-10-995-561-982	Sequence 982, App
21	103.5	6.7	182	US-10-601-368-25	Sequence 25, Appl
22	100	6.5	678	US-11-102-240-34	Sequence 34, Appl
23	99.5	6.5	182	US-10-601-368-7	Sequence 7, Appl
24	95.5	6.2	1179	US-11-097-125-1	Sequence 1, Appl
25	95.5	6.2	1196	US-10-995-561-921	Sequence 921, App

26	95	6.2	1167	US-11-097-125-2	Sequence 2, Appl
27	94	6.1	353	US-11-137-465-44	Sequence 44, Appl
28	94	6.1	448	US-11-137-465-45	Sequence 45, Appl
29	91.5	6.0	627	US-10-467-657-5432	Sequence 5432, App
30	91	5.9	1167	US-10-601-368-18	Sequence 18, Appl
31	82	5.3	1062	US-11-137-465-43	Sequence 43, Appl
32	81	5.3	1804	US-10-513-786-2	Sequence 2, Appl
33	81	5.3	3704	US-10-513-786-1	Sequence 1, Appl
34	79.5	5.2	904	US-10-793-826-1	Sequence 5, Appl
35	77.5	5.0	319	US-10-793-826-1040	Sequence 1040, App
36	77.5	5.0	415	US-10-763-712A-25	Sequence 25, Appl
37	77.5	5.0	436	US-10-763-712A-5	Sequence 5, Appl
38	76.5	5.0	1798	US-10-995-561-1033	Sequence 1033, App
39	76.5	5.0	1798	US-10-995-561-1034	Sequence 1034, App
40	76	4.9	469	US-10-467-657-4370	Sequence 4370, App
41	75.5	4.9	1933	US-10-523-912-2	Sequence 2, Appl
42	74	4.8	384	US-10-510-386-158	Sequence 158, App
43	74	4.8	509	US-10-793-826-2880	Sequence 2880, App
44	74	4.8	619	US-10-999-886-3	Sequence 3, Appl
45	74	4.8	640	US-10-999-886-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-11-186-284-199
Sequence 199, Application US/11186284
Publication No. US2005026493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kametkar, Shubhanga
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, AND
FILE REFERENCE: MEMO1-029P2RM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 199
LENGTH: 564
TYPE: PRT
ORGANISM: Homo Sapiens
US-11-186-284-199

Query Match 100.0%; Score 1536; DB 7; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.3e-135;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGRREDGGPACYGGFGLYFIIDKSGSVLHNNIYYFVEQLAHKFIISQILMSFIIFS 60
DB 27 GGGGRREDGGPACYGGFGLYFIIDKSGSVLHNNIYYFVEQLAHKFIISQILMSFIIFS 86
QY 61 TRGTTMLKLTEDBEQIRGIEELQKVLPGSDTYMHGCFERASQIYYENQGRITASVIT 120
DB 87 TRGTTMLKLTEDBEQIRGIEELQKVLPGSDTYMHGCFERASQIYYENQGRITASVIT 146
QY 121 ALTDGELHEDLFFYSEREARSRDLGAIYCVGKDFNFRQLARIADSKDHVPVNDGFQ 180

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Db 147 ALDGLHEDLFFYSEBRANRSDLAIVYCVKDFNETQLARIADSKDHVPVNDGRQ 206
|||
Qy 181 ALOGIHSLTKSCITIIAABPSTICAGSEFOVYVNGNGRRARNDRLCSKINDSVT 240
|||
Db 207 ALOGIHSLTKSCITIIAABPSTICAGSEFOVYVNGNGRRARNDRLCSKINDSVT 266
|||
Qy 241 LNEKPSVDEDTYLLCPAPILKEVGMKALQVSNNDGLSPISSEVITTTTHCSDGS 295
|||
Db 267 LNEKPSVDEDTYLLCPAPILKEVGMKALQVSNNDGLSPISSEVITTTTHCSDGS 321
|||

RESULT 2
US-11-080-026-4
; Sequence 4, Application US/11080026
; Publication No. US20050260192A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; FILE REFERENCE: CFBP-P02-021
; CURRENT APPLICATION NUMBER: US/11/080,026
; CURRENT FILING DATE: 2005-03-15
; PRIOR APPLICATION NUMBER: 09/945,265
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,700
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-026-4

Query Match 9.5%; Score 145.5; DB 7; Length 1152;
Best Local Similarity 26.2%; Pred. No. 1.1e-05;
Matches 60; Conservative 45; Mismatches 81; Indels 43; Gaps 12;

Qy 18 DLYFILDKSGSV-LHHMNEIYFVEQLAHK-ISPQLMSFIVSTRGTLMLKLTED- 72
|||
Db 150 DIAFLIDGSGSIIPIHPRRKKEFVST- -VMEQLKSKSLPS- -LMQSESEFRH 199
|||
Qy 73 - - - - -RQIQGLELQKLP- -GQDTYMHGEPERASEQIYYENRQYTA- -SVIIALT 123
|||
Db 200 FTPEKQNNPNPRSLVAKPIYQLL- -GRTHATATGIRKVRLEFNITNGARKNAFKILVIT 257
|||
Qy 124 DGLHEDLFFYSE- -REANRSRDLAGIVYCVKDFNETQLAR- - - - -IADS- -KDHVP 174
|||
Db 258 DGEKFDPLGIEDVIEPADRE- -GVIRYVIGVDARSRKSKQELNTISKPRDHFVQ 314
|||
Qy 175 VNDGFALQGIHSLTKSCITIIAABPSTICAGSEFOVYVNGNGRRAR 223
|||
Db 315 VNN- -FEALTKTIQNLREK- - - - -IFAIGTQTGSSSSPHEHMQEGFSA 358
|||

RESULT 3
US-11-186-284-26
; Sequence 26, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangt
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
```

```
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 3063
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-26

Query Match 8.5%; Score 131; DB 7; Length 3063;
Best Local Similarity 29.8%; Pred. No. 0.00099;
Matches 59; Conservative 38; Mismatches 75; Indels 26; Gaps 13;

Qy 18 DLYFILDKSGSV-LHHMNEIYFVEQLAHK-ISP-QLMSFIVSTR- -RGTMLKLT 71
|||
Db 440 DIVFLVDSGYSIGIANFVVRAPLEVLVYKFSIPRQVQISLVQVSRDPDTEFTLKKFTK 499
|||
Qy 72 DGEQIRQGLELQKLP- -GQDTYMHGEPERASEQIYYENRQYR- -ASVIIALDGL 127
|||
Db 500 VEDII- - - - -EAINTPPYRGSTNGKANTYVREKLEFVSK- -GSRSNVPRKWLITDGK- 552
|||
Qy 128 HEDLFFYSEBRANRSDLAIVYCVKDFNETQLARIAD- -SKDHVPVNDGFALQGI 185
|||
Db 553 SSDAF- - - - -RDPALKLRNSVVEIFAVGVKDAVASELEAISPPAEHTVFTVED- -FDAFQRI 608
|||
Qy 186 IHSILKSCIEI- - - - -LAA 200
|||
Db 609 SFELTQSTICLRIEQLA 626
|||

RESULT 4
US-11-057-047-2
; Sequence 2, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilleson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; TITLE OF INVENTION: Methods Related Thereto
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057,047
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/536,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; PRIOR FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-057-047-2

Query Match 7.4%; Score 113.5; DB 7; Length 739;
Best Local Similarity 19.6%; Pred. No. 0.006;
Matches 66; Conservative 63; Mismatches 109; Indels 99; Gaps 17;
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0Y      2  OGGREDD-GPA-----CYGPFILFLDSSGV-----LHNNELIYFVEOLAH 45
Db      218  EGVADBDHGHPGEOQRKRIVLDPSSGMNIIYVLDDSSDSTIGASNFTGAKKCLVNLIEKVAS 277
0Y      46  KFISPOLMSPFVIFSTRGTTLMKLT-----DREQIRQGLEEL-----QKVLPGDPTMHGEG 97
Db      278  YGVKR--RYGLVTATYTPKIIWKVSEADSSNADWTTKQNLNEINETHDKLXSGTNT----- 330
0Y      98  FERASEQIYENR-----OGY-RTASVITIALTDG-----ELHEDLFPFYSE 136
Db      331  -KKAQAVYMSMWSPEDVPEEGMNRTRAVIILMTDGLHNMGGDPITVIDEIRDLIYICKD 389
0Y      137  REARNSRDLGAIYVYCG--VKDFNETOLARIADSDOHFPVYNDGFOALQGIHSLTKKSC 194
Db      390  RKNPREDYLDVYFVGVGLVNOVINNALASKKDEQHFKYKD--MENLEDVFOYOMIDES- 447
0Y      195  IEIIAEPSTICAGESFOVVVVRGNGFERBARVNDRLGSPKINDSVTLNEKPFPSVDIYLL 254
Db      448  -----QSLSLIC-----GMVWERRKGD-----YHKOPWAKISV-- 476
0Y      255  CPAPILKEVMKALQVSMNDGLSFISSSVITITTHC 291
Db      477  ----IRPSKGHESCMG-----AVSIEFYULIAHC 502

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RESULT 5
US-11-057-047-1
/ Sequence 1, Application US/11057047
/ Publication No. US20050260198A1
/ GENERAL INFORMATION:
/ APPLICANT: Holers, Vernon
/ APPLICANT: Thurman, Joshua
/ APPLICANT: Taube, Christian
/ APPLICANT: Gelfand, Erwin
/ APPLICANT: Gilkeson, Gary
/ TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
/ TITLE OF INVENTION: Methods Related Thereto
/ FILE REFERENCE: 2848-66
/ CURRENT APPLICATION NUMBER: US/11/057,047
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,594
/ PRIOR FILING DATE: 2004-02-10
/ PRIOR APPLICATION NUMBER: 60/636,239
/ PRIOR FILING DATE: 2004-12-14
/ PRIOR APPLICATION NUMBER: US04/015040
/ PRIOR FILING DATE: 2004-05-13
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1
/ LENGTH: 764
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-057-047-1

Query Match      7 4*: Score 113.5; DB 7; Length 764;
Beet Local Similarity 19.6%; Pred. No. 0.0062;
Matches 66; Conservative 63; Mismatches 109; Indels 99; Gaps 17;

QY 2 QGGRREDS-GPA-----CYGFDLYFILDKSGSV-----LHHNIEIYFVEQLAH 45
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 243 EGVADAEHDHGEGEQQRKIVLDPSGSNMIIYLVLDSSDSIGASNFGAKKCLVNIIEKVAS 302
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY 46 KPISEQLAMSTIVSTRTCTLMKLE---DREQIRQGLEL---QKVLFGSGTYVMEHG 97
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 303 YGVKR--RYGLVYATVATYKPIWKVSEADSSNADWYTKQLINIEYDHLKSGTYT----- 355
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY 98 PERASEQIYENR-----QGV-RTASVITATFDG-----BLHEDLPFYSE 136
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 356 -KKALQAYYSMMSWEDDVPPEGKMRTRVITILMTDGLHNMGGDDPTVIDEIRDLILYIGKD 414
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY 137 REANRSRDLGAIYVCV--VKDFNETQIARIADSKDHVFPVNDGFRQALQGIHSILKSC 194
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

```

```

Db      415 RKRPRDDYDVVYFGVGLPQVNNALASKKQNEHQHFKYKD-MENIEDVFYOMDES- 472
Oy      195 IETLAAPRTICAGSEFQVVGNGFRRARNDVRLGCFKINDSVLTNEKFFSVEDPYLL 254
Db      473 -----QSLSTC-----GVMWEHRKGD-----YHKQPMQAKISV-- 501
Oy      255 CPAPILKEVGMKRAALQVSMNDLSPTSSVITTHTC 291
Db      502 ----LRPSKQHSCKMG-----AVSEYFVTLTAHC 527

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RESULT 6
US-10-821-234-1034
; Sequence 1034, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Steache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OR INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1034
; LENGTH: 798
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-1034

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[illegible]

```
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerltzen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P330R1C128
/ CURRENT APPLICATION NUMBER: US/10/131,826A
/ PRIOR FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: 60/049911
/ PRIOR FILING DATE: 1997-06-18
/ PRIOR APPLICATION NUMBER: 60/056974
/ PRIOR FILING DATE: 1997-08-26
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059115
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059117
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059122
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059184
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059352
/ PRIOR FILING DATE: 1997-09-19
/ PRIOR APPLICATION NUMBER: 60/059588
/ PRIOR FILING DATE: 1997-09-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 294
/ LENGTH: 915
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-131-826A-294

Query Match      7.4%; Score 113.5; DB 6; Length 915;
Best Local Similarity 22.4%; Pred. No. 0.008;
Matches 55; Conservative 53; Mismatches 103; Indels 35; Gaps 13;

QY 18 DLYFIIDKSGSV-LHHMNEIYVF-VEQLAHKFIISPOL-RMSFVIFSTRTGTL-----MKL 69
DB 57 DLVFIIDSSRSVNTHYAKKEFIYDLOFLDIGPVTYVGLQY---GSTVKNBSPLKT 113

QY 70 TEDREQIQGLLEBLQVLPQGDITYMHGFEPRASQIYENRQYR-----TASVIITLTD 124
DB 114 FKRKSEVERAVKMRHLSTGWTGLAIQY---ALNTAFSEAGARPLRENVPRVIMVTD 170

QY 125 GEIHEDLFYSEAREARSRDLGAIYCVGV--KDFNETQLARLADSKDHFPPVNDGQAL 182
DB 171 GRQDSV---AEVAAKARDTGILIFAIIGVGVDFNTLKSIGSEPHEDHVLVAN-FSQI 225

QY 183 QGIHHSILKKSCTEILAAEPSTICAGESFOVVRGNGFRHAR-----NVDRLCSFKIND 237
DB 226 EFTLSVFOKKLCTAHMCSLHENCA--HFCINIPGSYVCRCKQGYILNSQDTTC--RIQD 261

QY 238 SVTLNE 243
DB 282 LCAMED 287

RESULT 8
US-11-113-424-39
/ Sequence 39, Application US/11113424
```

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/ Publication No. US20050260713A1
/ GENERAL INFORMATION:
/ APPLICANT: Gangolli et al.
/ TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-225
/ CURRENT APPLICATION NUMBER: US/11/113,424
/ PRIOR FILING DATE: 2005-04-21
/ PRIOR APPLICATION NUMBER: 60/256,704
/ PRIOR FILING DATE: 2000-12-19
/ PRIOR APPLICATION NUMBER: 60/311,590
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: 60/257,314
/ PRIOR FILING DATE: 2000-12-20
/ PRIOR APPLICATION NUMBER: 60/311,613
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: 60/315,617
/ PRIOR FILING DATE: 2001-08-29
/ PRIOR APPLICATION NUMBER: 60/307,506
/ PRIOR FILING DATE: 2001-07-24
/ PRIOR APPLICATION NUMBER: 60/322,358
/ PRIOR FILING DATE: 2001-09-14
/ PRIOR APPLICATION NUMBER: 60/294,075
/ PRIOR FILING DATE: 2001-05-29
/ PRIOR APPLICATION NUMBER: 60/288,153
/ PRIOR FILING DATE: 2001-05-02
/ NUMBER OF SEQ ID NOS: 190
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 39
/ LENGTH: 956
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-113-424-39

Query Match      7.4%; Score 113.5; DB 7; Length 956;
Best Local Similarity 22.4%; Pred. No. 0.0085;
Matches 55; Conservative 53; Mismatches 103; Indels 35; Gaps 13;

QY 18 DLYFIIDKSGSV-LHHMNEIYVF-VEQLAHKFIISPOL-RMSFVIFSTRTGTL-----MKL 69
DB 57 DLVFIIDSSRSVNTHYAKKEFIYDLOFLDIGPVTYVGLQY---GSTVKNBSPLKT 113

QY 70 TEDREQIQGLLEBLQVLPQGDITYMHGFEPRASQIYENRQYR-----TASVIITLTD 124
DB 114 FKRKSEVERAVKMRHLSTGWTGLAIQY---ALNTAFSEAGARPLRENVPRVIMVTD 170

QY 125 GEIHEDLFYSEAREARSRDLGAIYCVGV--KDFNETQLARLADSKDHFPPVNDGQAL 182
DB 171 GRQDSV---AEVAAKARDTGILIFAIIGVGVDFNTLKSIGSEPHEDHVLVAN-FSQI 225

QY 183 QGIHHSILKKSCTEILAAEPSTICAGESFOVVRGNGFRHAR-----NVDRLCSFKIND 237
DB 226 EFTLSVFOKKLCTAHMCSLHENCA--HFCINIPGSYVCRCKQGYILNSQDTTC--RIQD 261

QY 238 SVTLNE 243
DB 282 LCAMED 287

RESULT 9
US-10-601-368-24
/ Sequence 24, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ PRIOR FILING DATE: 2003-06-23
/ CURRENT APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
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/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: PstSeq for Windows Version 3.0.
/ SEQ ID NO 24
/ LENGTH: 1141
/ TYPE: prt
/ ORGANISM: Mus musculus
/ JS-10-601-368-24

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Query Match	7.2%	Score 111;	DB 6;	Length 1141;
Best Local Similarity	24.1%;	Pred. No. 0.019;		
Matches 49;	Conservative 28;	Mismatches 88;	Indels 38;	Gaps 9;

QY 13 CYGGFDYDYLFDSDGSYLHNNHNIYYEVQLAHK-ISP-QLRMSFIYESTRGTLMLKT 70
Db 159 CQYTMDDIYVLDSSNSI-YPMWEVQHFLLNLKFLIPGQIQVGIYGGDAVHEPHL- 216
QY 71 EDREQIIRQGLEELQKVLPGDGYMHGEF---RASEQIYYERQSGTRASYIALTDGEL 127
Db 217 NDYRSYVDVVEAASHLEQRGTFETRAFGIEFARSEAPQGGKRAK--KMIYITDGS 278
QY 128 HED-----LFYSEERANSRDLGAIYCVGVKD---FNETQ 161
Db 275 HDSPDLEKVIROSEKQNDYRYAVAVLYGYYNRRGNIPEPFLNBIKTIASDPDDKHFWNTD 333

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335 EAAL--KDIVDALGDRIFSLEG 354

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RESULT 10
US-10-601-368-22
? Sequence 22, Application US/10601368
? Publication No. US20050260702A1
? GENERAL INFORMATION:
? APPLICANT: Pan, Yang
? APPLICANT: Lore, Jose M.
? TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
? FILE REFERENCE: 07334-275001
? CURRENT APPLICATION NUMBER: US/10/601,368
? CURRENT FILING DATE: 2003-06-23
? PRIOR APPLICATION NUMBER: US/09/561,263A
? PRIOR FILING DATE: 2000-04-27
? PRIOR APPLICATION NUMBER: US 09/322,790
? PRIOR FILING DATE: 1999-05-28
? NUMBER OF SEQ ID NOS: 40
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 22
? LENGTH: 1166
? TYPE: PRT
? ORGANISM: Mus musculus
? US-10-601-368-22

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Query Match 7.2%; Score 111; DB 6; Length 1166;
Best Local Similarity 24.1%; Pred. NO. 0.019;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

QY 13 CYGSPDLUTFLDKSGSVLHNNHEIYYFVYQGLNHR-1SP-OLRSPMFIYSIRGTLTKLT 70
Db 137 CQTYMDIVVLDDSNISI-YPMWEVQFHLNLIKFFYIGGQIVGIGVYGEDAVNEFHL- 194
QY 71 EDREQIRQGLEELQKTLPGGDYTMHEGFE---RASEQIYENRQGYRATSYIALTLGEL 127
Db 195 NDVRSKVDVVAASHLEQRGCTETRTAPDIEFARBEAQKGRKQAK--KMIIYITGGS 253
QY 128 HED-----LFYSESEANRSBDLGIYYCVGKQ---FNETQ 161
Db 253 HDSPDLEKVIROSEKQNDTRVAVAVLGYNRRGINPETFLEIKIYIASDPDKKHFNVTD 312
QY 162 LARIADSKDHVPVNDGFOALOG 184
Db 313 EAAL---KDIVDALGRIFSLG 332

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RESULT 11
US-10-601-368-21
; Sequence 21, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PasteSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1188
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(22)
US-10-601-368-21

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Query Match 7.2%; Score 111; DB 6; Length 1188;
Best Local Similarity 24.1%; Pred. No. 0.02;
Matches 49; Conservative 28; Mismatches 88; Indels 36; Gaps 9;

[illegible]

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12      RESULT 12
13      US-11-057-047-6
14      Sequence 6, Application US/11057047
15      Publication No. US20050260196A1
16      GENERAL INFORMATION:
17      APPLICANT: Holers, Vernon
18      APPLICANT: Thurman, Joshua
19      APPLICANT: Taube, Christian
20      APPLICANT: Gelfand, Erwin
21      APPLICANT: Gilkeson, Gary
22      TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
23      TITLE OF INVENTION: Methods Related Thereto
24      FILE REFERENCE: 2848--66
25      CURRENT APPLICATION NUMBER: US/11/057,047
26      CURRENT FILING DATE: 2005-02-10
27      PRIOR APPLICATION NUMBER: 60/543,594
28      PRIOR FILING DATE: 2004-02-10
29      PRIOR APPLICATION NUMBER: 60/636,239
30      PRIOR FILING DATE: 2004-12-14
31      PRIOR APPLICATION NUMBER: US04/015040
32      PRIOR FILING DATE: 2004-05-13
33      NUMBER OF SEQ ID NOS: 6
34      SOFTWARE: PatentIn version 3.3
35      SEQ ID NO 6
36      LENGTH: 761
37      TYPE: prt
38      ?
39      ?

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LOCATION: (1) ... (22)
US-10-601-368-3

Query Match 7.0%; Score 107; DB 6; Length 1188;
Best Local Similarity 24.1%; Pred. No. 0.046;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

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QY 13 CYGFDLYFILDKSGSVLHMHNEIYFVEQLAHKF-ISP-QLNMFIVFSTRGTTLMKLT 70
    |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |
DB 159 CQYMDIIVIVLDGNSI-YFWVEVQHFLINILKKFYIGPGIQGVGVQGEDVHHEFHL- 216
    |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |
QY 71 EDREQIRQGLEELQKVLPGGDTYMHGFE--RASEQIYYENRQGYRTASVITLTDGEL 127
    |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |
DB 217 NDYRSVADVVEAASHIEQRGTEETRTAFGIEFARSEAFQKGRKAK--KMIIVITDGES 274
    |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |
QY 128 HED-----LFFYSERANRSRDLGAIYVCVGD---FNETQ 161
    |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |
DB 275 HDSPDLEKVIQSERDNVTRYAVAVLGYNRRGINPETFLNEIKYIASDPDDKHFFVVTD 334
    |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |
QY 162 LARIADSKDHVPFVNDGFOALOG 184
    |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |
DB 335 EAML---KDIYDALGDRIFSLEG 354
    |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |

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Job time : 5.33534 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:01:37 ; Search time 207.111 Seconds
(without alignments)
2531.884 Million cell updates/sec

Title: US-09-970-076-2_COPY_27_321

Perfect score: 1536
Sequence: 1 GCGGREDGACGACGFDLY.....GLSFSSVITTTTSCDSG 295

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0970076.@CGN_1_1-535.@runat_14122005_11850_20999 -NCPU=6 -ICPU=3
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA:*
1: /cg2_6/ptodata/1/ina/1.COMB.seq:*
2: /cg2_6/ptodata/1/ina/5.COMB.seq:*
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5: /cg2_6/ptodata/1/ina/H.COMB.seq:*
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7: /cg2_6/ptodata/1/ina/PP.COMB.seq:*
8: /cg2_6/ptodata/1/ina/RB.COMB.seq:*
9: /cg2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1263	82.2	1609	3	US-09-620-312D-8
2	790.5	51.5	2234	3	US-10-104-047-669
3	709	46.2	1492	3	US-09-774-528-297
4	709	46.2	1492	3	US-10-120-988-297
5	662	43.1	3981	3	US-09-799-451-250
6	166	10.8	3519	2	US-08-286-889-45
7	166	10.8	3519	2	US-08-485-618-45
8	166	10.8	3519	2	US-08-362-652-45
9	166	10.8	3519	2	US-08-605-672-45

10	166	10.8	3519	2	US-08-482-293A-45	Sequence 45, Appl
11	166	10.8	3519	2	US-08-943-363-45	Sequence 45, Appl
12	166	10.8	3519	3	US-09-193-043-45	Sequence 45, Appl
13	166	10.8	3519	3	US-09-688-307A-45	Sequence 45, Appl
14	166	10.8	3519	3	US-09-350-259-45	Sequence 45, Appl
15	166	10.8	3803	3	US-08-485-618-52	Sequence 52, Appl
16	166	10.8	3803	2	US-08-362-652-52	Sequence 52, Appl
17	166	10.8	3803	2	US-08-605-672-52	Sequence 52, Appl
18	166	10.8	3803	2	US-08-482-293A-52	Sequence 52, Appl
19	166	10.8	3803	2	US-08-943-363-52	Sequence 52, Appl
20	166	10.8	3803	3	US-09-193-043-52	Sequence 52, Appl
21	166	10.8	3803	3	US-09-688-307A-52	Sequence 52, Appl
22	166	10.8	3803	3	US-09-350-259-52	Sequence 52, Appl
23	159.5	10.4	3528	2	US-08-286-889-36	Sequence 36, Appl
24	159.5	10.4	3528	2	US-08-485-618-36	Sequence 36, Appl
25	159.5	10.4	3528	2	US-08-362-652-36	Sequence 36, Appl
26	159.5	10.4	3528	2	US-08-605-672-36	Sequence 36, Appl
27	159.5	10.4	3528	2	US-08-482-293A-36	Sequence 36, Appl
28	159.5	10.4	3528	2	US-08-943-363-36	Sequence 36, Appl
29	159.5	10.4	3528	3	US-09-193-043-36	Sequence 36, Appl
30	159.5	10.4	3528	3	US-09-688-307A-36	Sequence 36, Appl
31	159.5	10.4	3528	3	US-09-350-259-36	Sequence 36, Appl
32	159.5	10.4	3528	2	US-08-485-618-54	Sequence 54, Appl
33	159.5	10.4	3528	2	US-08-362-652-54	Sequence 54, Appl
34	159.5	10.4	3528	2	US-08-605-672-54	Sequence 54, Appl
35	159.5	10.4	3528	2	US-08-482-293A-54	Sequence 54, Appl
36	159.5	10.4	3528	2	US-08-943-363-54	Sequence 54, Appl
37	159.5	10.4	3528	3	US-09-193-043-54	Sequence 54, Appl
38	159.5	10.4	3528	3	US-09-688-307A-54	Sequence 54, Appl
39	159.5	10.4	3528	3	US-09-350-259-54	Sequence 54, Appl
40	156	10.2	2499	2	US-08-485-618-96	Sequence 96, Appl
41	156	10.2	2499	2	US-08-605-672-96	Sequence 96, Appl
42	156	10.2	2499	2	US-08-482-293A-96	Sequence 96, Appl
43	156	10.2	2499	2	US-08-943-363-96	Sequence 96, Appl
44	156	10.2	2499	3	US-09-193-043-96	Sequence 96, Appl
45	156	10.2	2499	3	US-09-688-307A-96	Sequence 96, Appl

ALIGNMENTS

RESULT 1
US-09-620-312D-8
; Sequence 8, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Y. Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jjian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghaast
; APPLICANT: Dzmanac, Radoje T.
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP28
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_Fl_genes Version 1.0

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/ SEQ ID NO 8
/ LENGTH: 1609
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (309)..(1202)
US-09-620-312D-8

Alignment Scores:
Pred. No.: 6,92e-154 Length: 1609
Score: 1263.00 Matches: 241
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 99.18% Mismatches: 0
Query Match: 82.23% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-2_COPY_27_321 (1-295) x US-09-620-312D-8 (1-1609)

QY 1 G1yG1ng1yG1yArGArG1uArG1yG1yProAlAcYrG1yG1yPheArPLeuYr 20
Db 387 GGGCAAGGGGAGCGAGGAGGATGGGGGTCCAGCCTGCTACGGCGATTGACCTGTAC 446
QY 21 Phe11e1uArP1ySerG1ySerVal1LeuH1e1TrPaNg1u1eTyTyTyPheVal 40
Db 447 TTCATTTTGGCAAAATCAGAGAGTGTGTCACACCTGGAATGAAATCTATTCTTTGTG 506
QY 41 G1uG1n1e1uAlaH1e1yPhe11eSerProG1n1e1uArGMeSerPhe11eVal1PheSer 60
Db 507 GAACAGTTGGCTCAAAATTCATCAGCCACAGTGAATGAAATGCTTTATTTGTTCTCC 566
QY 61 ThrArG1yThrThr1e1uMeTy1eSerProG1n1e1uArPArG1uG1n1eArG1nG1yLeu 80
Db 567 ACCCGAGAAACAACCTTAATGAACCTACAGAAAGACAGAAACAATCCCTCAAGGCTTA 666
QY 81 G1uG1u1e1uG1n1yVal1e1uProG1yArPThrTyMeH1eG1uG1yPheG1uArG 100
Db 627 GAAGAAGTCCAGAAAGTTCTGCAGAGGAGACACTTACATGATGAAGATTGAAAGG 686
QY 101 AlAserG1uG1n1eTyTyTyTyG1uAerArG1nG1yTyTyArGThr1AserVal11e11e 120
Db 687 GCCAGTGAAGCATTTATTTATGAAACAGCAAGGGTACAGACAGCCGTCATCATTT 746
QY 121 AlA1e1uThrArPArG1yG1u1e1uH1eG1uArPLeuPhePheTyTySerG1uArG1uAlAer 140
Db 747 GCTTTGACTGATGGAAGACTCCATGAAGATCTCTTTTTCATTTCAAGAGAGGAGCTAAT 806
QY 141 ArgSerArGArPLeuG1yAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAl 160
Db 807 AGGCTCGAATCTTGGTGCAATTTGTTACTGTGTGTGTGAAAGATTTCATATGAGACA 866
QY 161 G1n1e1uAlArG11e1AaerSer1yAerH1eVal1PheProVal1AerArPArG1yPheG1n 180
Db 867 CAGCTGCGCGAATGGGAGCAGTAAGATCATGTGTTTCCCGTAATGACGGCTTTCAG 926
QY 181 AlA1e1uG1nG1y11e11eH1e1Ser11e1e1u1y1e1ySerCy11eG1u11e1uAlAlAl 200
Db 927 GCTCTGGAAGGATCATCCATCTCATTTTGAAGAAGTCCGCATCGAAATTCATAGCAGCT 986
QY 201 G1uProSerThr11eCyAlAlAlG1y1e1ySerPheG1nVal1Val1ArG1yAerG1yPhe 220
Db 987 GAACATCCACATATGTGAGAGAGAGTCAATTCATTTCAATGTCGAGAGAGAAACGGCTTC 1046
QY 221 ArgH1e1AlArGArNVal1AerArGVal1e1uCySerPhe1y11eAaerArPArG1yThr 240
Db 1047 CGACATGCCGCAACGTGACAGGGTCTCTGACGTTCAAGATCAATGACTCGGTGACA 1106
QY 241 LeuAerG1u 243
Db 1107 CTCAGTAAG 1115

RESULT 2
US-10-104-047-669
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/ Sequence 669, Application US/10104047
/ Patent No. 6943241
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: No. 6943241el full length cDNA
/ FILE REFERENCE: H1-A0105
/ CURRENT FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER:
/ PRIORITY FILING DATE:
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: Patentln Ver. 2.1
/ LENGTH: 2234
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-104-047-669

Alignment Scores:
Pred. No.: 3.77e-92 Length: 2234
Score: 790.50 Matches: 157
Percent Similarity: 71.53% Conservative: 54
Best Local Similarity: 53.22% Mismatches: 81
Query Match: 51.46% Indels: 3
DB: 3 Gaps: 2

US-09-970-076-2_COPY_27_321 (1-295) x US-10-104-047-669 (1-2234)

QY 1 G1yG1ng1yG1y---ArGArG1uArPArG1yG1yProAlAcYrG1yG1yPheArPLeu 19
Db 604 GGTCCCGGGGGCTGTGTGCGCCCGCAGAGCAGCCCTCTGCAAGAACCTTTGATCTC 663
QY 20 TyPhe11e1uArP1ySerG1ySerVal1LeuH1e1TrPaNg1u1eTyTyTyPhe 39
Db 664 TACTTGCTCTGAGCAAGCTGTGAGATGTGGCAATTAATCGAATTAATTAATTTTC 723
QY 40 ValG1uG1n1e1uAlaH1e1yPhe11eSerProG1n1e1uArGMeSerPhe11eVal1Phe 59
Db 724 GTACAGCAACTTGGCGAGATTTTGAGCCCTGAAATGAAATGATTAATCTTCAATTTGTTT 783
QY 60 SerThrArG1yThrThr1e1uMeTy1eSerProG1n1e1uArPArG1uG1n1eArG1nG1y 79
Db 784 TCTTCAGCAACATTTATTTTGGCCATTAACTGAGACAGAGCAAAATCACTAAAGC 843
QY 80 LeuG1uG1n1e1uG1n1yVal1e1uProG1yArPThrTyMeH1eG1uG1yPheG1u 99
Db 844 TTGAGAGATTTAAAGCTGTAGTCTCCATAGAGAAACATATATCAATGAAGACTAAAG 903
QY 100 ArgAlAserG1uG1n1eTyTyTyTyG1uAerArG1nG1yTyTyArGThrAlAserVal11e 119
Db 904 CTAGCGAATGAACAATTT-----CAGAAAGCAGAGGCTTGAAACCTCCAGTATCATTA 957
QY 120 11eAlA1e1uThrArPArG1yG1u1e1uH1eG1uArPLeuPhePheTyTySerG1uArG1uAlA 139
Db 958 ATTGCTCTGACAGATGGCAAGTTGACGGTCTGTGTCATCATATGACAGAAAGAGCA 1017
QY 140 AaerArGArPArPLeuG1yAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAl 159
Db 1018 AAGATATCCAGGCTCACTGGGGCTAGTATTATGTGTGTGTCTCTGATTTTGAACAA 1077
QY 160 ThnG1n1e1uAlArG11e1AaerSer1yAerH1eVal1PheProVal1AerArPArG1yPhe 179
Db 1078 GCACAGCTTGAAAGAAATTCGTATTCACAGAGCAAGTTTCCCTGTCAAAAGGTGATTT 1137
QY 180 G1nAlA1e1uG1nG1y11e11eH1e1Ser11e1e1u1y1e1ySerCy11eG1u11e1uAlAl 199
Db 1138 CAGGCTCTTAAAGGAATTAATTTATTAATCAAGCTCAAGTCACTGAATCCATAGAA 1197
QY 200 AlaG1uProSerThr11eCyAlAlAlG1y1e1ySerPheG1nVal1Val1ArG1yAerG1y 219
Db 1198 TTGCAGCCCTCAAGATGTGTGTGTGGGAGAGAAATTTCAATATTTCTTAAGTGAAGAGCA 1257
QY 220 PheArG1e1AlArGArNVal1AerArGVal1e1uCySerPhe1y11eAaerArPArG1yThr 239
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Db      1258 TTATGCTGGGAGTCCGGAATGGAGTGTCTCTGCACCTTACCTGTAATGAACAATAT 1317
      |||
Qy      240 ThrleuengluYrProPheSeValGluAphThrTyLeuLeuCySerProAlaProIle 259
      |||
Db      1318 ACAACGAGTGAACCAAGTGTGTACAGCTTAATCTTAATCTTGTGCTGCACCTATC 1377
      |||
Qy      260 LeuYegluValGlyMetLysAlaLeuGluInValSerMetAanAapGlyLeuSerPhe 279
      |||
Db      1378 CTGAATAAAGCTGGAAGAACTCTTGATGTTTCAGAGGCTTTAAATGAGAGAAATCTGTC 1437
      |||
Qy      280 ILeSerSeValIleIleThrThrHisCySerAapGly 294
      |||
Db      1438 ATTTCAGATCATTAATTCATCAGACCAAGATGTTCTAACGGG 1482

RESULT 3
US-09-974-528-297
; Sequence 297, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyun
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pc_fl_genes Version 2.0
; SEQ ID NO 297
; LENGTH: 1492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79)..(1434)
US-09-974-528-297

Alignment Scores:
Pred. No.: 7,98e-82 Length: 1492
Score: 709.00 Matches: 139
Percent Similarity: 72.35% Conservative: 52
Best Local Similarity: 52.65% Mismatches: 71
Query Match: 46.16% Gaps: 2
DB: 3

US-09-970-076-2_COPY_27_321 (1-295) x US-09-974-528-297 (1-1492)

Qy      31 HieHetrPangluYrTyTyPheValGluGluInleuAlaHlsYrAphleSePro 50
      |||
Db      16 AAATACCTGATGTAATTAATTTGATACAGCACTTGGGAGAGATTGTAGCCCT 75
      |||
Qy      51 GluLeuAArgMetSerPheIleValPheSerThraArgLyThrThrLeuMetLysLeuThr 70
      |||
Db      76 GAATAGATATATCTTTCATGTTCTCTCAGAGAACTATTAATTTGCCATTAAT 135
      |||
Qy      71 GluAphArgGluGluInleuArgGlyLeuGluGluInleuGlyValLeuProGlyGly 90
      |||
Db      136 GGAACAGAGGCGCAAAATCAGTAAAGGCTTGAGAGATTAAACCTGTTAGTCCAGTGA 195
      |||
Qy      91 AepHrTyRMetHlsGluGlyPheGluAArgLAserGluGluInleuYrTyGluAanArg 110
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Db      196 GAGCATATATCCATGAAAGGCTAAAGCTAAGCTAGCGAATGAACAAT-----CAGAAAGCA 249
      |||
Qy      111 GluGlyTyRArgThraLAserValIleIleAlaLeuThraArgGlyGluLeuHisGluAap 130
      |||
Db      250 GAGAGCTTGAACCTCAGATATATTCCTCTGACAGATGGCAAGTGGACGCTGTG 309
      |||
Qy      131 LeuPheHetrYrSerGluAArgGluAlaAanArgSerArgAapLeuGlyValIleValTyR 150
      |||
Db      310 GTGCCATCATATGCAAGAAAGGCAAGATATCCAGGTCACCTTGAGGAGCTAGTGTAT 369
      |||
Qy      151 CySeValGlyValLysAapPheAanGluThrGluInleuAlaArgIleAlaAapSerLysAap 170
      |||
Db      370 TGCTTGGGGCTCTTGAATTTTGAACAAGCAGCTTAAGAAATTCGATTCAGAGAG 429
      |||
Qy      171 HieValPheProValAanAapGlyPheGluAlaLeuGluGlyIleHlsSerIleLeu 190
      |||
Db      430 CAAGTTTCCCTGCAAGAGGATTCAGGCTCTTAAGAAATTAATTAATTTCTACTA 489
      |||
Qy      191 LysLysSerCysIleGluIleLeuAlaGluAProSerThrIleCySeAlaGlyGluSer 210
      |||
Db      490 GCTCAGTCATGTAAGTAATCTGAATTCGAGCCCTCAAGTGTCTGTGGGGAGGAA 549
      |||
Qy      211 PheGluValValAlaArgGlyAanGlyPheAArgHisAlaArgAenValAapArgValLeu 230
      |||
Db      550 TTTCAGATTCCTTAAGTGAAGAGATTCATGCTGGGCGATCGGAATGGCAGTCTCTC 609
      |||
Qy      231 CySerPheLysIleAanAapSerValThrleuAanGluYrProPheSeValGluAap 250
      |||
Db      610 TGCACTTACACTGTAATGAACATATATACAGAGTGTAAACCAAGTAAGTGTACACTT 669
      |||
Qy      251 ThrTyRleuLeuCySerProAlaProIleLeuLysGluValGlyMetLysAlaLeuGlu 270
      |||
Db      670 AATTCATGCTTGTCTGCACTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 729
      |||
Qy      271 ValSerMetAanAapGlyLeuSerPheIleSerSeValIleIleThrThrHis 290
      |||
Db      730 GTAGAGCTTAATGAGAAATCTGTATTCATTCAGATCATTAATTCACAGCAAGAA 789
      |||
Qy      291 CySerAapGly 294
      |||
Db      790 TGTCTTAACGG 801

RESULT 4
US-10-120-988-297
; Sequence 297, Application US/10120988
; Patent No. 6919193
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Ren, Feiyun
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6919193el Nucleic Acids and
; FILE REFERENCE: 802CON
; CURRENT APPLICATION NUMBER: US/10/120,988
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/774,528
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pc_fl_genes Version 2.0
; SEQ ID NO 297
; LENGTH: 1492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79)..(1434)
US-10-120-988-297

Alignment Scores:
```

Pred. No.: 7.98e-82 Length: 1492
Score: 709.00 Matches: 139
Percent Similarity: 72.35% Conservative: 52
Best Local Similarity: 52.65% Mismatches: 71
Query Match: 46.16% Indels: 2
DB: 3 Gaps: 1

US-09-970-076-2_COPY_27_321 (1-295) x US-10-120-988-297 (1-1492)

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QY H1eH1eT1pA8n8l1u1eT1rY1rPheVal1G1u1eU1aH1a1yS1pHe1leS1eP1ro 50
DB 16 AATAC1GGAATTATTAATTAATTCGACAGACCTTGGAGAGATTGGAGCCCT 75
QY 51 G1n1eU1aRw1eS1ePhe1leVal1PheS1eTh1rA1rG1y1Th1r1eU1eU1yS1eU1a1r 70
DB 76 GAATAGGATTAATCTTTCATGTTGTTTCTTCACAGCACTATTAATTTGGCATTAAC 135
QY 71 G1u1aP1aRg1u1n1le1aRg1n1y1eU1G1u1eU1n1yS1a1l1eU1P1oG1y1 90
DB 136 GGAGACAGAGGCAAAATCAGTAAGGCTTGAGGATTTAAACGTGTACTCCAGTAAG 195
QY 91 AaP1Th1r1eU1eU1G1u1eU1aRg1a1S1eRg1u1n1le1rY1rG1u1a1n1aRg 110
DB 196 GAGACATATATCCATGAGAGCTTAAGCTAGCCATGACAAATL-----CAGAAAGCA 249
QY 111 G1n1y1Y1z1aRg1Th1a1S1eR1a1l1e1a1eU1Th1aRg1y1G1u1eU1H1a1S1u1aP 130
DB 250 GAGAGCTTGAAACCTCCATATCATATATGCTGTGACATGGAAGTTGGACGGCTG 309
QY 131 L1eU1Phe1Th1eRg1u1aRg1u1a1a1a1S1eR1aRg1aP1eU1G1a1a1e1a1l1e1a1Y1r 150
DB 310 GTCACATCATATCAGAGAAAGGCAAAAGATATCCAGTCTGGGCTAGTGTATT 369
QY 151 C1e1V1a1G1y1a1y1a1S1aPhe1a1n8l1u1Th1r1eU1a1aRg11e1a1aP1eS1eR1y1aP 170
DB 370 TGGTTGGGGTCTCTGATTGTAACAGACAGCTTGAAAGAAATGCTGATCCAGAG 429
QY 171 H1e1a1Phe1P1o1a1a1a1a1a1Phe1G1y1Phe1G1a1eU1n1y1l1e1e1H1e1S1eR1l1eU 190
DB 430 CAAGTTTCCCTGCAAGGTGATTTCAAGCTCTTAAGAAATTAATTTCTATATCTA 489
QY 191 L1y1e1y1S1eR1C1y1l1eG1u1l1eU1a1a1a1G1u1P1r1oS1eR1Th1r1eC1y1a1a1G1y1u1S1eR 210
DB 490 GCTCAGCATGATCTGAATCTTAAGATTCAGCCCTCAAGTGTCTGTGTGGGGAGAA 549
QY 211 PheG1a1V1a1y1a1aRg1y1a1n8l1y1Phe1aRg1H1a1aRg1a1a1aP1aRg1a1y1eU 230
DB 550 TTTCAAGTTGTCTTAAGTGAAGAGATTCATCTGCGGCACTCGGAATGGCAGGTCTC 609
QY 231 C1y1eS1eR1Phe1y1l1e1a1n8P1eR1V1a1Th1r1eU1a1n8l1u1y1S1P1r1oPheS1eR1V1a1G1u1aP 250
DB 610 TGCACCTTACCTGTAATTAAGACATATACAGAGCTTAAGAACCAAGTAATGTACAGCTT 669
QY 251 Th1r1r1eU1eU1C1y1P1r1o1a1P1r1o1l1eU1y1S1G1u1a1G1y1eU1y1a1a1a1eU1n 270
DB 670 AATTCATGCTTTGCTGCACTATCTGAATTAAGCTGAGAACTCTTGATGTTTCA 729
QY 271 V1a1S1eR1eR1a1n8P1y1eU1S1eR1Phe1l1eS1eR1S1eR1V1a1l1e1Th1r1r1h1S 290
DB 730 GTAGAGCTTAAAGAGAAATCTGTCAATTCAGGATCATTAATGTACAGCCACAGAA 789
QY 291 C1y1eS1eR1aP1y1 294
DB 790 TGTTCATACGG 801
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RESULT 5
US-09-799-451-250
; Sequence 250, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ry1e

```
/ APPLICANT: Asundi, Vinod  
/ APPLICANT: Ren, Feiyan  
/ APPLICANT: Zhang, Jie  
/ APPLICANT: Xue, Aidong J.  
/ APPLICANT: Zhao, Qing A.  
/ APPLICANT: Wang, Jian-Rui  
/ APPLICANT: Ma, Yungting  
/ APPLICANT: Yamazaki, Victoria  
/ APPLICANT: Chen, Rui-hong  
/ APPLICANT: Wang, Zhiwei  
/ APPLICANT: Wang, Dunrui  
/ APPLICANT: Yang, Yonghong  
/ APPLICANT: Wehrman, Tom  
/ APPLICANT: Ghosh, Reena  
/ APPLICANT: Drmanac, Radoje T.  
/ TITLE OF INVENTION: No. 6783969e1 Nucleic Acids and  
/ FILE REFERENCE: Polypeptides  
/ CURRENT APPLICATION NUMBER: US/09/799,451  
/ CURRENT FILING DATE: 2001-03-05  
/ SOFTWARE: PL_FL_genes Version 2.0  
/ SEQ ID NO 250  
/ LENGTH: 3981  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: CDS  
/ LOCATION: (287)..(1118)  
US-09-799-451-250
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Alignment Scores:
Pred. No.: 5.11e-75 Length: 3981
Score: 662.00 Matches: 129
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 43.10% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-2_COPY_27_321 (1-295) x US-09-799-451-250 (1-3981)

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QY 167 AaP1eR1y1aP1H1a1Phe1P1o1a1a1a1a1a1Phe1G1y1Phe1G1a1eU1n1y1l1e1e 186
DB 3 GACAGTAAGATCATCTGTTCCCGTAATGACGGCTTTCAGGCTGTGCAAGCATCATC 62
QY 187 H1S1eR1l1eU1y1a1y1e1y1S1eR1C1y1l1eG1u1l1eU1a1a1a1G1u1P1r1oS1eR1Th1r1eC1y1 206
DB 63 CACTCAATTTGAAAGATCTGATCGATGAAATTTCTAGCACTGACCAATTCACCATATGT 122
QY 207 A1a1G1y1u1S1eR1Phe1G1n1a1y1a1aRg1y1a1n8l1y1Phe1aRg1H1a1aRg1a1a1aP1aRg1a1y1eU 226
DB 123 GCGAGAGATCATTTCAAGTTGTCGTGAGAGAAAGGGCTTCGACATGCGCAACGTG 182
QY 227 AaP1aRg1a1eU1C1y1S1eR1Phe1y1l1e1a1n8P1eR1V1a1Th1r1eU1a1n8l1u1y1S1P1r1oPhe 246
DB 183 GACAGGGTCTCTGCACTTCAAGATCAATGACTCGCTCACTCACTCAATGAGAAAGCCCTT 242
QY 247 S1eR1V1a1G1u1aP1Th1r1r1eU1eU1C1y1P1r1o1a1P1r1o1l1eU1y1S1G1u1a1G1y1eU1y1a1 266
DB 243 TCTGTGAAGATATCTTAATTTACTGTGTCCAGCCCTTAATCTTAAGAAAGTTGGCATGAA 302
QY 267 A1a1a1eU1n1y1a1S1eR1eR1a1n8P1y1eU1S1eR1Phe1l1eS1eR1S1eR1V1a1l1e1Th1r1r1h1S 286
DB 303 GCTGCACTCCAGGTCAGCATGAAGATGGGCTCTCTTAATCTCCAGTTCTGTCAATCATC 362
QY 287 Th1r1Th1H1eC1y1S1eR1aP1y1S1eR 295
DB 363 ACCACCACACACTGTTCGACGGTTC 389
```

RESULT 6
US-08-286-889-45
; Sequence 45, Application US/08286889
; Patent No. 5470953

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seer Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-286-889-45
Alignment Scores:
Pred. No.: 1.54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.81% Indels: 30
DB: 2 Gaps: 12
US-09-970-076-2_COPY_27_321 (1-295) x US-08-286-889-45 (1-3519)
QY 11 ProbaCyeTyrGly--GlyPheAspLeuTyrPheIleLeuAspLysSerGlySerVal 29
DB 481 CCAAGAGTCCAGACAGACAGATGACATGCTTCTCTGATTAAGCTCCGGGACATT 540
QY 30 ---LeuH1sh1sTPraEngluIeTyrTyrPheValgluInleuAhi1sYpPheIle 48
DB 541 GATCAAGTACCTTACCCAGATGAGAGCTTCTGCTCAAGCTTGAAGGGCGAATTGGCG 600
QY 49 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrIleuMetLys 68
DB 601 AGCACGACGACCTGCTCTCCGATGCAATACCAACATCTGAAAGCTCATTTTACC 660
QY 69 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGluGluLeu 83
DB 661 TTACGGAATTCAAGACAGACGCTGAGCCCTCAGAGCTGGATGCGCATGCTCAGCTC 720
QY 84 GlnIyValValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgAlaSerGlu 103
DB 721 CAA-----GGCCTGACGTACACAGCTCGGGCATCCAGAAAGTGTGAAA 765

QY 104 GlnIleTyrTrgIuAsnArgGlnGlyTyrArgThrAla---SerValIleIleAlaLeu 122
DB 766 GAGTATTTCATACCAAGAAATGGGGCCGAAAAAGTCCAGAAAGATACATTAATGTCATC 825
QY 123 ThrAspGlyGluLeuH1sh1sGluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsn 140
DB 826 ACAGATGGGCAAAATTCAGAGACCCCTCGAGATATGACATGTCATCCCTGAAAGCAGAG 885
QY 141 ArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValYAsp---PheAsnGlu 159
DB 886 AAAGCT-----GGATCATTCGCTATGATAGGGGTGGAGATGCTCCGGGAA 936
QY 160 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 173
DB 937 CCCATGCTCCCTACGAGAGCTGAAACACCATTTGGCTCAGCTCCCTCGCAGACCATGTTTC 996
QY 174 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleuLysSer 193
DB 997 AAGGTGGGCAAT---TTGTAGACATTCGACGATCCAGGGGCAAAATTCAGAGAAA--- 1050
QY 194 CysIleGluIleuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 213
DB 1051 -----ATCTTGCCATTGAAAGAACCGAATCAAGTCAAGTCAAGTACTCTTTCACACAC 1101
QY 214 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 227
DB 1102 GAGATGTACAGAGAGTTTCAGCTCAGCTCTCTCAATGAT 1143
RESULT 7
US-08-485-618-45 Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seer Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:

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/ LENGTH: 3519 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 52..3519
US-08-485-618-45

Alignment Scores:
Pred. No.: 1,54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.81% Indels: 30
DB: Gaps: 12

US-09-970-076-2_COPY_27_321 (1-295) x US-08-485-618-45 (1-3519)
QY 11 ProAlaCyetyrGly---GlyPheAspLeuTyPheIleuAspLysSerGlySerVal 29
DB 481 CCAGAGTGTCCAGAGACAGAGATGAGCATTTGCTTCTGTATGATGGCTCCGACAGATT 540
QY 30 ---LeuHiHieHieTrrpangluileTyTyPheValGluGlnLeuAlahisLysPheIle 48
DB 541 GATCAAGAATGACTTACCCAGATGAAGAGACTTCGTCAAAAGCTTGATGGCCAGTTGGCG 600
QY 49 SerProGlnLeuArgetSerPheIleValPheSerThrArgGlyThrPheLeuMetLys 68
DB 601 AGCACCAGACAGCTGTTCTCTCCGTATGCAATACCTCAAAACCTCTGAAGACTCATTTTACC 660
QY 69 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGlnGluLeu 83
DB 661 TTACCGGAATTCAGAGACAGACCTGAGACCTCAGAGCTGTGATGCCATCGTCCAGCTC 720
QY 84 GlnLysValIleuProGlyGlyAspThrTyTmetHieGluGlyPheGluArgAlaSerGlu 103
DB 721 CAA-----GGCCGTGACGTACACAGACCTCGGGCATCCAGAAAGTGTGTA 765
QY 104 GlnIleTyTyTgluAsnArgGlnGlyTyArgThrAla---SerValIleIleAlaLeu 122
DB 766 GAGCTATTTCATGACAGAAATGGGGCCGAAAAAGTCCAGAAAGATTAATTTGTCATC 825
QY 123 ThrAspGlyGluLeuHieHieGluAspLeuPhePheTySerGlu-----ArgGluAlaAsn 140
DB 826 ACAGATGGCAGAAATTCAGAGACCCCTGAGATATGACATGTCATCCTCGAAGCAGAG 885
QY 141 ArgSerArgAspLeuGlyAlaIleValTyTyCyValGlyValIysAsp---PheAsnGlu 159
DB 886 AAGGCT-----GGGATCATTCGGCTATGCTATAGGGGTGGAGATGCTTCCGGGAA 936
QY 160 ---ThcGlnLeuAlaArgIle-----AlaAspSerLysAspPheIleValPhe 173
DB 937 CCCACTGCTCCCTAAGAGAGCTGAACACCATGGCTCAGCTCCCTGCGAGCAGCAGTGTTC 996
QY 174 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 193
DB 997 AAGTGGGCAAT---TTTGAAGCATTCGCGAGCATTCAGAGCGCAATTCAGAGAAA--- 1050
QY 194 CysIleGluIleLeuAlaAlaGluProSerThrIleCyValaGlyLysSerPheGlnVal 213
DB 1051 -----ATCTTTGCCATTGAAGAACCGAATCAAGTCAAGTACTGCTTTCACACAC 1101
QY 214 ValValaArgGlyAsnGlyPheAspGhiAlaArgAsnValAsp 227
DB 1102 GAGATGTCAACAAGAGTTTCAGCTCAGCTCTCAATGAT 1143

RESULT 8
US-08-362-652-45
/ Sequence 45: Application US/08362652
/ Patent No. 5766850
/ GENERAL INFORMATION:

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/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 93
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/362,652
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32391
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ. ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3519 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 52..3519
US-08-362-652-45

Alignment Scores:
Pred. No.: 1,54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.81% Indels: 30
DB: Gaps: 12

US-09-970-076-2_COPY_27_321 (1-295) x US-08-362-652-45 (1-3519)
QY 11 ProAlaCyetyrGly---GlyPheAspLeuTyPheIleuAspLysSerGlySerVal 29
DB 481 CCAGAGTGTCCAGAGACAGAGATGAGCATTTGCTTCTGTATGATGGCTCCGACAGATT 540
QY 30 ---LeuHiHieHieTrrpangluileTyTyPheValGluGlnLeuAlahisLysPheIle 48
DB 541 GATCAAGAATGACTTACCCAGATGAAGAGACTTCGTCAAAAGCTTGATGGCCAGTTGGCG 600
QY 49 SerProGlnLeuArgetSerPheIleValPheSerThrArgGlyThrPheLeuMetLys 68
DB 601 AGCACCAGACAGCTGTTCTCTCCGTATGCAATACCTCAAAACCTCTGAAGACTCATTTTACC 660
QY 69 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGlnGluLeu 83
DB 661 TTACCGGAATTCAGAGACAGACCTGAGACCTCAGAGCTGTGATGCCATCGTCCAGCTC 720
QY 84 GlnLysValIleuProGlyGlyAspThrTyTmetHieGluGlyPheGluArgAlaSerGlu 103

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Db 721 CAA-----GGCTGACGTAACAGACCTCGGCAATCCAGAAAGTGTAAG 765
Qy 104 GlnIleTyrTyrGluAsnArgGlnGlyTyrArgThraIa---SerValIleIleAlaIleu 122
Db 766 GAGCTATTTCATACCAAGAAATGGGCCCCGAAAGAGTCCAGAAAGATTAATGTCATC 825
Qy 123 ThrAspGlyGluLeuHsiGluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsn 140
Db 826 ACAAGATGGGCAAGAAATTCAGACAGACCCCTGGAGTATAGACATGTCATCCTCGAAGCAGAG 885
Qy 141 ArgSerArgAspLeuGlyAlaIleValTyrCyValaGlyValysAsp---PheAsnGlu 159
Db 886 AAAGCT-----GGGATCATTCGGCTATGCTATAGAGGGGAGAGATTCCTCCGGGAA 936
Qy 160 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 173
Db 937 CCCACTGCCCTACAGAGCTGMAACCATTTGGCTCAGCTCCCTCCGACGAGACAGTGTTC 996
Qy 174 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 193
Db 997 AAGTGGGCAAT---TTGTAGCACTTCGACGATCCAGCCGCAAAATTCAGAGAA--- 1050
Qy 194 CysIleGluIleLeuAlaIleValProSerThrIleCysAlaGlyLysSerPheGlnVal 213
Db 1051 -----ATCTTGCCATTGAAAGAAACCAATCAAGTCAAGTCAATGCTCTTCACAGAC 1101
Qy 214 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 227
Db 1102 GAGATGTCAAGAAAGTTTCAGCTCAGCTCTCAATGAT 1143

RESULT 9
US-08-605-672-45
/ Sequence 45, Application US/08605672
/ Patent No. 5817515
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vlieten, Monica
/ TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/605,672
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856

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/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3519 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 52..3519
/ US-08-605-672-45

Alignment Scores:
Pred. No.: 154e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.81% Indels: 30
DB: 2 Gaps: 12

US-09-970-076-2_COPY_27_321 (1-295) x US-08-605-672-45 (1-3519)

Qy 11 ProAlaCysTyrGly---GlyPheAspLeuTyrPheIleLeuAspLysSerGlySerVal 29
Db 481 CCAAGTGTCCAGGACAAAGATGAGATGATGCTTCTGTAATGATGCTCCGACGATC 540
Qy 30 ---LeuHisIleTyrAsnGlyIleTyrTyrPheValGluGlnLeuAlaHsiLysPheIle 48
Db 541 GATCAAGATGACTTTATCCAGATGAGATGAGACTGCTCAAACTTTGATGGGCAAGTGGCG 600
Qy 49 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 68
Db 601 AGCACCAAGCACTTCGTTCTCTCCATGATCAATTAACAACATCTGAAGACTCATTTTACC 660
Qy 69 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGluLeu 83
Db 661 TTCACGGAATTCAAAGACAGACCTGAGCCCTCAGAGCTGGTGAATGCCATGTCACATC 720
Qy 84 GlnLysValLeuProGlyIleAspThrTyrMechIleGluIlePheGluArgAlaSerGlu 103
Db 721 CAA-----GGCTGACCTGATACAGACCTCGGCAATCCAGAAAGTGTAAG 765
Qy 104 GlnIleTyrTyrGluAsnArgGlnGlyTyrArgThraIa---SerValIleIleAlaIleu 122
Db 766 GAGCTATTTCATACCAAGAAATGGGCCCCGAAAGTCCAGAAAGATTAATGTCATC 825
Qy 123 ThrAspGlyGluLeuHsiGluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsn 140
Db 826 ACAAGATGGGCAAGAAATTCAGACAGACCCCTGGAGTATAGACATGTCATCCTGAAGCAGAG 885
Qy 141 ArgSerArgAspLeuGlyAlaIleValTyrCyValaGlyValysAsp---PheAsnGlu 159
Db 886 AAAGCT-----GGGATCATTCGGCTATGCTATAGAGGGTGGAGATGCTCCCGGAA 936
Qy 160 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 173
Db 937 CCCACTGCCCTACAGAGCTGMAACCATTTGGCTCAGCTCCCTCCGACGAGACAGTGTTC 996
Qy 174 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 193
Db 997 AAGTGGGCAAT---TTGTAGCACTTCGACGATCCAGGAGGCAAAATTCAGAGAA--- 1050
Qy 194 CysIleGluIleLeuAlaIleValProSerThrIleCysAlaGlyLysSerPheGlnVal 213
Db 1051 -----ATCTTGCCATTGAAAGAAACCAATCAAGTCAAGTCAATGCTCTTCACAGAC 1101
Qy 214 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 227
Db 1102 GAGATGTCAAGAAAGTTTCAGCTCAGCTCTCAATGAT 1143

RESULT 10
US-08-482-293A-45
/ Sequence 45, Application US/08482293A

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REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-943-363-45

Alignment Scores:
Pred. No.: 1.54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.81% Indels: 30
DB: Gaps: 12

US-09-970-076-2_COPY_27_321 (1-295) x US-08-943-363-45 (1-3519)

QY 11 ProAlaCyArTyGly--GlyPheArLeuTyPheIleLeuArLySeRgLySeRVal 29
DB 481 CCAGAGTGTCCAGACAAAGATGACATTCCTTCTGATGTGATGCTCGGACGACTT 540
QY 30 ---LeuH1eH1eTTPraEngIuIeTyTyTyPheValGluGlnLeuAlaH1eLyPheIle 48
DB 541 GATCAAAAGTACTTACCCAGATGAAGACTTCCTCAAGCTTTGATGGCCAGTTGGCG 600
QY 49 SerProGlnLeuArGMeSerPheIleValPheSerThArGlyThrThrLeuMetLyS 68
DB 601 AGACACGACGACCTGTTCTCCGTGATGCAATACCAAAATCCGAAGACTCATTTTACC 660
QY 69 LeuThGluArPArG-----GluGlnIleArGlnIleuGlnIleu 83
DB 661 TTCACGGAATTCAGAGACGCTGAAGCTTCAGAGCTGTGATGCATGCTCCAGACTC 720
QY 84 GlnLyValLeuProGlyGlyArPThrTyMeH1eGlnIlePheGlnArGAlaSeRgLy 103
DB 721 CAA-----GGCTGACGTACACAGCTCGGACATCCGAAAGTGGTGA 765
QY 104 GlnIleTyTyGlnLeuArGlnIleTyTyArGThrAla---SerValIleIleAlaLeu 122
DB 766 GAGCTATTTCATGACAAAGATGGGCCCCGAAAAAGTCCCAAGAAATTAATTCATC 825
QY 123 ThrArGlyGluLeuH1eGluArLeuPhePheTySeRgLy-----ArgGluAlaAsn 140
DB 826 ACAGATGGGCAAAATTCAGAGACCCCTGAGATATGACATGTCATCCCTGAAGCAGAG 885
QY 141 ArgSerArGArPLeuGlyAlaIleValTyTyCyValGlyValLyAsp---PheArGln 159
DB 886 AAAGCT-----GGGATCATTCGCTATGATAGAGGGTGGAGATGCTTCGGGAA 926
QY 160 ---ThGlnLeuAlaArgIle-----AlaArSerLyAsPArH1eValPhe 173
DB 937 CCCACTGCTCCATGACGAGCTGAACACCATGGCTGAGCTCCCTGCGACGACACAGTTC 996
QY 174 ProValArPArGlyPheGlnAlaLeuGlnIleIleH1eSerIleLeuLyArLySeR 193
DB 997 AAGGTGGGCAAT---TTGTAGCACTTCGACAGCATCAGCGGCAAAATTCAGGAA--- 1050
QY 194 CyAlleGluIleLeuAlaIleGluProSerThrIleCyValaGlyGluSeRPhGlnVal 213
DB 1051 -----ATCTTGGCATTTGAAGGACCAAGATCAAGGTCAAGTACTGCTTCACGAC 1101
QY 214 ValValArGlyLeuEngIyPheArGThH1eAlaArgArValArP 227
DB 227
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DB 1102 GAGATGTCAAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 12
US-09-193-043-45
Sequence 45, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT FILING DATE: US/09/193,043
EARLIER FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23/286,889
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 45
LENGTH: 3519
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (52)..(3516)
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer

US-09-193-043-45

Alignment Scores:
Pred. No.: 1.54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.81% Indels: 30
DB: Gaps: 12

US-09-970-076-2_COPY_27_321 (1-295) x US-09-193-043-45 (1-3519)

QY 11 ProAlaCyArTyGly--GlyPheArLeuTyPheIleLeuArLySeRgLySeRVal 29
DB 481 CCAGAGTGTCCAGACAAAGATGACATTCCTTCTGATGTGATGCTCGGACGACTT 540
QY 30 ---LeuH1eH1eTTPraEngIuIeTyTyTyPheValGluGlnLeuAlaH1eLyPheIle 48
DB 541 GATCAAAAGTACTTACCCAGATGAAGACTTCCTCAAGCTTTGATGGCCAGTTGGCG 600
QY 49 SerProGlnLeuArGMeSerPheIleValPheSerThArGlyThrThrLeuMetLyS 68
DB 601 AGACACGACGACCTGTTCTCCGTGATGCAATACCAAAATCCGAAGACTCATTTTACC 660
QY 69 LeuThGluArPArG-----GluGlnIleArGlnIleuGlnIleu 83
DB 661 TTCACGGAATTCAGAGACGCTGAAGCTTCAGAGCTGTGATGCATGCTCCAGACTC 720
QY 84 GlnLyValLeuProGlyGlyArPThrTyMeH1eGlnIlePheGlnArGAlaSeRgLy 103
DB 721 CAA-----GGCTGACGTACACAGCTCGGACATCCGAAAGTGGTGA 765
QY 104 GlnIleTyTyGlnLeuArGlnIleTyTyArGThrAla---SerValIleIleAlaLeu 122
DB 766 GAGCTATTTCATGACAAAGATGGGCCCCGAAAAAGTCCCAAGAAATTAATTCATC 825
QY 123 ThrArGlyGluLeuH1eGluArLeuPhePheTySeRgLy-----ArgGluAlaAsn 140
DB 826 ACAGATGGGCAAAATTCAGAGACCCCTGAGATATGACATGTCATCCCTGAAGCAGAG 885
QY 141 ArgSerArGArPLeuGlyAlaIleValTyTyCyValGlyValLyAsp---PheArGln 159
DB 159
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Db      886 AAAGCT-----GGGATCATTCCTATGCTATAGGGGTGGAGATGCTCCGGGAA 936
Qy      160 ---ThGlnLeuAlaArgIle-----AlaAspSerIysAspHisValPhe 173
Db      937 CCCACTGCCCTACAGAGCAAGAACACCACTGGCTCAGCTCCCTCGACAGACACGCTGTC 996
Qy      174 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIysIysSer 193
Db      997 AAGGTGGGCAAT---TTTGTAGCACTTCGACGATCCAGCGGCAATTTCAGAGAA--- 1050
Qy      194 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 213
Db      1051 -----ATCTTTCCTCATTTGAAGAACCAATCAAGCAAGTAGTTCCTTCAGACAC 1101
Qy      214 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 227
Db      1102 GAGATGTCACAGAGGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 13
US-09-688-307A-45
; Sequence 45, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688,307A
; PRIORITY FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3516)
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-688-307A-45

Alignment Scores:
Pred. No.:      1,54e-10      Length:      3519
Score:          166.00      Matches:      66
Percent Similarity: 46.15%      Conservative: 42
Best Local Similarity: 28.21%      Mismatches: 96
Query Match:      10.81%      Indels:      30
DB:              3          Gaps:      12

US-09-970-076-2_COPY_27_321 (1-295) x US-09-688-307A-45 (1-3519)
Qy      11 ProAlaCysArgGly---GlyPheAspLeuTyrrPheIleLeuAspIysSerGlySerVal 29
Db      481 CCAGAGGTGCCAGGACAGAGATGACATTCCTTCGTATGATGCTCCGGGACGACAT 540
Qy      30 ---LeuHisThrPheAsnGluIleTyrrPheValGluGlnIleAlaHisIysPheIle 48
Db      541 GATCAAAAGTAGACTTACCCAGATGAAGACTCTGTCAAAGCTTGATGGCGCGATTGGCG 600
Qy      49 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetIys 68
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Db      601 ACCACAGCAGCCTCGTTCCTCCCTGATGCAMTCTCAAAATCTGAAAGCTCATTTTACC 660
Qy      69 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGluGluLeu 83
Db      661 TTCAGGAAATTCAAGAGCAGCAGCCTCAGACCTCAGAGCCTGTGGATGCCATCTCCAGCTC 720
Qy      84 GlnIysValLeuProGlyValAspThrTyrrMetHisGluGlyPheGluArgAlaSerGlu 103
Db      721 CAA-----GGCTGACGTACACAGCCTCGGGCATCCAGAAAGTGCTGA 765
Qy      104 GlnIleTyrrTyrrGluAsnArgGlnGlyTyrrAlaGlnThrAla---SerValIleIleAlaLeu 122
Db      766 GAGCTATTTCATAGCAAGAAATGGAGGCCCGAAAGAGTCCCAAGAGATTAATTGTCAATC 825
Qy      123 ThrAspGlyGluLeuHisGluIleAspLeuPhePheTyrrSerGlu-----ArgGluAlaAsn 140
Db      826 ACGATGGGCAAAATTCCAGAGACCCCTCGAGTATGACATGTATCCCTCGAAGCAGAG 885
Qy      141 ArgSerArgAspLeuGlyValAlaIleValTyrrCysValGlyValIysAsp---PheAsnGlu 159
Db      886 AAAGCT-----GGGATCATTCGCTATGCTATAGGGGTGGAGATGCTCCGGGAA 936
Qy      160 ---ThGlnLeuAlaArgIle-----AlaAspSerIysAspHisValPhe 173
Db      937 CCCACTGCCCTACAGAGCTGAACACCACTGGCTCAGCTCCCTCGACAGACACGCTGTC 996
Qy      174 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIysIysSer 193
Db      997 AAGGTGGGCAAT---TTTGTAGCACTTCGACGATCCAGCGGCAATTTCAGAGAA--- 1050
Qy      194 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 213
Db      1051 -----ATCTTTCCTCATTTGAAGAACCAATCAAGCAAGTAGTTCCTTCAGACAC 1101
Qy      214 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 227
Db      1102 GAGATGTCACAGAGGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 14
US-09-350-259-45
; Sequence 45, Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6620915el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3516)
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-350-259-45
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QY      123 ThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsn 140
      |||||:::
Db      775 ACAGATGGGCAGAAATTTCAGAGACCCCTGGAGTATAGACATGTCACTCCCTGAAGCAGAG 834
QY      141 ArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAsp--PheAsnGlu 159
      :::::
Db      835 AAAGCT-----GGGATCATTCGCTATGCTATAGGGGTGGAGATGCTTCGGGAA 885
QY      160 ---ThrGluLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 173
      |||||:::
Db      886 CCCACTGCCCTTACAGAGAGCTGAACACCATTTGGCTCAGCTCCCTCGCAGAGCACGTGTTTC 945
QY      174 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysIleSer 193
      |||||:::
Db      946 AAGGTGGGCAAT---TTTGAGCACTTCGACGATCCAGCGGCAGAAATTCAGAGAAA--- 999
QY      194 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyLysSerPheGlnVal 213
      |||||:::
Db      1000 -----ATCTTGGCATTGAAGGAAACCGAATCAAGTCAAGTATTCTTTTCAGCAC 1050
QY      214 ValValArgGlyLysAsnGlyPheArgHisAlaArgAsnValAsp 227
      :::::
Db      1051 GAGATGTACACAGAAAGTTTCAGCTCAGCTCTCTCATGTGAT 1092
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Search completed: December 18, 2005, 07:34:00
Job time : 225.111 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:35:12 ; Search time 945.104 Seconds
(without alignments)
2581.163 Million cell updates/sec

Title: US-09-970-076-2_COPY_27_321

Perfect score: 1536
Sequence: 1 GCGGRREDGACVCGFDLY.....GLSFSSVITTTTCSDSG 295

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh
-Q=/cg2_1/USPTO.epool/US0970076/runat_14122005_11852_21035/app_query.fasta_1_2410
-DB=Published_Applications_NA_Main -OPMT=fastap -SUFFIX=rnprobm -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blomsun62
-TRANS=human40.csl -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US0970076 @CGN_1_1_2715 @runat_14122005_11852_21035
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:

1:	/cg2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2:	/cg2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3:	/cg2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4:	/cg2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5:	/cg2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6:	/cg2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7:	/cg2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8:	/cg2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9:	/cg2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10:	/cg2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1536	100.0	1414	10	US-11-047-278-1
2	1536	100.0	1454	6	US-10-133-937-58
3	1536	100.0	1454	6	US-10-159-563-58
4	1536	100.0	5540	3	US-09-918-715-176
5	1536	100.0	5540	3	US-09-918-715-231
6	1536	100.0	5540	6	US-10-301-822-198
7	1536	100.0	5540	8	US-10-474-794-176
8	1536	100.0	5540	8	US-10-474-794-231

9	1536	100.0	5540	9	US-10-979-159-176	Sequence 176, App
10	1536	100.0	5540	9	US-10-979-159-231	Sequence 231, App
11	1536	100.0	5540	10	US-11-047-278-5	Sequence 5, Appl
12	1532	99.7	1674	6	US-10-038-307-17	Sequence 17, Appl
13	1532	99.7	1674	6	US-10-201-292-17	Sequence 17, Appl
14	1521	99.0	1650	6	US-10-038-307-13	Sequence 13, Appl
15	1521	99.0	1650	6	US-10-038-307-15	Sequence 15, Appl
16	1521	99.0	1650	6	US-10-201-292-13	Sequence 13, Appl
17	1521	99.0	1650	6	US-10-201-292-15	Sequence 15, Appl
18	1520	99.0	1056	6	US-10-038-307-23	Sequence 23, Appl
19	1520	99.0	1056	6	US-10-201-292-23	Sequence 23, Appl
20	1520	99.0	1713	6	US-10-038-307-19	Sequence 19, Appl
21	1520	99.0	1713	6	US-10-201-292-19	Sequence 19, Appl
22	1520	99.0	2112	10	US-11-047-278-7	Sequence 7, Appl
23	1520	99.0	2272	3	US-09-796-753-11	Sequence 11, Appl
24	1520	99.0	2272	6	US-10-038-307-1	Sequence 1, Appl
25	1520	99.0	2272	6	US-10-201-292-1	Sequence 1, Appl
26	1520	99.0	2353	5	US-10-198-846-9957	Sequence 9957, Ap
27	1519	98.9	5220	3	US-09-918-715-186	Sequence 186, App
28	1519	98.9	5220	3	US-09-918-715-300	Sequence 300, App
29	1519	98.9	5220	8	US-10-474-794-186	Sequence 186, App
30	1519	98.9	5220	8	US-10-474-794-300	Sequence 300, App
31	1519	98.9	5220	9	US-10-979-159-186	Sequence 186, App
32	1519	98.9	5220	9	US-10-979-159-300	Sequence 300, App
33	1511	98.4	1650	6	US-10-038-307-9	Sequence 9, Appl
34	1511	98.4	1650	6	US-10-201-292-9	Sequence 9, Appl
35	1507	98.1	1008	6	US-10-038-307-25	Sequence 25, Appl
36	1507	98.1	1008	6	US-10-201-292-25	Sequence 25, Appl
37	1505.5	98.0	1047	6	US-10-038-307-21	Sequence 21, Appl
38	1505.5	98.0	1047	6	US-10-201-292-21	Sequence 21, Appl
39	1500	97.7	1623	6	US-10-038-307-11	Sequence 11, Appl
40	1500	97.7	1623	6	US-10-201-292-11	Sequence 11, Appl
41	1419	92.4	1608	6	US-10-201-292-35	Sequence 35, Appl
42	1391	90.6	2397	6	US-10-062-674-1757	Sequence 1757, Ap
43	1294	84.2	1534	6	US-10-201-292-33	Sequence 33, Appl
44	1263	82.2	1436	10	US-11-047-278-9	Sequence 9, Appl
45	1263	82.2	1609	5	US-10-037-270-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-11-047-278-1
; Sequence 1, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: McGridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; PRIOR FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)..(1207)
US-11-047-278-1
Alignment Scores:
Pred. No.: 3,246-186
Score: 1536.00
Length: 1414
Matches: 295
Percent Similarity: 100.00%
Conservative: 0

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-970-076-2_COPY_27_321 (1-295) x US-11-047-278-1 (1-1414)
QY 1 GYGLNGIYGIYARARGLUAPRGYGLYPROALCYETRYGJLYPHEAPLEUTYR 20
DB 182 GGGCAAGGGGAGCGAGGAGATGGGGGCTCCAGCCGTGACGGCGATTGACCTGTAC 241
QY 21 PHEILEUAPLYSERGYSERVALLEUHIHISTPANGIUIETRYTPHEVAL 40
DB 242 TTCATTTTGGACAAATCAGAGATGTGCTCACCACCTGGAATGAAATCTATTCTTTG 301
QY 41 GUGLNUAHLAHSYSPHEILSERPROGJLNUARGMESERPHEILEVALPHESE 60
DB 302 GAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAAATGTCCTTTATTGTTTCTCC 361
QY 61 THRARGJLYTHRLEUWETLYSEUThRGJUAAPRGJUGJNLEARGJNGJLEU 80
DB 362 ACCCGAGAACACCTTAAATGAACTGACAGAAAGACAGAAACAAATCCGTCAAGGCTTA 421
QY 81 GUGJLNUGLNUYVALLEUPROGJLYASPThRYMECHISGLUGJYPHEGJUA 100
DB 422 GAAGAACTCCAGAAAGTTCTGCCAGAGAGACCTTACATGATGAAGATTGAAAGG 481
QY 101 ALASERGLUGJNLEUTRYRGJUAAPRGJNGJLYTRARThRLASERVALILE 120
DB 482 GCCAGTGAGCAATTTATGAAACAGCAAGGTTACAGACAGCCAGCTCATCAT 541
QY 121 ALALEUThRAPJLYLEUHIHISGLUAPLYSPHEPHEThYRSERGJUAARGJUAASN 140
DB 542 GCTTTGACTGAGAGAACTCCATGAAGATCTCTTTTCTATTCAAGAGAGGAGCTAAT 601
QY 141 ARGSEARGLAPLEUGJYALILEVALTRYCYVALIGJLYVALYASPPHEANGJUTHR 160
DB 602 AGGCTCGAGATCTTGTCAAATTTGATTCTGTGCTGTAAGATTTTCAATGAGACA 661
QY 161 GJLNUAHLARGLILEALASPSERYASPHISVALPHEPROVALASNAPSGJYPHEGJN 180
DB 662 CAGCTGCCCCGAGATGCGGACAGTAAGATCATGTGTCGCCGTAATGACGGCTTCAG 721
QY 181 ALALEUGJNGLYILEIHISERJLEUJLYSSECYSLIEGJULEUJLEUJALALA 200
DB 722 GCTCTGAGAGCATCATCCACTCAATTTTGAAGAAGCTCGCATCGAAATTCATGACGCT 781
QY 201 GIUPROSEThRIIECYVALAGJYUSERPHEGJNVALYVALARGJYANGJYPHE 220
DB 782 GAACCATCCACATATGTGACGAGAGACTCAATTCAGTGTGAGAGAGAAACGGCTTC 841
QY 221 ARGHISALARGANVALAPARGVALLEUCYSESPHELYSILEASNAPSERVALTHR 240
DB 842 CGACATGCCCGCAACGTGACAGGGTCTCTGACGCTTCAGATCAATGACTGGGTACA 901
QY 241 LEUASNGJULYSPROPHESERVALGUASPThRYLEUJLEUCYSPROALAPROJLEU 260
DB 902 CTCATAGAGAGACCTTTTCTGTGAGAGACACTTATTATTCAGTGTCCAGGCGCTATCTTA 961
QY 261 LYGJLNUALGYMETLYSALALALEUGJNVALSERMETASNPARGJLYLEUSERPHEILE 280
DB 962 AAAGAAATTTGACATGAAAGCTGCACTCAGGTCCAGCTGAGAACGATGCGCTCTTTATTC 1021
QY 281 SESERSEVALILEIETHRThRHISCYSESPARGJLYSER 295
DB 1022 TCCAGTTCGTGATCATCACCAACACACTGTTCTGACGGTTC 1066
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```
APPLICANT: Peterson, Carsten
APPLICANT: Melzer, Paul
TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
TITLE OF INVENTION: OTHER BIOLOGICAL STATES
FILE REFERENCE: 11613.56US01
CURRENT APPLICATION NUMBER: US/10/133,937
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58
LENGTH: 1454
TYPE: DNA
ORGANISM: Homo sapiens
US-10-133-937-58
Alignment Scores:
Pred. No.: 3,39e-186 Length: 1454
Score: 1536.00 Matches: 295
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-970-076-2_COPY_27_321 (1-295) x US-10-133-937-58 (1-1454)
QY 1 GYGLNGIYGIYARARGLUAPRGYGLYPROALCYETRYGJLYPHEAPLEUTYR 20
DB 222 GGGCAAGGGGAGCGAGGAGATGGGGGCTCCAGCCGTGACGGCGATTGACCTGTAC 281
QY 21 PHEILEUAPLYSERGYSERVALLEUHIHISTPANGIUIETRYTPHEVAL 40
DB 282 TTCATTTTGGACAAATCAGAGATGTGCTGACACCACTGGAATGAAATCTATTCTTTG 341
QY 41 GJLNUAHLAHSYSPHEILSERPROGJLNUARGMESERPHEILEVALPHESE 60
DB 342 GAACATTTGGCTCAAAATTCATCAGCCCAAGTTGAAATGTCCTTTATTTGTTTCTCC 401
QY 61 THRARGJLYTHRLEUWETLYSEUThRGJUAAPRGJUGJNLEARGJNGJLEU 80
DB 402 ACCCGAGAACACCTTAAATGAACTGACAGAAAGACAGAAACAAATCCGTCAAGGCTTA 461
QY 81 GJLNUAHLNUYVALLEUPROGJLYASPThRYMECHISGLUGJYPHEGJUA 100
DB 462 GAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGATGAAGATTGAAAGG 521
QY 101 ALASERGLUGJNLEUTRYRGJUAAPRGJNGJLYTRARThRLASERVALILE 120
DB 522 GCCAGTGAGCAATTTATGAAACAGCAAGGTTACAGACAGCCAGCTCATCAT 581
QY 121 ALALEUThRAPJLYLEUHIHISGLUAPLYSPHEPHEThYRSERGJUAARGJUAASN 140
DB 582 GCTTTGACTGAGAGAACTCCATGAAGATCTCTTTTCTATTCAAGAGGAGGCTAAT 641
QY 141 ARGSEARGLAPLEUGJYALILEVALTRYCYVALIGJLYVALYASPPHEANGJUTHR 160
DB 642 AGGCTCGAGATCTTGTCCAATTTGTTACTGTGCTGTAAGATTTCAATGAGACA 701
QY 161 GJLNUAHLARGLILEALASPSERYASPHISVALPHEPROVALASNAPSGJYPHEGJN 180
DB 702 CAGCTGCCCCGAGATGCGGACAGTAAGATCATGTGTTCCGCTGATGACGGCTTCAG 761
QY 181 ALALEUGJNGLYILEIHISERJLEUJLYSSECYSLIEGJULEUJLEUJALALA 200
DB 762 GCTCTGAGAGCATCATCCACTCAATTTTGAAGAAGTCTGATCGAAATTCATGACGCT 821
QY 201 GIUPROSEThRIIECYVALAGJYUSERPHEGJNVALYVALARGJYANGJYPHE 220
DB 822 GAACATTCACCATATGTGACAGAGAGTCAATTTCAAGTGTGAGAGAAACGGCTTC 881
QY 221 ARGHISALARGANVALAPARGVALLEUCYSESPHELYSILEASNAPSERVALTHR 240
DB 882 CGACATGCCCGCAACGTGACAGGGTCTCTGACGCTTCAATGATCATGACTGGGTACA 941
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QY 241 LeuansgluysPpoheserValgluaspThrtThrtleuLeuCyprolaProilaLeu 260
DB 942 CTCAATGAGAGCCCTTTCTGTGGAACACTTATTCTGTCTCCAGCCCTATCTTA 1001
QY 261 LysgluValgluMetlysaalaleuInvalserMetanaapgluLeuSerPheile 280
DB 1002 AAAAGAGTGGCATGAAAGCTGCACCTCCAGCTCAGATGAAAGATGGCTCTTTATTC 1061
QY 281 SerSerSerValleileThrtThrtThrtThrtThrtThrtThrtThrtThrt 295
DB 1062 TCCAGTCTGTCTCATCATCACCAACACACTGTCTGACGGTTC 1106

RESULT 3
US-10-159-563-58
Sequence 58, Application US/10159563
Publication No. US2004009154A1
GENERAL INFORMATION:
APPLICANT: Khan, Javed
APPLICANT: Ringner, Markus
APPLICANT: Peterson, Carsten
APPLICANT: Meltzer, Paul
TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
FILE REFERENCE: 11613.56US11
CURRENT APPLICATION NUMBER: US/10/159,563
PRIOR FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 10/133,937
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 444
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58
LENGTH: 1454
TYPE: DNA
ORGANISM: Homo sapiens
US-10-159-563-58

Alignment Scores:
Pred. No.: 3,396-186 Length: 1454
Score: 1536.00 Matches: 295
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_27_321 (1-295) x US-10-159-563-58 (1-1454)

QY 1 GlyIngluylgIyArgrgIuaspgluylgIyProilaCystrgIygluYpneaspLeuTyr 20
DB 222 GGGCAAGGGGAGCCAGGAGAGATGGGGGTCTCACTCTGACGGGATTTGACCTGTAC 281
QY 21 PheileuaspIySerIySerValleuHsiestrapangluileTyrTyrPheVal 40
DB 282 TTTCAATTTTGGACAATCAGAAAGTGTCTGCACCACTGGAATGAAATCTATTACTTGTG 341
QY 41 GluInleuHsielylePheileSerProgluInleuargMetSerPheileValPheSer 60
DB 342 GAACAGTTGGCTCAAAATTCATCAGCCCACTGGAAGTCTTTATTGTTTCTCC 401
QY 61 ThrtArgluThrtThrtleuMetlysaalaleuThrtgluaspArggluInleargGluYleu 80
DB 402 ACCGAGAGAACACTTATATGAACTGACAGAAACAGAAACAAATCCGTCAGAGCTTA 461
QY 81 GluInleuInleuValleuPheProgluYlYaspThrtThrtThrtThrtThrtThrt 100
DB 462 GAAGAACTCCAGAAAGTCTCCAGAGAGACCTTAATGATGAAAGATTTGAAAGG 521
QY 101 AlaSerGluInleuTyrTyrGluaspArggluInleuYrargTrrAlaSerValleile 120
DB 522 GCCAGTGAAGCATTTATATGAAACAGAAAGGATGAGAGACGCGATCATCAATT 581
QY 121 AlaLeuThrtArpIygluLeuHsielyleuaspLeuPhePheTyrSerGluargGluAlaasn 140

DB 582 GCTTTGATGATGAGAACTCCATGAAGATCTTTTCTATTTCAGAGAGGAGCTAAT 641
QY 141 ArgSerArpaspLeuInleuValleileTyrCyValgluYlYaspPheaspLeuThrt 160
DB 642 AGGTCTGAAGATCTGTGTGCAATTTGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 701
QY 161 GluInleuAlaArgIleAlaApseryAspHsiValPheProValaenapgluYpHeGln 180
DB 702 CAGCTGGCCGGATTTGGACAGATGAGATCATGTGTTCCTCCGTAATGACGGCTTTCAG 761
QY 181 AlaLeuIngluYlIleleHsiestryleuYlYaserysileguileuAlaAla 200
DB 762 GCTCTGCAAGCATCATCACTCAATTTTGAAGAAGCTTCGATCGAAATTTAGACAGCT 821
QY 201 GluProSerThrtIleCyValgluYlYaseryPheGluValYalYargGluYasnGluYpHe 220
DB 822 GAACATCCACCAATGTGAGAGAGTCAATTCAGATTTCCGTAAGAGAAACGGCTTC 881
QY 221 ArgHsiAlaArgAsnValaPArGValleuCySerPheYlIleAenapSerValThrt 240
DB 882 CGACATCCCGCAACGTGAGACAGGGTCTCTGACGTTCAAGATCATGATCGGTACACA 941
QY 241 LeuansgluysPpoheserValgluaspThrtThrtleuLeuCyprolaProilaLeu 260
DB 942 CTCAATGAGAGCCCTTTCTGTGGAAGACATTATTACTGTGTCCAGCGCTATCTTA 1001
QY 261 LysgluValgluMetlysaalaleuInvalserMetanaapgluLeuSerPheile 280
DB 1002 AAAAGAGTGGCATGAAAGCTGCACCTCCAGTCAAGATGAAAGATGGCTCTTTATTC 1061
QY 281 SerSerSerValleileThrtThrtThrtThrtThrtThrtThrtThrtThrt 295
DB 1062 TCCAGTCTGTCTCATCATCACCAACACACTGTCTGACGGTTC 1106

RESULT 4
US-09-918-715-176
Sequence 176, Application US/09918715
Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 176
LENGTH: 5540
TYPE: DNA
ORGANISM: Homo sapiens
US-09-918-715-176

Alignment Scores:
Pred. No.: 2,876-185 Length: 5540
Score: 1536.00 Matches: 295
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-2_COPY_27_321 (1-295) x US-09-918-715-176 (1-5540)

QY 1 GlyIngluylgIyArgrgIuaspgluylgIyProilaCystrgIygluYpneaspLeuTyr 20
DB 222 GGGCAAGGGGAGCGAGGAGAGATGGGGGTCTCACTCTGACGGGATTTGACCTGTAC 281

QY 21 Phe1LeuAspLysSerGlySerValLeuH1e1eTTPanGlu1LeTyrPheVal 40
282 TTCATTTTGGCAAAATCAGAAATGTGTCTCACCACTGGAAATTAATCTTATCTTGTG 341
QY 41 GluGlnLeuA1aH1e1ySpher1eSerProGlnLeuArgMetSerPhe1LeValPheSer 60
342 GAACAGTTGGCTCAAAATTCATCAGCCACAGCTTGAGATGTCCTTATTTGTTTCTCC 401
QY 61 ThrArgGlyThrThreuleuMetLysLeuThrGluAspArgGluGln1LeaArgGlnGlyLeu 80
402 ACCCGAGGAAACAACCTTAATGAACCTGACAGAAAGACAGAAACAATTCCTCAAGGCTTA 461
QY 81 GluGlnLeuGln1yValLeuProGlyGlyAspThrTyrMetH1eGluGlyPheGluArg 100
462 GAAGAACTCCAGAAAGTCTCGCAGAGAGAGACATTAATGATGAAGATTTGAAAG 521
QY 101 AlaSerGluGln1LeTyrTyrGluAanaArgGlnGlyTyrArgThrAlaSerVal1le1le 120
522 GCCAGTGAGCAGATTTATTTATGAAAAACAGACAAGGGTACAGACAGCCAGCTCATCAT 581
QY 121 AlaLeuThrAspGlyGluLeuH1eGluAspLeuPhePheTyrSerGluArgGluA1aen 140
582 GCTTTGACGATGAGAACTCCATGAAATCTCTTTTCTATTCAAGAGAGGAGGCTAAT 641
QY 141 ArgSerArgAspLeuGlyAla1leValTyrCyValGlyVal1yAspPheAenGluThr 160
642 AGGTCTCGAGATCTTGCTGCAATTTGTTACTGTGTGTGTGAAGATTTCAATGAGACA 701
QY 161 GlnLeuA1aArg1Lea1aAspSerLysAspH1eValPheProValaAspGlyPheGln 180
702 CAGCTGGCCGAGATTGGGAGACATGAAAGATCATGTGTTCCTGTAATGACGCTTTCAG 761
QY 181 AlaLeuGlnGly1Le1leH1eSer1LeuLysLysSerCyVal1eGlu1LeuA1a1a 200
762 GCTCTGAGAGCATCATCACTCAATTTTGAAGAGCTCGCATCGAAATCTTAAGAGCT 821
QY 201 GluProSerThr1LeCyValaGlyGlySerPheGlnVal1Val1ArgGlyAenGlyPhe 220
822 GAACATCCACCAATGTGTGAGAGAGCTCATTTCAAGTTCGTGAGAGAGAAACGCTTC 881
QY 221 ArgH1eA1aArgAenValaAspArgValLeuCySerPheLys1LeaAspSerVal1Thr 240
882 CGACATGCCGCAACGAGACAGGGTCTCTGCAAGCTTCAAGATCATGATCGGTGACA 941
QY 241 LeuAsnGluLysProPheSerValGluAspThrTyrLeuLeuCyProAlaPro1leu 260
942 CTCATGAGAAAGCCCTTTCTGTGAGAGATTAATTACTGTGTCCAGGCGCTATCTTA 1001
QY 261 LysGluValaGlyMetLysA1a1aLeuGlnValSerMetAAspGlyLeuSerPhe1e 280
1002 AAAGAACTTGGCATGAAGCTGCACTCCAGGTCAAGCATGAACGATGGCTCTCTTTAT 1061
QY 281 SerSerSerVal1le1leThrThrH1eCySerAspGlySer 295
1062 TCAGTCTGTCTCATCATCACACACACACTGTTCTGACGCTTC 1106
Db 1062 TCAGTCTGTCTCATCATCACACACACACTGTTCTGACGCTTC 1106

RESULT 5

US-09-918-715-231
; Sequence 231, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918, 715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11

; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 231
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-231
Alignment Scores:
Pred. No.: 2,87e-185 Length: 5540
Score: 1536.00 Matches: 295
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-09-970-076-2_COPY_27_321 (1-295) x US-09-918-715-231 (1-5540)
QY 1 G1yGlnGlyGlyArgArgGluAspGlyGlyProAlaCyTyrGlyGlyPheAspLeuTyr 20
Db 222 GGGCAAGGGGAGACGACGAGAGATGGGGTCCAGCTGCTACGCGGATTTGACCTGTAC 281
QY 21 Phe1LeuAspLysSerGlySerValLeuH1e1eTTPanGlu1LeTyrPheVal 40
Db 282 TTCATTTTGGCAAAATCAGAAATGTGTCTCACCACTGGAAATTAATCTTATCTTGTG 341
QY 41 GluGlnLeuA1aH1e1ySpher1eSerProGlnLeuArgMetSerPhe1LeValPheSer 60
Db 342 GAACAGTTGGCTCAAAATTCATCAGCCACAGGTGAGAAATCTTATTTGTTTCTCC 401
QY 61 ThrArgGlyThrThreuleuMetLysLeuThrGluAspArgGluGln1LeaArgGlnGlyLeu 80
Db 402 ACCCGAGGAAACAACCTTAATGAACCTGACAGAAAGACAGAAACAATTCCTCAAGGCTTA 461
QY 81 GluGlnLeuGln1yValLeuProGlyGlyAspThrTyrMetH1eGluGlyPheGluArg 100
Db 462 GAAGAACTCCAGAAAGTCTCGCAGAGAGAGACATTAATGATGAAGATTTGAAAG 521
QY 101 AlaSerGluGln1LeTyrTyrGluAanaArgGlnGlyTyrArgThrAlaSerVal1le1le 120
Db 522 GCCAGTGAGCAGATTTATTTATGAAAAACAGACAAGGGTACAGACAGCCAGCTCATCAT 581
QY 121 AlaLeuThrAspGlyGluLeuH1eGluAspLeuPhePheTyrSerGluArgGluA1aen 140
Db 582 GCTTTGACGATGAGAACTCCATGAAGATCTCTTTTCTATTCAAGAGAGGCTAAT 641
QY 141 ArgSerArgAspLeuGlyAla1leValTyrCyValaGlyVal1yAspPheAenGluThr 160
Db 642 AGGTCTCGAGATCTTGCTGCAATTTGTTACTGTGTGTGTGAAGATTTCAATGAGACA 701
QY 161 GlnLeuA1aArg1Lea1aAspSerLysAspH1eValPheProValaAspGlyPheGln 180
Db 702 CAGCTGGCCGAGATTGGGAGACATGAAAGATCATGTGTTCCTGTAATGACGCTTTCAG 761
QY 181 AlaLeuGlnGly1Le1leH1eSer1LeuLysLysSerCyVal1eGlu1LeuA1a1a 200
Db 762 GCTCTGAGAGCATCATCACTCAATTTTGAAGAACTCTGATCGAAATTCAGACAGCT 821
QY 201 GluProSerThr1LeCyValaGlyGlySerPheGlnVal1Val1ArgGlyAenGlyPhe 220
Db 822 GAACATCCACCAATGTGTGAGAGATTAATTACTGTGTCCAGGCGCTATCTTA 1001
QY 221 ArgH1eA1aArgAenValaAspArgValLeuCySerPheLys1LeaAspSerVal1Thr 240
Db 882 CGACATGCCGCAACGAGACAGGGTCTCTGCAAGCTTCAAGATCATGATCGGTGACA 941
QY 241 LeuAsnGluLysProPheSerValGluAspThrTyrLeuLeuCyProAlaPro1leu 260
Db 942 CTCATGAGAAAGCCCTTTCTGTGAGAGATCTTATTTACTGTGTCCAGGCGCTATCTTA 1001
QY 261 LysGluValaGlyMetLysA1a1aLeuGlnValSerMetAAspGlyLeuSerPhe1e 280

Db 1002 AAGAGTGGCATGAAAGTCGACCTCAGGTGACGATGAAAGTGGCTCTTTATC 1061
Qy 281 SerSerValIleIleThrThrThiAcYSerAppGlySer 295
Db 1062 TCCAGTCTGTCTCATCATCACCACACACTGTTCTGACGGTTCC 1106

RESULT 6

US-10-301-822-198
Sequence 198, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MEMO1-029P2RNM
CURRENT APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 198
LENGTH: 5540
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (144)...(1838)
US-10-301-822-198

Alignment Scores:

Pred. No.: 2.87e-185 Length: 5540
Score: 1536.00 Matches: 295
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-970-076-2_copy_27_321 (1-295) x US-10-301-822-198 (1-5540)

Qy 1 G1yG1ng1yG1yA9yAG1yA9PG1yG1yPro1aCy9yG1yG1yPheA9PLeuTyR 20
Db 222 GCGGAGGGGAGCCGAGGAGGATGGGGTCTGACCTGCTACCGGATTTGACCTGTAC 281
Qy 21 PheIleuA9PLeuS9ySerValIeuhIshIstrPa9ngIuIeTyRtyrPheVal 40
Db 282 TTCATTTTGGACAATCAGAAAGTGTGCTGCACCACTGGAATGAATCTATTACTTTGTG 341
Qy 41 G1uG1u1euh1A9Ie9yPheIleS9yProG1u1euh9yMetS9rPheIleValPheS9r 60
Db 342 GAACAGTTGGCTCAAAATTCATCAGCCCACTTGAAAGTCTTTATTTGTTTCTCC 401
Qy 61 ThrArg1yThrThrLeuMetLeuTh9rG1uA9PAr9G1uG1u1eA9G1ng1yLeu 80
Db 402 ACCGAGGAAACAACCTTAATGAACCTGACAGAAACAAATCCGTCAGGCTTA 461
Qy 81 G1uG1u1euh1y9yValIeuh9yProG1yG1yA9PThrTyRMetH9g1uG1yPheG1uA9 100
Db 462 GAAGAACTCCAGAAAGTTCTGCGAGGAGAGACACTTATCATGCAATGAAGATTGAAAG 521

Qy 101 A1aSerG1uG1u1eTyRtyrG1uA9PAr9G1ng1yTyA9rThrA1aSerValIle 120
Db 522 GCGAGTACGAGANTTTATTTGAAAACAGACAGAGGATACAGACGCGATCATATT 581
Qy 121 A1aLeuThrA9PGLyG1u1euhI9g1uA9PLeuPheTyRtyrSerG1uA9G1uA1a9n 140
Db 582 GCTTGACATGAGAACTCCATGAAGATCTCTTTTCTATTTCAGAGAGGAGCTAAT 641
Qy 141 ArgSerTh9rPheLeuG1yA1aIeValTyRtyrCy9yValG1yValIyA9PAr9PheA9nG1uThr 160
Db 642 AGGTCTGAATCTTGGTGAATTTGACTGTGTGTGTGAAAGATTTCAATGAAGACA 701
Qy 161 G1u1euh1A9rG1leA1a9PSe9yLeA9PShI9yValPheProValA9nA9PGLyPheG1n 180
Db 702 CAGCTGCGCGGATTTGGGACAGTAAAGATCATGTGTTCCCGTAATGACGCTTCA 761
Qy 181 A1aLeuG1ng1yIleIleIshI9ySerIleu1yA9ySerCy9yIleG1u1euh1A1a 200
Db 762 GCTCTGCAAGCATCATCCACTCAATTTGAAAGATCCGATCGAAATTTCTAGCAGCT 821
Qy 201 G1uPAr9SerThrIleCy9yA1aG1yG1uSerPheG1nValIyA1a9rG1yA9nG1yPhe 220
Db 822 GAACATCCACCATATGTGACAGAGACTCATTCMAAGTGTCTGAGAGAGAAACGGCTTC 881
Qy 221 ArgH1sA1a9r9nValA9PAr9ValIe9ySerPheIyS1leA9nA9PSe9yValThr 240
Db 882 CGACATCCCGCAACGTCGACAGGCTCTTCGACGCTTCAAGATCATGATCGGTACA 941
Qy 241 LeuA9ng1u1ySPAr9PheS9yValG1uA9PThrTyRLeu9yCy9yProA1a9rIleu 260
Db 942 CTCAATAGAAAGCCCTTTCTGTGAGATATTATTATTCATGTGTCCAGCGCTATCTTA 1001
Qy 261 Ly9g1uValG1yMetLy9yA1aIeG1nValIe9ySerMetA9nA9PGLyLeuSerPheIle 280
Db 1002 AAGAAAGTTGCATGAAGCTGCATCCAGGTGACATGAACGATGGCTCTCTTTATC 1061
Qy 281 SerSerValIleIleThrThrThiAcYSerAppGlySer 295
Db 1062 TCCAGTCTGTCTCATCATCACCACACACTGTTCTGACGGTTCC 1106

RESULT 7

US-10-474-794-176
Sequence 176, Application US/10474794
Publication No. US20040213793A1
GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
PRIOR FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 176
LENGTH: 5540
TYPE: DNA
ORGANISM: Homo sapiens
US-10-474-794-176

Alignment Scores:
Pred. No.: 2.87e-185 Length: 5540
Score: 1536.00 Matches: 295
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-970-076-2_copy_27_321 (1..295) x US-10-474-794-176 (1..55410)

QY	1	GIYNGIYGIYA	gagargGluaspGlyI	ProAlaCyTYrGIYGIY	PhheAspLeuTYr	20
Db	222	GGGCAAGGGGAG	CGCAGGAGAGATGGGGGGT	CCAGCTTC	AGCGGGATTTGACCTGTAC	281
QY	21	PhelIleuAspIYsSerGIYSerIaIleuHishI	STPAnGluIleTYrTYrPhheAl	40		
Db	282	TTCAATTGGACAAAT	CGAAGTGTCTGCACCACTGGAAATGAAT	CTTATTACTTGTG	341	
QY	41	GIuGIuLeuAlaHishIYsPheI	eserProGIuLeuIqMecSerPheIleValI	Pheser	60	
Db	342	GAAcAGTTGGCTCA	CAAAATTCATCATCGCCACAGTTGAAGAAATG	CTCTTATTGTTTCTCC	401	
QY	61	ThraIrgIYThrThrLeuMecIYleuThrGIu	AspIrgIuGIuGIuIleIargIuGIYleu	80		
Db	402	ACCCAGAGAACAA	CCCTTAATGAATCGACAGAGACAGAAACAAAT	CCGTCAAGGCGCTA	461	
QY	81	GIuGIuLeuGIuIlyYsValIleuProGIYGI	YAspThrTYrMecHishIuGIYPhheGIuIrg	100		
Db	462	GAAGAACTCCAGAA	AGTTCTGCGAGAGAGAGACATTTACATGACAA	GAAGAAATTTGAAGG	521	
QY	101	AlAserGIuGIuIleTYrTYrGIuAsnIrgGIu	IYrArgThrAlAserValIleIle	120		
Db	522	GCCAGTAGACAGAT	TATTATGAAGAACAGACAGAGGTACAGACAG	CGCGTCTACTT	581	
QY	121	AlAleuThraSpGIYGIuLeuHishIuAspLeu	PhheIeTYrSerGIuIrgIuAlAsn	140		
Db	582	GCTTTGACTGATGG	AGAACTCCATMAATCTTTTCTATTCAGAAAGG	AGGCTAAT	641	
QY	141	ArgSerIaAspAlleuGIYAlaIleValIYrCy	sValIGIYAllyAspPhheAsnGIuThr	160		
Db	642	AGGTTCAGAGATCT	GGGCAATGTTTACTGTGTGTGAGAAAGATTTCA	ATGACACA	701	
QY	161	GIuLeuAlaArgIleAlaAspSerIYsAspHish	ValI	PheProValAsnAspGIYPhheGIu	180	
Db	702	CAGCTGGCCCGAT	TGGCGGACAGTAAAGATCATGTGTTCCCGTAA	AGAGCGCTTCAG	761	
QY	181	AlAleuGIuGIYIleIleHishSerIleuIYs	YsSerCYsIIeGIuIleuAlaIa	200		
Db	762	GCTTCGACAGGAT	CATCATCACTTTTGAAGAGTCTGCATGAAT	CTTAGCGACT	821	
QY	201	GIuProSerThrIleCyAlaGIYGIuSerPhe	GIuValIValIValIArgGIYAsnGIYPhhe	220		
Db	822	GAACCATCCACCA	NTATGTGCAGAGAAAGTCATTCAAGTTGCGAGAG	AGAAACGGCTTC	881	
QY	221	ArgHishIaArgAsnValIAspIrgValIleu	CysSerPhelYsIIeAsnAspSerValIThr	240		
Db	882	CGACATGCCCGCA	AGTGCAGGAGTCTCTGCAGCTTCMAATGA	ACTCGGTACA	941	
QY	241	LeuAsnGIuIYsProPheSerValIGIuAspThr	IYrIleuLeuCYsProAlaProIleu	260		
Db	942	CTCAATGAGAAAG	CCCTTTTCTGTGAAAGTACTTATTACTGTGCCAG	CGGCTACTTA	1001	
QY	261	LYsGIuValIIGYMeIYAlaIAlaLeuGIuVal	IserMecAsnAspGIYleuSerPheIle	280		
Db	1002	AAAGAAAGTGGAT	AAAGCTGCATCCAGGTCACAGAAAGAGAGG	CGCTCTTTTATTC	1061	
QY	281	SerSerSerValIleIleIleThrThrThrHish	CysSerAspGIYSer	295		
Db	1062	TCCAGTTCTGTCA	TATCATCACCAACACACTGTTC	TGACGGTTCC	1106	

RESULT 8
US-10-474-794-231
; Sequence 231, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	52
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QY      1  GYGLNGLYGIVARGRGIVARPGIYGLIYPRQALCYETRYGIVGLYPHEAPLEUTYR  20
DB      222 GGGCAAGGGGAGCGCAGGAGATGGGGGTCAGCGCTGACGGCGATTGACCTGTAC  281
QY      21  PHEILEUAPLYSERGISYERVALLEUHIHISTRPANGLULETYRTPHEVAL  40
DB      282 TTCATTTTGGACAATTCAGGAAGTGTGCTGACCACTGGAATGAAATCTATTACTTGTG  341
QY      41  GUGLNULEUAIHISYRPHLEISERPROGLNULEUARGMERSERPHEILEVALPHESE  60
DB      342 GAACAGTGGCTCAAAATTCATCAGCCACAGTGAAGATGCTTATTGTTTCTCC  401
QY      61  THRARGLYTHRTHREUMELYSLEUTHRGIVASPARGLUGINILEARGINGLYLEU  80
DB      402 ACCCGAGAACCACTTAATGAACTGACAGAAACAGAAACAAATCCGTCAAGGCTTA  461
QY      81  GUGLNULEUINLYVALLEUPROGLIYGLIYASPTHTYRMECHISGLUGIYPHEGLUARG  100
DB      462 GAAGAACTCCAGAAAGTTCTGCAGAGAGAGACACTTACATGATGAAAGATTGAAAG  521
QY     101  ALASERGLUGINILETYRTRYGUASPARGLINGLYTRYRGRHRLASERVALILELE  120
DB     522 GCCAGTGAAGCATTTATATGAAAAACAGCAAGGGTACAGACAGCCAGCTCATCTATT  581
QY     121  ALALEUTHRASPGLIYGLIYUENHISGLUASPLEUPHEPHETRYSERGIUARGIUALAASN  140
DB     582 GCTTTGACTGATGAGAACTCCATGAAAGATCTCTTTTTCATTCAGAGAGAGGCTTAAT  641
QY     141  ARGSEARARGAPLEUGIYALILEVALTRYCYVALIGLYVALIYASAPRHEANGIUTHR  160
DB     642 AGGTCTCGAATCTGTGTCATATTGTTACTGTGTGTTGTAAGATTTCATATGAGACA  701
QY     161  GINLEUAIARGILEHISYRPHLEISERPROGLNULEUARGMERSERPHEILEVALPHESE  180
DB     702 CAGCTGGCCCGAGTGGGAGCAGTGAAGATCATGTGTTCCCGTAATGACGGCTTCAG  761
QY     181  ALALEUNGINLYILEHISERILEUHIYSEYSECYSIILEGJUILEUAIALA  200
DB     762 GCTCTGCAAGCATCATCTCAATTTTGAAGAAGCTTCGATCAAAATTCATGACAGCT  821
QY     201  GIUPROSETHRIEYALAGIYGLIYUASPTHTYRMECHISGLUGIYPHEGLUARG  220
DB     822 GAACCATCCACCATATGTGAGAGAGATCATTTCAATGTCGTGAGAGAAACGGCTTC  881
QY     221  ARGHIALARGASVALASPARGVALLLEUCYSESERPHEIYSLIENASAPSERVALITHR  240
DB     882 CGACATGCCCGCAACGTGACAGGGTCTCTGACGCTTCAAGATCAATGACCTGGTACA  941
QY     241  LEUASNGIUTYSPROPHESERVALIGLUASPTHTYRLEUENUCYSPROALAPROILELEU  260
DB     942 CTCAATGAGAAAGCCCTTTTCTGTGAGAGATTCATTATTACTGTCTCAAGCGCTATCTTA  1001
QY     261  LYEGLIYVALIYMETIYSAIALAILEUINVAISERMERASAPRGLIYSEUERPHEILE  280
DB     1002 AAAGAAGTTGACATGAAGCTGCACTCCAGGTCAAGTGAACGATGCGCTCTTTATTC  1061
QY     281  SERSESERVALILEITHRTHRHIECYSESERPGLIYSER  295
DB     1062 TCCAGTTCGTGCATCATCACCAACACACACTGTTCGACGTTCC  1106

RESULT 11
US-11-047-278-5
; Sequence 5, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
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; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144) .. (1835)
US-11-047-278-5

Alignment Scores:
Pred. No.: 2,876-185 Length: 5540
Score: 1536.00 Matches: 295
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-970-076-2_COPY_27_321 (1-295) x US-11-047-278-5 (1-5540)

QY      1  GYGLNGLYGIVARGRGIVARPGIYGLIYPRQALCYETRYGIVGLYPHEAPLEUTYR  20
DB      222 GGGCAAGGGGAGCGCAGGAGATGGGGGTCAGCGCTGACGGCGATTGACCTGTAC  281
QY      21  PHEILEUAPLYSERGISYERVALLEUHIHISTRPANGLULETYRTPHEVAL  40
DB      282 TTCATTTTGGACAATTCAGGAAGTGTGCTGACCACTGGAATGAAATCTATTACTTGTG  341
QY      41  GUGLNULEUAIHISYRPHLEISERPROGLNULEUARGMERSERPHEILEVALPHESE  60
DB      342 GAACAGTGGCTCAAAATTCATCAGCCACAGTGAAGATGCTTATTGTTTCTCC  401
QY      61  THRARGLYTHRTHREUMELYSLEUTHRGIVASPARGLUGINILEARGINGLYLEU  80
DB      402 ACCCGAGAACCACTTAATGAACTGACAGAAACAGAAACAAATCCGTCAAGGCTTA  461
QY      81  GUGLNULEUINLYVALLEUPROGLIYGLIYASPTHTYRMECHISGLUGIYPHEGLUARG  100
DB      462 GAAGAACTCCAGAAAGTTCTGCAGAGAGACACTTACATGATGAAGATTGAAAG  521
QY      101  ALASERGLUGINILETYRTRYGUASPARGLINGLYTRYRGRHRLASERVALILELE  120
DB      522 GCCAGTGAAGCATTTATATGAAAAACAGCAAGGGTACAGACAGCCAGCTCATCTATT  581
QY      121  ALALEUTHRASPGLIYGLIYUENHISGLUASPLEUPHEPHETRYSERGIUARGIUALAASN  140
DB      582 GCTTTGACTGATGAGAACTCCATGAAAGTCTTTTTCATTCAGAGAGAGGCTTAAT  641
QY      141  ARGSEARARGAPLEUGIYALILEVALTRYCYVALIGLYVALIYASAPRHEANGIUTHR  160
DB      642 AGGTCTCGAATCTGTGTCATATTGTTACTGTGTGTTGTAAGATTTCATATGAGACA  701
QY      161  GINLEUAIARGILEHISYRPHLEISYRPHISVALPHEPROVALIENASAPSERVALITHR  180
DB      702 CAGCTGGCCCGGATTCGAGCAGTGAAGATCATGTGTTCCGTGAATGACGGCTTCAG  761
QY      181  ALALEUNGINLYILEHISERILEUHIYSEYSECYSIILEGJUILEUAIALA  200
DB      762 GCTCTGCAAGCATCATCTCAATTTTGAAGAAGCTTCGATCAAAATTCATGACAGCT  821
QY      201  GIUPROSETHRIEYALAGIYGLIYUASPTHTYRMECHISGLUGIYPHEGLUARG  220
DB      822 GAACCATCCACCATATGTGAGAGAGTCAATTCAGATGTCGTGAGAGAAACGGCTTC  881
QY      221  ARGHIALARGASVALASPARGVALLLEUCYSESERPHEIYSLIENASAPSERVALITHR  240
DB      882 CGACATGCCCGCAACGTGACAGGGTCTCTGACGCTTCAAGATCAATGACCTGGTACA  941
```



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Oy      241  leuAnGuIyVpProPhSeSeVaIgiuAspThrTYleuIeuCySePcoIAProIleu 260
Db      942  CTCATGAGAACCCCTTTCTGTGTGGAGACTTATTATCTGTCTCCAGCGCTATCTTTA 1001
Oy      261  LygIuVaIgiMeIyAlaIaIeugInVaISeMetAsnAspGIyLeuSePheIle 280
Db      1002  AAAGAGTTGGCATGAAGCTGCATCTCCAGGTCAACATGAAGAGTGGCTCTCTTTATC 1061

RESULT 12
US-10-038-307-17
US-Sequence 17, Application US/10038307
US-Publication No. US20030134786A1
US-GENERAL INFORMATION:
US-APPLICANT: James B. ROTTMAN
US-APPLICANT: Theresa L. O'KEEFE
US-APPLICANT: Engin OZKANAK
US-APPLICANT: Judith J. HEALEY
US-TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
US-FILE REFERENCE: 7853-253-999
US-CURRENT APPLICATION NUMBER: US/10/038,307
US-CURRENT FILING DATE: 2002-06-28
US-NUMBER OF SEQ ID NOS: 26
US-SOFTWARE: FastSeq for Windows Version 4.0
US-SEQ ID NO 17
US-LENGTH: 1674
US-TYPE: DNA
US-ORGANISM: Homo sapiens
US-US-10-038-307-17

```

Alignment Scores:		
Pred. No.:	1,396-185	length: 1674
Score:	1532.00	Matches: 294
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	99.74%	Indels: 0
DB:	6	Gaps: 0

Oy	1	GIYGLNGIYGLVAYRQARGLWAPRGIYGLYPRCALAQSRYTGLYGLYPHEAPRLEUTYR	20
Db	91	GGGCAAGGGGGAGCGCAGGAGGATGGGGGGCTCCAGCTGTACAGCGGATTTGACCTGTAC	150
Oy	21	PHEIIIELEUAPRLYASERGLYSERVALLEUHIHISTTPAANGULIETRYTYRPHAEVAL	40
Db	151	TTTCATTTTGGACAAATACAGAAAGTGTGCTGCACACCTGGAAATAAATCTATTCTTTGTG	210
Oy	41	GIUGIINLEUAIHISTYAPHEIIIESRPRGILNLEUARYMETERPHEIIIEVALPHESER	60
Db	211	GAACAGTTGGCTCACAAATTCACACCCACAGTTGGAAATGTCTTTAATGTGTTCTCC	270
Oy	61	THIRAXGLYTHRTRHEUMECTLYSELEUTRGLIAPRARGIUGIINLEARGIINGLYLEU	80
Db	271	ACCCGAGGACAACTTAATGAAACTGACAGGAAGACAGAAACAAATCCGTCAAGGCTTA	330
Oy	81	GIUGIULEUGLINLYEVALLEUPRPGIYGLYAPRTHRYMECHISGLUGIYPHEGLIARG	100
Db	331	GAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACACTTACATGATGAGATTTGANAAG	390
Oy	101	ALASERGLUGIINILETYRTYRGLIUAENARGIINGLYTYRZARTHRALASERVALILEIE	120
Db	391	GCCAGTGAACAATTTATTATATGAAAACAGACAAAGGTTACAGGACGCCAGCTCATCTT	450
Oy	121	ALALEUTHRAPRGLYGLIULEUHIISGLIUAAPRLEUPHEPHERYTSERGIUARGIUALAASN	140
Db	451	GCTTTGACATGAGGAGAACTCCATGANAATCTCTTTTTCATTCAAGAGAGGAGGCTAAT	510
Oy	141	ARGSERARGAPRLEUGIIVALAILEVALTYRCYSEVALGLYVALIYAPRPHAEANGIUTHR	160

Db	511	AGGCTCGAGATCTTGGTGCATTTGTTTACTGTGTGGTGGAAAGATTTCATGAGACA	570
Oy	161	GLNLEUALAARGILEALASPSERLYSAAPHISVALPHEPROVALASMAPGILYPHEG	180
Db	571	CAGCTGGCCGGATTCGGAGCAGTAAGATCATGTGTTTCCCGTGAATGACGGCTTTCAG	630
Oy	181	ALALEUNGILYILELLEHISSERLILEULYSLYSSERYGILLEGILILEUALALA	200
Db	631	GCCTGTGAAGGCMATCATCCATCAATTTTGAAGAAAGTCTTCATCGAAATTCAGAGCT	690
Oy	201	GLUPROSETHRIILECYVALAGLYGUSERPHEGINVALVALARGGILYASNGILYPHE	220
Db	691	GAACCATCCACCATATGTGCAGAGAGTGTCATTTCAAGTTGTCGTAGAGGAAACGGCTTC	750
Oy	221	ARGHISALARGANVALASPARGVALLEUCYSSERPELHISILEASMAPSERVALTHR	240
Db	751	CGACATGCCCGCAACTGACAGGAGGCTCTCTGCACCTTCMAAGATCAATGACATCGGTACA	810
Oy	241	LEUASNGILULYAPROPHESERVALGLUAPHTRHYRILEULENCYAPROVALPROILEU	260
Db	811	CTCAATGAGAAAGCCCTTTTCTGTGGAGATACTTATTACTGTGTCCAGGCCATCTTA	870
Oy	261	LYSGILVALGILYMETYLVALALALEUGINVALSERMETSAMAPGILYLEUSERPHEILE	280
Db	871	AAAGAAGTTGGCATGTGAACCTGCACCTCCACAGGCACACATGAAGACGATGGCTCTCTTTATC	930
Oy	281	SERSESERVALILELLETHRTHRTHRHISCYSEARAPGILY 294	
Db	931	TCCAGTTCGTGTCATCATCCACACACACCTGTTCTGTAGCGGT 972	

```

RESULT 13
US-10-201-292-17
: Sequence 17, Application US/10201292
: Publication No. US20030144192A1
: GENERAL INFORMATION:
: APPLICANT: James B. ROTHMAN
: APPLICANT: Theresa L. O'KEEFE
: APPLICANT: Engin OZKAYNAK
: APPLICANT: Judith J. HEALEY
: TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
: FILE REFERENCE: 7853-253-999
: CURRENT APPLICATION NUMBER: US/10/201,292
: CURRENT FILING DATE: 2003-02-14
: NUMBER OF SEQ ID NOS: 36
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 17
: LENGTH: 1674
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-201-292-17

```

Alignment Scores:			
Pred. No.:	1,39e-185		
Score:	1532.00		
Percent Similarity:	100.00%		
Best Local Similarity:	100.00%		
Query Match:	99.74%		
DB:	6		
Gaps: 0			
US-09-970-076-2_COPY_27_321 (1-295) x US-10-292-17 (1-1674)			
Oy	1	GLYGLGLGLYARARGGLUAPGLYGLYPROALACYSYRGLYGLYPHEAPLEUTYR	20
Db	91	GGGCAAGGGGGACGCGAGGAGATGGGGTCCAGCTGCTCCGCGGATTTGACCTGTAC	150
Oy	21	PHEILLEUAPLYSERGLYSERVALLEUHSIHSITPAENGILILEYRTRYRYPHEVAL	40
Db	151	TTGATTTTGGACAAACACGAGAGTGTGCTGCACCACTGATGAAACTATTACTTTGTG	210
Oy	41	GLUGLNUALAHISLYSPHEILLESERPROGILNUARQMETSERPHEILLEVALPHESER	60
Db	211	GAACAGTTGGCTCCAAATTCATTCAGGCCACAGTTGAAGAAAGTCTTATATATGGTTCTCC	270

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QY      61 ThrATGGLYThrThreumeclybLeuthrgluAspArggluGlnllearglnglyleu 80
      271 ACCCGAGGAAACAACCTTAATGAACTGACAGAAAGACAGAAACAATCCGTCAAGGCTTA 330
QY      81 gluGluLeuGlnlyValLeuProglyIYAspThrTYrMechisgluGlyPhegluArg 100
      331 GAAAGAACTCCAGAAATCTTCCAGAGAGAGACACTTAATGATGATGATGATGATGAAAG 390
QY     101 AlAspGluGlnlleTYrTYrGluAspArgGlnGlyTYrArgThrAlAspVallle 120
      391 GCCAGTACAGATTATTAATGAAACAGAAAGGATACAGACAGCCAGCCGATCATATT 450
QY     121 AlAlAspThrAspGlygluLeuuhisgluAspLeuPhePheTYrSerGluArggluAlaAsn 140
      451 GCTTTGACATGATGAGAACTCCATGAAAGATCTTTTTCATTCAGAGAGGAGGCTTAAT 510
QY     141 ArgSerArgAspLeuGlyAlaAlaIleValTYrCyValGlyValIYAspPheAsnGluThr 160
      511 AGGTCGAGATCTTGTCATTTGTCATTTGTCATTTGTCATTTGTCATTTGTCATTTGTCAT 570
QY     161 GlnLeuAlaArgIleAlaAspSerIYAspPheIYAspPheProValAspArgIYPheGln 180
      571 CAGCTGCGCCGAGTTCGCGACAGTAAAGATCATGTGTCCTCGTGAATGACGGCTTTCAAG 630
QY     181 AlAlAspGlnGlyIleIleHisSerIleLeuIYAspSerCyAlleGluIleLeuAlaAla 200
      631 GCTTCGAAAGGATCATCTCCATTTTGAAGAAGTCCGTCGATCBAATTCGACAGCT 690
QY     201 GluProSerThrIleCyValaglyIYAspPheGlnValIYValIYArgGlyAsnGlyPhe 220
      691 GAAACCATCCACCATATGTGACAGAGAGTCAATTCAGATGTCGTGAGAGGAAACGGCTTC 750
QY     221 ArgHisAlaArgAsnValAspArgValIYAspSerPheIYAspPheIleAspSerValThr 240
      751 CGACATGCCCGACAGTGCAGAGGTCCTGACGCTTCAAGATCATGATCGTGCAC 810
QY     241 LeuAsnGluYAspProPheSerValIYAspThrTYrIleuLeuCyAspProAlaProIleLeu 260
      811 CTCGAAGAAAGCCCTTTCTGCGAAAGATCTTAATTTCTGTCGACAGGCTTAATCTTA 870
QY     261 IYAspGluValGlyMetIYAspAlaAlaLeuGlnValSerMechAspArgIYLeuSerPheIle 280
      871 AAGAAGTGGCATGAAGCTGCATCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCC 930
QY     281 SerSerSerValIleIleThrThrThrHisCySerAspGly 294
      931 TCCAGTTCGTCAATCATCACACACACACACTGTTCTGACGCT 972
Db
RESULT 14
US-10-038-307-13
; Sequence 13, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: JUDITH J. HEALEY
; APPLICANT: JUDITH J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PASTESEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-13
Alignment Scores:
Pred. No.: 3,52e-184 Length: 1650
Score: 1521.00 Matches: 293
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Percent Similarity: 99.32%
Best Local Similarity: 99.32%
Query Match: 99.02%
DB: 6 Gaps: 0
US-09-970-076-2_COPY_27_321 (1-295) x US-10-038-307-13 (1-1650)
QY      1 glYnglnglyIYArgArggluAspGlyIYProAlaCyAspTYrGlyIYAspPheAspLeuTYr 20
      79 GGGCAAGGGGAGCGCAGGAGGATGGGGGTCCAGCTGCTTACGGGAGATTTGACCTGTAC 138
QY     21 PheIleLeuAspIYSerGlySerValIleuhisIleTPAsnGlnlleTYrTYrPheVal 40
      139 TTCATTTTGGACAAATCAGAAAGTGTGTCGACCACTGGAATGAATCTTAATCTTTGTG 198
QY     41 GluGlnLeuAlaHisIYAspPheIleSerProGlnLeuAspMetSerPheIleValPheSer 60
      199 GAAACGTTGGCTCACAAATTCATGACCCACGTTGAGAAATGCTTTATTTGTTTCTTC 258
QY     61 ThrATGGLYThrThreumeclybLeuthrgluAspArggluGlnllearglnglyleu 80
      259 ACCCGAGGAAACAACCTTAATGAACTGACAGAAAGACAGAAACAATCCGTCAAGGCTTA 318
QY     81 gluGluLeuGlnlyValLeuProglyIYAspThrTYrMechisgluGlyPhegluArg 100
      319 GAAAGAACTCCAGAAAGTTCCTGCGAGAGAGACACTTAATCATGATGATGATGATGAAAG 378
QY     101 AlAspGluGlnlleTYrTYrGluAspArgGlnGlyTYrArgThrAlAspVallle 120
      379 GCCAGTACAGCAATTTATTAATGAAACAGAAAGGATACAGAGACCCGCTCATCAT 438
QY     121 AlAlAspThrAspGlygluLeuuhisgluAspLeuPhePheTYrSerGluArggluAlaAsn 140
      439 GCTTTGACATGAGGAACTCCATGAAATCTTTTTCATTCAGAGAGGAGGCTTAAT 498
QY     141 ArgSerArgAspLeuGlyAlaAlaIleValTYrCyValGlyValIYAspPheAsnGluThr 160
      499 AGGTCGAGATCTTGTCGCAATTTGTCATGTCGTGTCGTCGTCGTCGTCGTCGTCGTCGTC 558
QY     161 GlnLeuAlaArgIleAlaAspSerIYAspPheIYAspPheProValAspArgIYPheGln 180
      559 CAGCTGCGCCGAGTTCGCGACAGTAAAGATCATGTGTTCCCGTGAAATGACGGCTTTCAAG 618
QY     181 AlAlAspGlnGlyIleIleHisSerIleLeuIYAspSerCyAlleGluIleLeuAlaAla 200
      619 GCTTCGAAAGGATCATCTCCATTTTGAAGAAGTCCGTGATCGAAATTCGACAGCT 678
QY     201 GluProSerThrIleCyValaglyIYAspPheGlnValIYValIYArgGlyAsnGlyPhe 220
      679 GAACCATCCACATATGTGACAGAGAGTCAATTCAGATGTCGTGTCGTCGTCGTCGTCGTC 738
QY     221 ArgHisAlaArgAsnValAspArgValIYAspSerPheIYAspPheIleAspSerValThr 240
      739 CGACATGCCCGACAGTGCAGAGGTCCTTCCAGCTTCAAGATCATGATCGTGCAC 798
QY     241 LeuAsnGluYAspProPheSerValIYAspThrTYrIleuLeuCyAspProAlaProIleLeu 260
      799 CTCGAAGAAAGCCCTTTCTGCGAAAGATCTTAATTTCTGTCGACAGGCTTAATCTTA 858
QY     261 IYAspGluValGlyMetIYAspAlaAlaLeuGlnValSerMechAspArgIYLeuSerPheIle 280
      859 AAGAAGTGGCATGAAGCTGCATCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAG 918
QY     281 SerSerSerValIleIleThrThrThrHisCySerAspGlySer 295
      919 TCCAGTTCGTCAATCATCACACACACACTGTTCTCCCAAAATCT 963
Db
RESULT 15
US-10-038-307-15
; Sequence 15, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:41:36 ; Search time 238.049 Seconds
(without alignments)
607.449 Million cell updates/sec

Title: US-09-970-076-2_COPY_27_321

Perfect score: 1536

Sequence: 1 GCGGRDGGPACVGGFDLY.....GLSFSSVITTTTHCSDS 295

Scoring table:

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Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA New -QFMT=fastap -SUFFIX=rnbn -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blonsum62
-TRANS=human40.csl -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076@cgn_1_1_675@runat_14122005_111853_21065
-NCPV=6 -ICPV=3 -NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:*

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2:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5:	/cgn2_6/ptodata/1/pubpna/PCF_NEW_PUB.seq:*
6:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
9:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
10:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1536	100.0	5540	7	US-11-186-284-198
2	145.5	9.5	4740	7	US-11-080-026-3
3	131	8.5	11447	7	US-11-186-284-25
4	122	7.9	2834	6	US-10-750-185-39040
5	113.5	7.4	1325	6	US-10-750-185-56394
6	113.5	7.4	2501	6	US-10-821-234-182
7	113.5	7.4	3449	6	US-10-131-826A-293
8	111	7.2	3564	6	US-10-601-368-20

9	111	7.2	4858	6	US-10-601-368-19	Sequence 19, Appl
10	107.5	7.0	3175	6	US-10-995-561-464	Sequence 464, App
11	107.5	7.0	3464	6	US-10-995-561-465	Sequence 465, App
12	107.5	7.0	3468	6	US-10-995-561-466	Sequence 466, App
13	107.5	7.0	3564	6	US-10-601-368-2	Sequence 2, Appl1
14	107	7.0	3967	7	US-11-000-463-574	Sequence 574, App
15	107	7.0	3969	7	US-11-000-463-102	Sequence 102, App
16	107	7.0	5042	6	US-10-601-368-1	Sequence 1, Appl1
17	105.5	6.9	3868	6	US-10-995-561-404	Sequence 404, App
18	103.5	6.7	2755	6	US-10-750-185-25375	Sequence 25375, A
19	101.5	6.6	47572	6	US-10-995-561-13356	Sequence 13356, A
20	100	6.5	2773	7	US-11-102-240-33	Sequence 33, Appl1
21	96	6.2	3884	6	US-10-601-368-17	Sequence 17, Appl
22	94	6.1	1062	7	US-11-137-465-11	Sequence 11, Appl1
23	94	6.1	1347	7	US-11-137-465-12	Sequence 12, Appl1
24	91.5	6.0	1881	6	US-10-467-657-5431	Sequence 5431, Ap
25	84.5	5.5	2715	6	US-10-507-275-4	Sequence 4, Appl1
26	82	5.3	3189	7	US-11-137-465-10	Sequence 10, Appl1
27	81.5	5.3	1688	6	US-10-510-386-157	Sequence 157, App
28	81	5.3	11115	6	US-10-513-786-6	Sequence 8, Appl1
29	81	5.3	11115	6	US-10-513-786-8	Sequence 4357, Ap
30	79.5	5.2	2317	6	US-10-793-626-4357	Sequence 3398, Ap
31	79.5	5.2	2987	6	US-10-793-626-3398	Sequence 6111, Ap
32	79.5	5.2	3366	6	US-10-467-657-6111	Sequence 42451, A
33	78.5	5.1	1895	6	US-10-750-185-42451	Sequence 3293, Ap
34	78	5.1	1329	6	US-10-467-657-3293	Sequence 3293, Ap
35	78	5.1	1443	6	US-10-467-657-3291	Sequence 1039, Ap
36	77.5	5.0	960	6	US-10-793-626-1039	Sequence 178, App
37	77.5	5.0	1311	6	US-10-763-712A-118	Sequence 91, Appl
38	77.5	5.0	20600	6	US-10-829-826B-91	Sequence 89, Appl
39	77.5	5.0	28586	6	US-10-829-826B-89	Sequence 90, Appl1
40	77.5	5.0	28586	6	US-10-829-826B-90	Sequence 7037, Ap
41	76.5	5.0	1548	6	US-10-467-657-7037	Sequence 4369, Ap
42	76	4.9	1407	6	US-10-523-912-1	Sequence 1, Appl1
43	75.5	4.9	8157	6	US-10-793-626-3648	Sequence 3648, Ap
44	75	4.9	3435	6	US-10-793-626-3648	Sequence 102, App
45	74.5	4.9	2361	6	US-10-467-962B-102	

ALIGNMENTS

RESULT 1
US-11-186-284-198
: Sequence 198, Application US/11186284
: Publication No. US20050266493A1
: GENERAL INFORMATION:
: APPLICANT: Millennium Pharmaceuticals, Inc.
: APPLICANT: Berger, Allison
: APPLICANT: Guillemette, Tracy L.
: APPLICANT: Kamackar, Shubhangi
: APPLICANT: Schlegel, Robert
: APPLICANT: Monahan, John E.
: APPLICANT: Thibodeau, Stephen N.
: APPLICANT: Burgart, Lawrence J.
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
: TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
: THERAPY OF COLON CANCER
: FILE REFERENCE: MP01-029P2RNM
: CURRENT APPLICATION NUMBER: US/11/186,284
: CURRENT FILING DATE: 2005-07-21
: PRIOR APPLICATION NUMBER: US/10/301,822
: PRIOR FILING DATE: 2002-11-21
: PRIOR APPLICATION NUMBER: US 60/339,971
: PRIOR FILING DATE: 2001-12-10
: PRIOR APPLICATION NUMBER: US 60/361,978
: PRIOR FILING DATE: 2002-03-05
: PRIOR APPLICATION NUMBER: US 60/381,988
: PRIOR FILING DATE: 2002-05-20
: NUMBER OF SEQ ID NOS: 228
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 198
: LENGTH: 5540
: TYPE: DNA

;	ORGANISM:	Homo Sapiens	
;	FEATURE:		
;	NAME/KEY:	CDS	
;	LOCATION:	(144) ... (1838)	
US-11-186-284-198			
Alignment Scores:			
Pred. No.:	3,42e-180	Length: 5540	
Score:	1536.00	Matches: 295	
Percent Similarity:	100.00%	Conservative: 0	
Best Local Similarity:	100.00%	Mismatches: 0	
Query Match:	100.00%	Indels: 0	
DB:	7	Gaps: 0	
US-09-970-076-2_COPY 27_321 (1-295) x US-11-186-284-198 (1-5540)			
QY	1	G1yGInG1yG1yAaGxAG1uAaPbQ1yG1yPfoA1aCyE7yG1yG1yPheAaPLeuTyR	20
DB	222	GGCGAAGGGAGCCAGAGAGATGGGGGCTCAGCTGCTCAGCGGATTTGACTGAC	281
QY	21	Phe11e1eUaAPLySeSeG1ySeVa11eUhiSh1aTPAaNG1u11eTyTyPheVa1	40
DB	282	TTCAATTTTGACAATTCAGAAATGTGTGTGCACCACTGAAATGAATCTATTACTTGTG	341
QY	41	GlUgInLeUa1aH1e1yPhe11eSeRProG1nLeUa1yMeSeSePhe11eVa1PheSeR	60
DB	342	GAACGTGGGTCCAAATTCATCAGCCCAAGTGAAGATGCTTTATGTTTCTCC	401
QY	61	ThRAaRG1yThrThrLeUeMeTySeThRG1uAaPaRG1uG1n11eARG1nG1yLeu	80
DB	402	ACCGAGGAACAACCTTAATGAACTGACAGAAACAGAAACAAATCCGTCAAGGCTTA	461
QY	81	GlUgInLeUg1nLyVa11eUProG1yG1yAaPThTyRMeCh1aG1uG1yPheG1uAaG	100
DB	462	GAAGAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATGACATGAAGATTGAAAG	521
QY	101	AlaSeRG1uG1n11eTyTyTyRG1uAaPaRG1nG1yTAaGThRa1aSeVa11e11e	120
DB	522	GCCAGTGAAGCATTTATTAAGAAAACAGAAAGGTACAGAGACAGCCAGCGTCATCAT	581
QY	121	AlaLeUThRaARGLyG1nLeUhiAG1uAaPLeUPheTySeSeG1uAaRG1uA1aAa	140
DB	582	GCTTTGATGATGAGAACTCCATGAAATCTCTTTTCTTTCAGAAAGGAGCTTAAT	641
QY	141	ARSeRaTaRPaRLeUg1yA1a11eVa1TyRcYVa1G1yVa1LyAaSPheAaNG1uThR	160
DB	642	AGGTGTGAGATCTTGTCGCAATGTTTAACTGTGTGTGTGAAGATTTCAAGAGACA	701
QY	161	G1nLeUa1aAaRG11e1a1aPSeSeTyAaPeh1eVa1PheProVa1AaPaRG1yPheG1n	180
DB	702	CAGCTGGCCCGGATTTGCCGACAGTAAGATCATGTGTCCCGTAATGAAGCGGCTTCAG	761
QY	181	AlaLeUg1nG1y11e11eH1eSeR11e1eUyLySeSeCyB11eG1n11eUa1a1a	200
DB	762	GCTGTGCAAGGATATCATCACTCAATTTTGAAGAGCTCTGATCGAAATTCAGACACT	821
QY	201	GlUPRoSeThr11eCyAaG1yG1uSeRPheG1nVa1Va1aJaRG1yAaNG1yPhe	220
DB	822	GAACATTCACCACTATGTGCAAGAGATCATTTCAAGTGTGTGTGAAGAAACGGCTTC	881
QY	221	ARgh1Sa1aARGaAaVa1AaPaRG1yA1eUCySeSePheLyB11eAaPaRSeVa1ThR	240
DB	882	COACATGCCCGCAAGTGGACAGAGGTCTCTGCACTTCAAGATCAATGATCGGTGACA	941
QY	241	LeUaNG1uLyPProPheSeSeVa1G1uAaPThTyTyLeUeUCySPfoA1aPro11eUe	260
DB	942	CTCAATGAGAAAGCCCTTTTGTGTGAAATATTTTATTAATGTGTGCCAGCCCTATCTTA	1001
QY	261	LySG1uVa1G1yMeTyAa1a1a1eUg1nVa1SeRMeCaAaPaRG1yLeuSeRPhe11e	280
DB	1002	AAAGAAAGTTGGCATAAAGCTGCATCCAGGTCACAGTAAGAAAGATGGCTCTCTTTTATC	1061
QY	281	SeRSeSeVa11e11eThrThrThRh1aCySeSeAaPaRG1ySeR	295

[illegible]

```

Oy 175 ValAlaNaBPgLyPhgGlaLaLeuGlnGlyIleIleHisSerIleLeuLybSerGys 194
Db 1015 GTGAATTAAC---TTTGAGCGCTTGAAGACATTACGAACCGCTTCGGAGAG--- 1065
Oy 195 IleguIleLeuAlaAlaGluProSerThrIleCySaIaGlyGluSerPhgGluValVal 214
Db 1066 -----ATCTTTGCCATCGAGGCTACTCAGACAGAGATGACAGCTCCCTTTGACATGAG 1119
Oy 215 ValArgGlyAsnGlyPheArgHisAla 223
Db 1120 ATGCTTCAGAAAGCTTCACGCCCTCC 1146

```

```

RESULT 3
US-11-186-284-25
; Sequence 25, Application US/11186284
; Publication No. US2005026493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPW01-02952RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/501,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11447
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(9192)
; US-11-186-284-25

```

Pred. No.:	0.000304	Length:	11447
Score:	131.00	Matches:	59
Percent Similarity:	46.99%	Conservative:	38
Best Local Similarity:	23.80%	Mismatches:	75
Query Match:	8.53%	Indels:	26
DB:	7	Gaps:	13

Oy	18	AspLeuTyrPheIleLeuAspLysSerGlySerVal---LeuMLeHTTPAspCduIule	36
Db	1318	GATATGCTGTTTTGGTGTGATGGCTCTATAGCATGGATGGATGCAAACTTGTAAAGTT	1377
Oy	37	TyrTyrPheValGluGlnLeuMLeHTLysPhe---IleSerPro---GlnLeuArgMet	54
Db	1378	AGAGCGCTTTTGGAGAGTCTTGTA AAAAGTTTGAAATTTACCAAAATAGGCTCAGAGT	1437
Oy	55	SerPheIleValPheSerThr-----ArgGlyThrThrLeuMetLysLeuThrGlu	71
Db	1438	AGCTCTTGCAATACAGCCGGAGATCCTATACCTAGCTCACCTTGGAAAAAATTCACCCAA	1497

```

Oy 72 AsprhrgluglnlIeargInglYleuGlnGluLeuGlnLysValIePro-----Gly 89
Db 1498 GTTGAAGATTAATATT-----GAAACAATAAACCTTCCTTACAGAGGA 1542
Oy 90 GLyAspThrTYrMeChIsglGlyPheGluAArgAlaSerGlnGlnIleTYrTYrGluAsn 109
Db 1543 GGATCTCAAAATTAAGTGGCAAAAGCAATGACTTATGTACAGAGAAATATTGTGCGCTAGC 1602A
Oy 110 ArgInglYTYrArgThr-----AlaSerValIleIleAlaLeuThrAspGlyGluLeu 127
Db 1603 AAG---GGATCAAAAGACAAATGTGCCAAAGGTCAATGATTCATTACACAGGATGGGAAA--- 1656
Oy 128 HisGluAspLeuPhePheTYrSerGluArgGlnAlaAsnArgSerArgAspLeuGlyAla 147
Db 1657 TCATCAAGATGCTTTC-----AGAGATCTCGATTAATAACTGAGAGAAATTCAGATGT 1707
Oy 148 IleValTYrCysValGlyValYAspPheAsnGluThrGlnLeuAlaArgIleAlaAsp 167
Db 1708 GAATTCCTTTCAGTTGGTGGTGAAGATGCGCTGGTCAGAAATTGAAAGCTATTGGCTCT 1767
Oy 168 -----SerLYAspArgHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGlyIle 185
Db 1768 CCTGCTCGAGAGACCACTGTGTTTACAGTGGAAAT---TTTGATGCTTTTTCAGAGGATA 1824A
Oy 186 IleHisSerIleLeuLYsLYsSerCysIleGluIle-----LeuAlaAla 200
Db 1825 TCTTTTGAACTCACACAGCTCTATTGCTTGGATTGAAATTGACAGAAATGGCGAGCT 1878

```

```

RESULT 4
US-10-750-185-39040/c
; Sequence 39040, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FATTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39040
; LENGTH: 2834
; TYPE: DNA
; ORGANISM: Bovine 198668680867914
US-10-750-185-39040

```

Alignment Scores:	
Pred. No.:	0.006475
Score:	123.00
Percent Similarity:	50.00%
Best Local Similarity:	29.03%
Query Match:	7.94%
DB:	6
Length:	2834
Matches:	54
Conservative:	39
Mismatches:	71
Indels:	24
Gaps:	10

[illegible]

```

Db      2004 GTCGACATTGAGTCCGTCAGTACTCGATGAAGTACGATCCAGTTTACCCCTCAGCCAG 1945
      73 ggtuglnlleahrglnlgluendlu-----gluleuglnlyvalleuprog 89
      1944 CACTCCAGTGTGGAGGCTTGGAGTACCGCTTGACAGCATCCACAG-----AAGG 1891
      89 ygliaerthrtymechi6glugl1phegluAalaserglnl1etyrtYrgluba 109
      1890 AGGGGGCACCMAATGGGTAGAGCCCTG---GGCAGATGATCCAGGTCTTTGCAACACT 1834
      109 narglnglYtYrYrglThralaserVallellealeuThraPrGlygluendi6gl 129
      1833 TGCTCCACAGCA--CGTGCCCTT--GGTATCTATTGTTGTACATGACGGCCAACTATAG 1776
      129 uAerleupherPhetysergluAarglualaenAargserAArgAerleuglYalale 149
      1775 CCGCGTG-----GCTGATGCTCGAAGCGCTGAGGGCCATGAGTCAACCT 1728
      149 lYrCyValglYVallyAerPhaenGluThrGlnleuAlaarglleAlaAerSerly 169
      1727 TTATGCAAGTTGAGTCAAGATCTAATATGCTGACCTTCAGAGATTCCTAA----- 1673
      169 aaerPhaValAerPhaerValaenAerGlyPheGlnAlaLeuglnlyllelehiAser 189
      1672 -GACAGAAATGTTTTCGTGCATGAT---TTTGAATCCTTGAAAGCATCCACAAGAA 1617
      189 eLeuLylyserCy 194
      1616 GGTACAAAGCATCTGT 1601

```

RESULT 5

```

US-10-750-185-56394
/ Sequence 56394, Application US/10750185
/ Publication No. US20050260603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFIELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ PRIOR FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 56394
/ LENGTH: 1325
/ TYPE: DNA
/ ORGANISM: Bovine 19866880505724
US-10-750-185-56394

```

Alignment Scores:

```

Pred. No.: 0.00171 Length: 1325
Score: 113.50 Matches: 58
Percent Similarity: 42.63% Conservative: 49
Best Local Similarity: 23.11% Mismatches: 93
Query Match: 7.39% Indels: 51
DB: 6 Gaps: 15

```

US-09-970-076-2_COPY_27_321 (1-295) x US-10-750-185-56394 (1-1325)

```

Qy      10 G1ProhlaCyserYrgly---GlyPhaAerleuThrPheilleuAerLyserGlySer 28
      456 GGGAGCCCTGTGGAACAAGCGAGCAGCTGTCTTTATCATGACACTACGACG 515
      29 Val---LeuHshlSTPAmGlnuileTyrtYrPhe---ValGlnleuAlaHleLy 46

```

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Db      516 GTCACACCCSAGSACTAGSAAAGSTCAAGAGTTTATGTTGACATCTCTGACATTCTTG 575
      47 PheIserProGlnleu---ArgMetSerPheilleValPheSerThraGlyThrt 65
      576 GACATTGGCCCTGACSTCAACCCGTGGGTGCTGCTCAATAT-----GGCAGCAG 626
      66 Leu-----MetLyLeuThrtYuaerAArgGlnlleAarglnlyLeu 80
      627 GTCAGAAACAGATTCTCTCTCAAGACCTTCAGAGAAAGTCCAGGTGAGCGTGCCTG 686
      81 GlnGlnleuGlnlyValleuProglYglYuarThrtYmetHie6glu6lYpHeGluA 100
      687 AAGAGATGCGCATCTGTCACAGGACCATGACGAGGCGCCGCGCCCTGAGGAGATGG 740
      101 AlaSerGlnl11etyrtYrglubaAarglnlytYrArg-----Thr 115
      741 ---GCCCTAACAATGCGCTTCTCGAAGAGAGGGGCGCCGCGCCCTGAGGAGATGG 797
      116 AlaSerVallelleAleuThraerGlyluLeuHieGluAerleupherPhetySer 135
      798 CCTCGGTCATATGATCGTGAATGAGAGGCGCCSAGAGTCCGCTG----- 845
      136 GlnAArgGlnAlaAenAerSerAArgAerleuGlnAlaAlleValtYrCyValglYVal 154
      846 GCCGAGTGGCGCAAAAGCCGGACACAGAGCATCTATCTTGGCATCGGTGGGC 905
      155 ---LyAerPhaenGluThrGlnleuAlaArglleAlaAerSerLyAerPhaValPhe 173
      906 CAGTGGATTTCAACAGCTGAAGCCATTTGGAGGAGCCSCACAGACACACGCTTTC 965
      174 ProValAenAerGlyPheGlnAlaLeuglnlyllelehiAserlleuLylyser 193
      966 CTGTGGCCAAAC---TTCAAGCAGATTGAGAGCTGACCTGATGTTCCAGAAAGATTG 1022
      194 Cyg-----lleGlnleuAlaAla-----Gln 201
      1023 TGCAATGAGTCTGCTCTGTGCTCTTCTCGGGCATTCGTTGGAATGAGTCAATTCA 1082
      202 ProSerThrtle-----CyAlaGlyGlyserPheGln 212
      1083 CCTTCCCGGATTATCTGTGCTACCTGCTGCCAATACCTGCTGCAAGGGTCTTTA 1142
      213 ValValAlaArgGlyAenGlyPheAerGlnleu 223
      1143 GCAAAGTCCAG-----ATAAGACACAGT 1166

```

RESULT 6

```

US-10-821-234-182/C
/ Sequence 182, Application US/10821234
/ Publication No. US2005025114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andartman, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ PRIOR FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pc_seq_genes Version 1.0
/ SEQ ID NO 182
/ LENGTH: 2501
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-821-234-182

```

Alignment Scores:

```

Pred. No.: 0.00452 Length: 2501
Score: 113.50 Matches: 66
Percent Similarity: 38.28% Conservative: 63

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Best Local Similarity: 19.58%      Mismatches: 109
Query Match: 7.39%      Indels: 99
DB: 6      Gaps: 17

US-09-970-076-2_COPY_27_321 (1-295) x US-10-821-234-182 (1-2501)

QY      2  GlnGlyGlyArgArgGlySerGly---GlyProAla----- 12
DB      1631 GAAGAGATCGATGCTGAGATGGGACGGGCAACAACAGAAAGCGAATGCTC 1572
QY      13  -----CyGlyGlyGlyPheAspLeuThrPheIleLeuAspGlySerGlySerVal--- 29
DB      1571 CTGAGACCTTCAGGCTCATCAATCACTACCTGCTAGATGATGATGACAGCATTTGGG 1512
QY      30  -----LeuHisIleTpaAngIuIleTyrTyrPheValGluGluIleuAlaHis 45
DB      1511 GCCAGCACTTCACAGAGCAAAAGTGTCTTACTCAATTAATTGAAAGGTGCAAGT 1452
QY      46  LysPheIleSerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThr 65
DB      1451 TATGCTGTGAAGCCA-----AGATATGCTCTAGTACATATGCAATACCCCAAAATT 1398
QY      66  LeuMetIleLeuThrGlu-----AspArgGluGlnIleArgGlnGlyLeuGlu 81
DB      1397 TGGGTCAAGTGTCTGAAGCAGACAGCATGATCAAGATGCGGCACGAAAGCTCAAT 1338
QY      82  GluLeu-----GlnIleValLeuProGlyGlyAspThrTyrMetHisGluGly 97
DB      1337 GAATATCAATTATGAAAGCACCAAGTTGAACTGAGGACTAACACC----- 1293
QY      98  PheGluIleAspGlnGluGlnIleTyrTyrGluAsnArg----- 110
DB      1292 ----AAGAAGGCCCCCGACGAGCTACAGCATGATGAGCTGGCCAGATGAGCTCCCTCT 1236
QY      111  GlnGlyTyr---ArgThrAlaSerValIleIleIleAspLeuThrAspGly----- 125
DB      1235 GAAGGCTGAACCGCACCCGCGATGATCATCTCTCATGACTGATGATGATGACAAACATG 1176
QY      126  -----GluLeuHisGluLeuAspLeuPhePheTyrSerGlu 136
DB      1175 GCGCGGAGCCCAATTACTGTCAATGATGATGATGATGCGGACCTTGATCATTTGCGAAGAT 1116
QY      137  ArgGluIleAsnArgSerArgAspLeuGlyValAlaIleValTyrCySerValGly-----Val 154
DB      1115 CGCAAAAACCCAGAGAGATATCTGTGATGTCTATGTGTTGGGCTCGGCGCTTTGGTG 1056
QY      155  LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerIleAspHisValPhePro 174
DB      1055 AACCAAGTGAACATCAATGCTTTGGCTTCCAAAGAAAGACATGCAATGTGTTCCAA 996
QY      175  ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIleValSerCyS 194
DB      995 GTCAAGAT---ATGAAAAACCTGGAGATGTTTTCACAAAGATCGATGAAGC--- 942
QY      195  IleGluIleLeuAlaIleGluProSerThrIleCyAlaIleGlyIleuSerPheGlnVal 214
DB      941 -----CACTCTCTAGTCTCTGT----- 924
QY      215  ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCySerPheIle 234
DB      923 -----GCGATGCTTGGAAACACAGAGAGGTATCCAT----- 891
QY      235  IleAsnAspSerValThrLeuAsnGluIleProPheSerValGluAspThrTyrLeuLeu 254
DB      890 -----TACCAACAGCAACCAAGCAGGCGACATCTCAAGTC----- 855
QY      255  CysProAlaProIleLeuIleValGlyMetIleValAlaLeuGlnValSerMetAsn 274
DB      854 -----ATTGCGCCCTTCAAAGGACACAGAGCTGTATGGG----- 819
QY      275  AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCyS 291
DB      818 -----GCTGCTGTCTGAGTACTTGTCTGCTGACAGACGACATTTGT 777

```

```

RESULT 7
US-10-131-826A-293
? Sequence 293, Application US/10131826A
? Publication No. US20050245730A1
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Beresini, Maureen
? APPLICANT: DeForge, Laura
? APPLICANT: Denoyere, Luc
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Gerlitsen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Gurney, Austin L.
? APPLICANT: Sherwood, Steven
? APPLICANT: Smith, Victoria
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Watanabe, Colin K
? APPLICANT: Wood, William
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE REFERENCE: P330R1C128
? CURRENT APPLICATION NUMBER: US/10/131,826A
? CURRENT FILING DATE: 2002-04-24
? PRIOR APPLICATION NUMBER: 60/049911
? PRIOR FILING DATE: 1997-06-18
? PRIOR APPLICATION NUMBER: 60/056974
? PRIOR FILING DATE: 1997-08-26
? PRIOR APPLICATION NUMBER: 60/059113
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059115
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059117
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059122
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059184
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059263
? PRIOR FILING DATE: 1997-09-18
? PRIOR APPLICATION NUMBER: 60/059352
? PRIOR FILING DATE: 1997-09-19
? PRIOR APPLICATION NUMBER: 60/059588
? PRIOR FILING DATE: 1997-09-19
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 550
? SEQ ID NO 293
? LENGTH: 3449
? TYPE: DNA
? ORGANISM: Homo Sapien
? US-10-131-826A-293

Alignment Scores:
Pred. No.: 0.0074      Length: 3449
Score: 113.50      Matches: 55
Percent Similarity: 43.90%      Conservative: 53
Best Local Similarity: 22.36%      Mismatches: 103
Query Match: 7.39%      Indels: 35
DB: 6      Gaps: 13

US-09-970-076-2_COPY_27_321 (1-295) x US-10-131-826A-293 (1-3449)

QY      18  AspLeuTyrPheIleLeuAspGlySerVal---LeuHisIleTpaAngIuIle 36
DB      372  GACCTGCTTTCATCTACATTCAGCTCTCGAGTGTCAACCCCATGACTATGCAAGCTC 431
QY      37  TyrTyrPhe---ValGluGlnLeuAlaHisIleAspPheIleSerProGlnLeu---ArgMet 54
DB      432  AAGAGTTCACTGTCGACATCTTGCATTTCTTGACATTTGCTCTGATGTACCCGAGTG 491

```

```
QY 55 SerPhe11eValPheSerThraGlyThrThrLeu-----MetLysLeu 69
   ::::
Db 492 GGCCTGCTCCAAAT-----GGCAGCATGCTCAAGAAATGATTCCTCCCAAGACC 542
QY 70 ThrGluAspArgGluGlnIleArgGlnGlyLeuGluGlnLeuGlnIleValLeuProGly 89
   ::::
Db 543 TTCANAGAGAGATCCAGCGAGTGAGCGTGTCTCAAGAGATGGAGCATGTGTCCACGGGG 602
QY 90 GlyAspThrTyrMetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsn 109
   ::::
Db 603 ACCATGACTGGGCTGGCCATCCAGTAT-----GCCCTGAACATGGCATTCCTAGAA 653
QY 110 ArgGlnGlyTyrArg-----ThrAlaSerValIleIleAlaLeuThrAsp 124
   ::::
Db 654 GCAGAGAGGGGGCCGGCCCTGAGAGAGAAATGTGCCACGGGTCTAATGATCGTGAAGAT 713
QY 125 GlyGluLeuHisGluAspLeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAsp 144
   ::::
Db 714 GGGAGACTCAGGACTCCGTG-----GCCAGGTGGCTGTCAAGCGACGGGAC 761
QY 145 LeuGlyAlaIleValIleValIleValIleValIleValIleValIleValIleValIleVal 162
   ::::
Db 762 ACGGCGATCTTAATCTTTGGCATTTGGTGGCCAGGTAGACTTCAACACTTGAAGTCC 821
QY 163 AlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnIleAlaLeu 182
   ::::
Db 822 ATTTGGAGATGAGCCCATGAGACATGCTTCTTGTGGCCAAAT---TTCAAGCCAGATT 878
QY 183 GlnGlyIleIleHisSerIleLeuLysSerCysIleGluIleLeuAlaIleGluPro 202
   ::::
Db 879 GAGACCTGCTGCTCCGTGTTCCAGAAAGTTGTGACAGCGCCACATGTGCACACCCCTG 938
QY 203 SerThrIleCysValIleGlySerPheGlnIleValIleValIleValIleValIleValIleVal 222
   ::::
Db 939 GAGCATTAACGTGCTC-----CACTTCTGCATCAACATCCTGCTCATACGTCTGCAGG 992
QY 223 AlaArg-----AsnValAspArgValLeuCysSerPheLysIleAsnAsp 237
   ::::
Db 993 TCGAACAAGAGCTACATTCCTCAACTCGGATCAGACAGACTTGC-----AGAATCCAGGAT 1046
QY 238 SerValThrLeuAsnGlu 243
   ::::
Db 1047 CTGTGTGCCATGGAGGAC 1064

RESULT 8
US-10-601-368-20
; Sequence 20, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 3564
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3564)
US-10-601-368-20

Alignment Scores:
Pred. No.: 0.016 Length: 3564
```

```
Score: 111.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 7.23% Indels: 38
DB: 6 Gaps: 9

US-09-970-076-2_COPY_27_321 (1-295) x US-10-601-368-20 (1-3564)

QY 13 CysTyrGlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHis 32
   ::::
Db 475 TCCGAGACTTAATGACATGCTCATGTCTTAATGGTCCAAAGCATC---TACCCC 531
QY 33 TyrAsnGluIleTyrTyrPheValGluGlnLeuAlaHisLysPhe---IleSerPro--- 50
   ::::
Db 532 TGGGTGAGGTCCCAACTTCTCCATCATATCTCCAAAAGTTCTACATTCGGCCCCGGCC 591
QY 51 GlnLeuArgMetSerPheIleValPheSerThraGlyThrThrLeuMetLysLeuThr 70
   ::::
Db 592 CAGATCCAGGTGGAATAGTCCAGTATGAGAAAGATGCCGTCCATGAGTTCCACTT--- 648
QY 71 GluAspArgGluGlnIleArgGlnGlyLeuGlnIleValIleValIleValIleValIleVal 90
   ::::
Db 649 AATGACTACAGGTCTGTAAAGATGTGTGAAAGCCGCCACATTTAGCAGAGAGA 708
QY 91 AspThrTyrMetHisGluGlyPheGlu-----ArgAlaSerGluGlnIleTyr 107
   ::::
Db 709 GGGAGAGAGACCCGACAGGCAATTTGGCATTTGCAAGTTCGAGGCTTTCAGAAAG 768
QY 108 GluAsnArgGlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeu 127
   ::::
Db 769 GGTGAGAGAAAGGGGCCAAG-----AAAGTATGATTTGTCTACGAGCGGGAATCC 822
QY 128 HisGluAsp----- 130
   ::::
Db 823 CACGACAGCCCAAGACTGAGAAAGTATCCGGCAGAGAGAGAGACAAGTACAGAG 882
QY 131 -----LeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeu 145
   ::::
Db 883 TAGCGTGTGCGCGTTTGGGCTACTACAAACCCAGGGGAGTCAATCCAGAGACTTTTCTCA 942
QY 146 GlyAlaIleValIleTyrCysValIleValIleValIleValIleValIleValIleValIleVal 161
   ::::
Db 943 AATGAATCAAAATACATCCGACGACCTTGCAGACACTTCTTCAACGTCAAGAT 1002
QY 162 LeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnIleAla 181
   ::::
Db 1003 GAGCGCGCGCTG-----AAGGACATTTGATGACCTTGGGACAGAGATCTTCAGC 1053
QY 182 LeuGlnGly 184
   ::::
Db 1054 TTGGAAGGC 1062

RESULT 9
US-10-601-368-19
; Sequence 19, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 4858
; TYPE: DNA
; ORGANISM: Mus musculus
```

```
FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)...(3591)
US-10-601-368-19

Alignment Scores:
Pred. No.: 0.0257 Length: 4858
Score: 111.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 7.23% Indels: 38
DB: Gaps: 9

US-09-970-076-2_COPY_27_321 (1-295) x US-10-601-368-19 (1-4858)

QY 13 CyetylglutylpheleapleuTyrrheleleuaplysSerGlySerValleuHleuHis 32
DB 502 TGCCAGACTTACATGACATGTCATGCTTAGATGCTCCACAGCAGCATC---TACCCC 558
QY 33 TrpAenGluIleTyrrheleValGluIleuAhaHleuPhe---IleSerPro--- 50
DB 559 TGGGTGAGGTCACACACTTCTCATCATATCTCCAAAGTCTTACATTGGCCCGCC 618
QY 51 GluLeuArgMetSerPheIleValPheSerThrArgGlyThrThrleuMetLysLeuThr 70
DB 619 CAGATCCAGGTCGGAATAGTCAGTATGAGAGAGATGCCCTCATGATTCACCTT--- 675
QY 71 GluAparGluGlnIleArgGlnGlyLeuGluLeuGlnLysValleuProGlyGly 90
DB 676 AATGACTACAGGTCTGTAAAGATGTGTGAGACCCGACCCACCATTTGAGCAGAGAGA 735
QY 91 AspThrTyrrMetHisGluGlyPheGlu-----ArgAlaSerGluGlnIleTyrr 107
DB 736 GGCACAGAGACCCCGACGCGCATTTGGCATTAATTGCAACCTGAGAGCTTTCCAGAG 795
QY 108 GluAparGluGlnGlyTyrrArgThrAlaSerValIleIleAlaLeuThrAparGlyGlu 127
DB 796 GGTGAGAAAGAGGGCGCAG-----AAAGTATGATTTGATCATCAGAGCGGGAATCC 849
QY 128 HisGluApar----- 130
DB 850 CACGACAGCCCGACACTCGAGAGAGTATCCGCGACGAGAGAGAGAGAGAGAGAGAGAG 909
QY 131 -----LeuphePheTyrrSerGluArgGluAlaAparSerArgAparLeu 145
DB 910 TAGCTGTGCGCTTTGGGCTACTACACCGAGGGGATCAATCCAGAGACTTTTCTA 969
QY 146 GlyAlaIleValTyrrCyValGlyValIleApar-----PheAenGluThrGln 161
DB 970 AATGAATCAATATCATTCGCGACGAGCCCTGACAGACAGACACTTCTTCAACGTCAAGAT 1029
QY 162 LeuAlaArgIleAlaAparSerLysAparHisValPheProValAparGlyPheGlnAla 181
DB 1030 GAGCGCGCCCTG-----AAGACATTTGTTGATCCCTTGGGAGACAGATCTTGACG 1080
QY 182 LeuGlnGly 184
DB 1081 TTGGAAGGC 1089

RESULT 10
; Sequence 464, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: C0001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FASTSEQ for Windows Version 4.0
```

```
; SEQ ID NO 464
; LENGTH: 3175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-464

Alignment Scores:
Pred. No.: 0.0366 Length: 3175
Score: 107.50 Matches: 50
Percent Similarity: 40.28% Conservative: 37
Best Local Similarity: 23.15% Mismatches: 84
Query Match: 7.00% Indels: 45
DB: Gaps: 9

US-09-970-076-2_COPY_27_321 (1-295) x US-10-995-561-464 (1-3175)

QY 19 LeuTyrrheIleleuAparLysSerGlySerVal----- 29
DB 243 GTGTAATTGCTGTCGACACCTCGAGAGAGGTGACATGAGTCCCGACGACATCTCG 302
QY 30 LeuHisIleThrPheGlnGly---IleTyrrPheValGluIleuAhaHleuLysPheIle 48
DB 303 CTCTCCACATGAGAGCAGTTCGTCGCGAGTATCATGCCAGCTGAGAGAGAGTTTAC 362
QY 49 SerProGluLeuArgMetSerPhe-----IleValPheSerThrArgGlyThr 64
DB 363 CTGACACAGGTGGCGCTGACCTGCGCTATGCGCGCTGACCTTCTTGACACAGGTGAG 422
QY 65 ThrleuMetLysLeuThrGluAparArgGluGlnIleArgGlnGlyLeuGluLeuGln 84
DB 423 GTGTTACGCCACCGGCGAGCAGACCGGGCTCTTCATCAAGAACTGACAGGCGATCAGC 482
QY 85 LysValleuProGlyGlyAparThrTyrrMetHisGluGlyPheGluAlaSerGluGln 104
DB 483 TCCTTCGCGCGGCGC-----ACCTTACCGAGCTGCGCTGCGCAATGACAGAGCAG 536
QY 105 IleTyrrGluAparArgGlnGlyTyrrArgThrAlaSerValIleIleAlaLeuThrApar 124
DB 537 ATCCGAGAGACCGCGACAGAGGCG-----ACGTCACATTCGCGCTGATCATCAGCAG 590
QY 125 GlyLeuLeuHisGluAparLeuPheTyrrSerGluArgGluAlaAparSerArgApar 144
DB 591 GGCACAGTCAACCGGACGCGCTGCGGGGATCATGAGCTGAGCGGCGCGCGAG 650
QY 145 LeuGlyAlaIleValTyrrCyVal-----GlyValLys 155
DB 651 GAGGCGATCCGCGCTTCGCGCGGCGCCCAACAGAGAGCTGAAGAGAGAGAGAGAGAG 710
QY 156 AspPheAenGluThr-----GlnLeuAlaArgIleAlaAparSerLysAparHisValPhe 173
DB 711 GACATGCCAGACAGCGCGCGACAGCTTACCGC-----AACGACTACGCCACC 758
QY 174 ProValAparAparGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu----- 190
DB 759 ATGCTGCCGATCTCCACCGAGATCACCAGACACCATCAACGCGATCATCAAGTCTATG 818
QY 191 -----LysLysSerGlyIleGluIle 197
DB 819 AACACAGAGACTACGAGAGAGTCTACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 866

RESULT 11
; Sequence 465, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: C0001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
```

```
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 465
/ LENGTH: 3464
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-465
```

Alignment Scores:

Pred. No.:	0.0418	Length:	3464
Score:	107.50	Matches:	50
Percent Similarity:	40.28%	Conservative:	37
Best Local Similarity:	23.15%	Mismatches:	84
Query Match:	7.00%	Indels:	45
DB:	6	Gaps:	9

US-09-970-076-2_COPY_27_321 (1-295) x US-10-995-561-465 (1-3464)

```
QY 19 LeuTYRPhel1LeuLysSerGlySerVal-----29
DB 243 GTGTACTTGTGCTGGACACTCGAGAGCGTCAACCATGCAATGCCCAAGCATCTTG 302
QY 30 LeuNH1stPAsnGlu---1LeTYRPhValGluGluLeuLah1stLysPhe1Le 48
DB 303 CTCTTCCACATGAAGCATTCGTGCGGCACTTCAAGCCAGCTGAGAAAGATTCTAC 362
QY 49 SerProGluLeuArgMetSerPhe-----1LeValPheSerThrArgGlyThr 64
DB 363 CTGGACCAAGTGGCGCTGAGCTGGCGCTAAGCGGCGCTGACTTCTTCAACAGGTGAG 422
QY 65 ThrLeuMetLysLeuThrGluAparArgGluGln1LeArgGlnGlyLeuGluLeuGln 84
DB 423 GTGTTCAGCCCAACCGGCGAGCAACCGGCGCTCTTCATCAAGAACTGCAAGGCGCATCAG 482
QY 85 LysValLeuProGlyLysPheThrTyMetH1sGluGlyPheGluArgL1AserGluGln 104
DB 483 TCTTTCGCGCGGCGC-----ACCTTCAACCACTGCGCGCTGCCCAATGACGAGAGCAG 536
QY 105 1LeTYRPh1LeuLysnArgGlnGlyTyArgThrAlaSerVal1Le1Lea1LeuThrAsp 124
DB 537 ATCCGCGAGAGACCGGCAAGAGGC-----ACGTCACACTGCCCGGTGCATCACCGCAG 590
QY 125 GlyGluLeuNH1sGluAparLeuPhePheTySerGluArgGluLah1stLysSerArgAsp 144
DB 591 GGCACAGTCACCGGCAAGCCCTGCGGCGCATCAAGCTGACAGCGGCGCGCGCGAG 650
QY 145 LeuGlyAla1LeValTyArgVal-----GlyValLys 155
DB 651 GAGGGCATCCGGCTCTTGGCGGTGCGCCCAACCAAGAACTGAAGAGAGAGGCGCTGCGG 710
QY 156 AepPheAAsnGluThr-----GlnLeuAlaArg1Lea1AAserLysAAsPhe1sValPhe 173
DB 711 GACATGCCAGACAGCGCGCAAGCTTACCG-----AACGACTAGCGCAGC 758
QY 174 ProValAAsnAparGlyPheGlnAlaLeuGlnGly1Le1LeH1sSer1Leu-----190
DB 759 ATGCTGCYCATCCACCGAGATCRAACAGACACCATCAACCGCATCATCAAGTCAATG 818
QY 191 -----LysLysSerCys1LeGlu1Le 197
DB 819 AAACACGAAGCTTACGAGAGTGTCTACAAAGTGAAGTGGCTGGAAATC 866
```

RESULT 12

```
US-10-995-561-466
/ Sequence 466, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: C4001553
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
```

```
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 466
/ LENGTH: 3468
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-466
```

Alignment Scores:

Pred. No.:	0.0419	Length:	3468
Score:	107.50	Matches:	50
Percent Similarity:	40.28%	Conservative:	37
Best Local Similarity:	23.15%	Mismatches:	84
Query Match:	7.00%	Indels:	45
DB:	6	Gaps:	9

US-09-970-076-2_COPY_27_321 (1-295) x US-10-995-561-466 (1-3468)

```
QY 19 LeuTYRPhel1LeuLysSerGlySerVal-----29
DB 243 GTGTACTTGTGCTGGACACTCGAGAGCGTCAACCATGCAATGCCCAAGCATCTTG 302
QY 30 LeuNH1stPAsnGlu---1LeTYRPhValGluGluLeuLah1stLysPhe1Le 48
DB 303 CTCTTCCACATGAAGCATTCGTGCGGCACTTCAAGCCAGCTGAGAAAGATTCTAC 362
QY 49 SerProGluLeuArgMetSerPhe-----1LeValPheSerThrArgGlyThr 64
DB 363 CTGGACCAAGTGGCGCTGAGCTGGCGCTAAGCGGCGCTGACTTCTTCAACAGGTGAG 422
QY 65 ThrLeuMetLysLeuThrGluAparArgGluGln1LeArgGlnGlyLeuGluLeuGln 84
DB 423 GTGTTCAGCCCAACCGGCGAGCAACCGGCGCTCTTCATCAAGAACTGCAAGGCGCATCAG 482
QY 85 LysValLeuProGlyLysPheThrTyMetH1sGluGlyPheGluArgL1AserGluGln 104
DB 483 TCTTTCGCGCGGCGC-----ACCTTCAACCACTGCGCGCTGCCCAATGACGAGAGCAG 536
QY 105 1LeTYRPh1LeuLysnArgGlnGlyTyArgThrAlaSerVal1Le1Lea1LeuThrAsp 124
DB 537 ATCCGCGAGAGACCGGCAAGAGGC-----ACGTCACACTGCCCGGTGCATCACCGCAG 590
QY 125 GlyGluLeuNH1sGluAparLeuPhePheTySerGluArgGluLah1stLysSerArgAsp 144
DB 591 GGCACAGTCACCGGCAAGCCCTGCGGCGCATCAAGCTGACAGCGGCGCGCGCGAG 650
QY 145 LeuGlyAla1LeValTyArgVal-----GlyValLys 155
DB 651 GAGGGCATCCGGCTCTTGGCGGTGCGCCCAACCAAGAACTGAAGAGAGAGGCGCTGCGG 710
QY 156 AepPheAAsnGluThr-----GlnLeuAlaArg1Lea1AAserLysAAsPhe1sValPhe 173
DB 711 GACATGCCAGACAGCGCGCAAGCTTACCG-----AACGACTAGCGCAGC 758
QY 174 ProValAAsnAparGlyPheGlnAlaLeuGlnGly1Le1LeH1sSer1Leu-----190
DB 759 ATGCTGCYCATCCACCGAGATCRAACAGACACCATCAACCGCATCATCAAGTCAATG 818
QY 191 -----LysLysSerCys1LeGlu1Le 197
DB 819 AAACACGAAGCTTACGAGAGTGTCTACAAAGTGAAGTGGCTGGAAATC 866
```

RESULT 13

```
US-10-601-368-2
/ Sequence 2, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
```

```

; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3564
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3564)
US-10-601-368-2

Alignment Scores:
Pred. No.: 0.0504 Length: 3564
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 6.97% Indels: 38
DB: Gaps: 9

US-09-970-076-2_COPY_27_321 (1-295) x US-10-601-368-2 (1-3564)
QY 13 CyeTyrGlyGlyPheAspLeuTyrPheIleuAspLysSerGlySerValLeuHis 32
DB 475 TGCCAGACCTACATGACATCGTCATTTCTCGATGCTCCACACAGCATC---TACCCC 531
QY 33 TrpAsnGluIleTyrTyrPheValGluGlnLeuAlaHisLysPhe---IleSerPro--- 50
DB 532 TGGGTGAGGTTTCAGCATCTTCATCATCAACATCTCTGAAAAGTTTACATTGGCCCGG 591
QY 51 GlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThr 70
DB 592 CAGATCCAGCTGTGAGTTGTGCAGTATGCGAAGATGTGTCATGATTCACCTC--- 648
QY 71 GluAspArgGluGlnIleArgGlnGlyLeuGluGlnLeuGlnValLeuProGlyGly 90
DB 649 AACGACTACACAGCTGTAAAAGATGTGTGAGAGCTGCCAGCCACATTCAGCAGAGAGA 708
QY 91 AspThrTyrMetHisGluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyr 107
DB 709 GGAACAGAGACCCGAGCGCATTTGGCATTTGAATTGSCAGCGCTTCAGAGGCTTCCAGAG 768
QY 108 GluAsnArgGlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeu 127
DB 769 GGTGAAAGGAAAGAGACCAAG-----AAGGTGATGATTGTATCAGATGGGGAGTCC 822
QY 128 HisGluAsp----- 130
DB 823 CACGACAGCCCGACAGCTCGAAGAGGTGATCCAGCAAGAGCAAGCAAGTAAACAAGA 882
QY 131 -----LeuPhePheTyrSerGlyArgGlyAlaAsnArgSerArgAspLeu 145
DB 883 TATCGCGTGCCTCGCTCGGCTACTACACCGCAGGGGGATCAATCCAGAACTTTTCTA 942
QY 146 GlyAlaIleValIleTyrCysValGlyValLysAsp-----PheAsnGluThrGln 161
DB 943 AATGAATCAAAATACATCGCCAGTACCCCTGATGACAAAGCATTTCTTCAATGTCACTGAT 1002
QY 162 LeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAla 181
DB 1003 GAGGCTCGCTTG-----AAGGACATTTGCGATGCCCTGGGGGACAGAAATCTTCAGC 1053
QY 182 LeuGlnGly 184
DB 1054 CTGGAAGGC 1062

RESULT 14
US-11-000-463-574
; Sequence 574, Application US/11000463
; Publication No. US20050266423A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Aundt, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Jie
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 574
; LENGTH: 3967
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-000-463-574

Alignment Scores:
Pred. No.: 0.0595 Length: 3967
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 6.97% Indels: 38
DB: Gaps: 9

US-09-970-076-2_COPY_27_321 (1-295) x US-11-000-463-574 (1-3967)
QY 13 CyeTyrGlyGlyPheAspLeuTyrPheIleuAspLysSerGlySerValLeuHis 32
DB 524 TGCCAGACCTACATGACATCGTCATTTCTCGATGCTCCACACAGCATC---TACCCC 580
QY 33 TrpAsnGluIleTyrTyrPheValGluGlnLeuAlaHisLysPhe---IleSerPro--- 50
DB 581 TGGGTGAGGTTTCAGCATCTTCATCATCAACATCTCTGAAAAGTTTACATTGGCCCGG 640
QY 51 GlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThr 70
DB 641 CAGATCCAGCTGTGAGTTGTGCAGTATGCGAAGATGTGTCATGATTCACCTC--- 697
QY 71 GluAspArgGluGlnIleArgGlnGlyLeuGluGlnLeuGlnValLeuProGlyGly 90
DB 698 AACGACTACACAGCTGTAAAAGATGTGTGAGAGCTGCCAGCCACATTCAGCAGAGAGA 757
QY 91 AspThrTyrMetHisGluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyr 107
DB 758 GGAACAGAGACCCGAGCGCATTTGGCATTTGAATTGSCAGCGCTTCAGAGGCTTCCAGAG 817
QY 108 GluAsnArgGlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeu 127
DB 818 GGTGAAAGGAAAGAGACCAAG-----AAGGTGATGATTGTATCAGATGGGGAGTCC 871
QY 128 HisGluAsp----- 130
```

```
DB 872 CACGACAGCCAGACCTGGAGAGGTGATCCAGCAAGGAAAGACAACTAACAGA 931
      |||:::
QY 131 -----LeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeu 145
      |||:::
DB 932 TATGCGTGCCGCTCTGCGCTACTACACCGGAGGAGATCATCCAGAACTTTCTA 991
      |||:::
QY 146 GYAlAlAlAlAlAlTyrCysValGlyValLysAsp-----PheAsnGluThrGln 161
      |||:::
DB 992 AATGAATCAATATCATCCGCGCATGACCTGATGACAGACCTTCTTCAATGTCACTGAT 1051
      |||:::
QY 162 LeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAla 181
      |||:::
DB 1052 GAGGCTGCCTTG-----AAGACATTTGCGATGCCCTGGGGACAGAACTTTCAGC 1102
      |||:::
QY 182 LeuGlnGly 184
      |||:::
DB 1103 CTGGAAGGC 1111

RESULT 15
US-11-000-463-102
/ Sequence 102, Application US/11000463
/ Publication No. US20050266423A1
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Qian, Xiaohong B.
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Zhang, Jie
/ APPLICANT: Zhou, Ping
/ APPLICANT: Cao, Yi-Cheng
/ APPLICANT: Dmanac, Radoje T.
/ TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
/ FILE REFERENCE: 785CIP4CN
/ CURRENT APPLICATION NUMBER: US/11/000,463
/ CURRENT FILING DATE: 2004-11-29
/ PRIOR APPLICATION NUMBER: 10/291,265
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: PCT/US01/02623
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 09/922,279
/ PRIOR FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: 09/491,404
/ PRIOR FILING DATE: 2000-01-25
/ PRIOR APPLICATION NUMBER: 09/617,746
/ PRIOR FILING DATE: 2000-07-17
/ PRIOR APPLICATION NUMBER: 09/631,451
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: 09/633,870
/ PRIOR FILING DATE: 2000-09-15
/ NUMBER OF SEQ ID NOS: 944
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 102
/ LENGTH: 3969
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (52)..(3618)
US-11-000-463-102

Alignment Scores:
Pred. No.: 0.0595 Length: 3969
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 6.97% Indels: 38
DB: 7 Gaps: 9
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US-09-970-076-2_COPY_27_321 (1-295) * US-11-000-463-102 (1-3969)

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QY 13 CysTyrGlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisHis 32
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DB 526 TCCAGACCTTACATGAGACATGCTCATTTGCTCGATGGCTCCAAAGCATC---TACCCC 582
      |||:::
QY 33 TTPAnGluIleTyrTyrPheValGluGlnLeuAlaHisLysPhe---IleSerPro--- 50
      |||:::
DB 583 TGGGTGGAGTTTCACACATCTCTCATCAACATCCGMAAAAGTTTACCTTGGCCCAAGG 642
      |||:::
QY 51 GlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThreuMetLysLeuThr 70
      |||:::
DB 643 CAGATTCAGGTGGAGTTTGCGATTCGATGCGCAAGATGTGTGCATGACCTTCACTTC 699
      |||:::
QY 71 GluAspArgGlyGlnIleArgGlnGlyLeuGlnLysValLeuProGlyGly 90
      |||:::
DB 700 AACGACTACAGTCTGTAAAGATGCGTGAAGCTCCAGCAGCATTTGACGACAGAGGA 759
      |||:::
QY 91 AspThrTyrMetHisGluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyr 107
      |||:::
DB 760 GGAACGAGAGACCCGAGCGGCATTTGGCATTTGAAATTTGCAGCGCTCAGAGGCTTTCAGAA 819
      |||:::
QY 108 GluAsnArgGlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeu 127
      |||:::
DB 820 GGTGAGAGGAAAGAGCCAG-----AAGTGATGATTGTCTATCACAGATGGGAGTCC 873
      |||:::
QY 128 HisGluAsp----- 130
      |||:::
DB 874 CACGACAGCCAGACCTGGAGAGGTGATCCAGCAAGGAAAGACAACTAACAGA 933
      |||:::
QY 131 -----LeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeu 145
      |||:::
DB 934 TATGCGTGCCGCTCTGCGCTACTACACCGGAGGAGATCATCCAGAACTTTCTA 993
      |||:::
QY 146 GYAlAlAlAlAlAlTyrCysValGlyValLysAsp-----PheAsnGluThrGln 161
      |||:::
DB 994 AATGAATCAATATCATCCGCGCATGACCTGATGACAGACCTTCTTCAATGTCACTGAT 1053
      |||:::
QY 162 LeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAla 181
      |||:::
DB 1054 GAGGCTGCCTTG-----AAGACATTTGCGATGCCCTGGGGACAGAACTTTCAGC 1104
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QY 182 LeuGlnGly 184
      |||:::
DB 1105 CTGGAAGGC 1113
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Search completed: December 19, 2005, 02:29:47
Job time : 260.049 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 11:02:37 : Search time 26.4228 Seconds
(Without alignments)
916.781 Million cell updates/sec

Title: US-09-970-076-2_COPY_28_320

Perfect score: 1526

Sequence: 1 QGGRREDGPGACVCGFDLYF.....DGLSFSSVITTTTCHSDG 293

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/prodata/1/1aa/6 COMB.pep.*
3: /cgn2_6/prodata/1/1aa/H.COMB.pep.*
4: /cgn2_6/prodata/1/1aa/PCUS.COMB.pep.*
5: /cgn2_6/prodata/1/1aa/RE.COMB.pep.*
6: /cgn2_6/prodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	786	51.5	488	2	US-10-104-047-2639
2	166	10.9	1155	1	US-08-286-889-46
3	166	10.9	1155	1	US-08-485-618-46
4	166	10.9	1155	1	US-08-362-652-46
5	166	10.9	1155	1	US-08-605-672-46
6	166	10.9	1155	1	US-08-482-293A-46
7	166	10.9	1155	1	US-08-943-363-46
8	166	10.9	1155	2	US-09-193-043-46
9	166	10.9	1155	2	US-09-688-307A-46
10	166	10.9	1155	2	US-09-350-259-46
11	166	10.9	1161	1	US-08-485-618-53
12	166	10.9	1161	1	US-08-362-652-53
13	166	10.9	1161	1	US-08-605-672-53
14	166	10.9	1161	1	US-08-482-293A-53
15	166	10.9	1161	1	US-08-943-363-53
16	166	10.9	1161	2	US-09-193-043-53
17	166	10.9	1161	2	US-09-688-307A-53
18	166	10.9	1161	2	US-09-350-259-53
19	159.5	10.5	1151	1	US-08-286-889-37
20	159.5	10.5	1151	1	US-08-485-618-37
21	159.5	10.5	1151	1	US-08-362-652-37
22	159.5	10.5	1151	1	US-08-605-672-37
23	159.5	10.5	1151	1	US-08-482-293A-37
24	159.5	10.5	1151	1	US-08-943-363-37
25	159.5	10.5	1151	2	US-09-193-043-37
26	159.5	10.5	1151	2	US-09-688-307A-37
27	159.5	10.5	1151	2	US-09-350-259-37

28	159.5	10.5	1161	1	US-08-485-618-55	Sequence 55, Appl
29	159.5	10.5	1161	1	US-08-362-652-55	Sequence 55, Appl
30	159.5	10.5	1161	1	US-08-605-672-55	Sequence 55, Appl
31	159.5	10.5	1161	1	US-08-482-293A-55	Sequence 55, Appl
32	159.5	10.5	1161	1	US-08-943-363-55	Sequence 55, Appl
33	159.5	10.5	1161	2	US-09-193-043-55	Sequence 55, Appl
34	159.5	10.5	1161	2	US-09-688-307A-55	Sequence 55, Appl
35	159.5	10.5	1161	2	US-09-350-259-55	Sequence 55, Appl
36	156	10.2	1161	1	US-08-173-497-2	Sequence 2, Appl
37	156	10.2	1161	1	US-08-286-889-2	Sequence 2, Appl
38	156	10.2	1161	1	US-08-485-618-2	Sequence 2, Appl
39	156	10.2	1161	1	US-08-485-618-99	Sequence 99, Appl
40	156	10.2	1161	1	US-08-362-652-2	Sequence 2, Appl
41	156	10.2	1161	1	US-08-605-672-2	Sequence 2, Appl
42	156	10.2	1161	1	US-08-482-293A-2	Sequence 99, Appl
43	156	10.2	1161	1	US-08-943-363-2	Sequence 2, Appl
44	156	10.2	1161	1	US-08-482-293A-99	Sequence 99, Appl
45	156	10.2	1161	1	US-08-943-363-2	Sequence 2, Appl

ALIGNMENTS

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RESULT 1
US-10-104-047-2639
; Sequence 2639, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIORITY APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2639
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2639

Query Match      51.5%; Score 786; DB 2; Length 488;
Best Local Similarity 53.9%; Pred. No. 1.7e-78;
Matches 153; Conservative 54; Mismatches 75; Indels 2; Gaps 1;

QY 10 PACYGFADLYFIDKSGSVLHNMNEIYFEVQLAHKFIQPLRMSPFVSTGRTIMKLT 69
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DB 37 PSGRAPFDLYFVLDKSGSVANMWEIYFVQALAEFVSPFEMRLSFVSSQNTIILPLT 96
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 70 EDREQIRQGLEBELQKVLPGSDTYMHGFERBASQIYENRQGYRTASVITATLDEBLED 129
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 97 GDRGKISKSGEDHDKRVSPEVETIYHGLKLANEQI--QKAGGKTSIIITLTDGKLDGL 154
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 130 LFFYSREARNSDGLAIYVCVKDQENETQLARINDSKHVPVNDGPGALGGIHSIL 189
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 155 VPSYAKAEKATISLSIGASVCGVLPDQQLRINDSKQVPPVKGFGALGGIHSIL 214
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 190 KKSCEIILAEPTTICAGESFOVVVRNGGFRHARNYRVLCSPKINDSVTLNKPFSVED 249
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DB 215 AQSCTEILBELQPSVCGEFGQIVLSGRGMLGSRNGSVLCITYVETITTSVKPVSQVL 274
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QY 250 TYLLCPAPILKEVGMKALQVSNMGLSFSSSVIITTTTCHSDG 293
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DB 275 NSMLCPAPILKAGETLIDVSVSPNGKSVISGLIATVATECSNG 318
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 2
US-08-286-889-46
; Sequence 46, Application US/08286889
; Patent No. 5470953
; GENERAL INFORMATION:
```

APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-889-46

Query Match 10.9%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYG-GFDLYFLIDSGSV-LHHMNEIYFVEQLAHKFI SPOLRMSFIVSTRGTTLMK 67
DB 144 PEPCGEMDI AFIDSGSIDQSDFTQMKDFVAKLMGQLASTSTSFSLQYSILKTHFT 203
QY 68 LTEDR-----EQIRQGLEIQLKVLPGSDTYMEGFERRASEQIYYENRGYRTA-SVIAL 121
DB 204 FTEFKSLSPQSLVDIVQLQ-----GLTYTAGIQLKVKELFHSKNGARKSAKILIVI 258
QY 122 TDEGLHEDLFFYSE--REANRSDLGAIYVCVGKD-FNE-TOLARI-----ADSKDHF 172
DB 259 TDQQRPRDPLEYHVIPEAKA---GIRYALVGDAFREPTALQELINTIGSAPSODHVF 315
QY 173 PVNDGFOALOGIHSILKSCIEILAEPSITCAGSFQVVRGNGFRHARNVD 226
DB 316 KVGN-FVALRSIQROIQEK-----IFALEGTESRSSSFQHEMSQEGFSSALSMD 364

RESULT 3
US-08-485-618-46
Sequence 46, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago

STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-46

Query Match 10.9%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYG-GFDLYFLIDSGSV-LHHMNEIYFVEQLAHKFI SPOLRMSFIVSTRGTTLMK 67
DB 144 PEPCGEMDI AFIDSGSIDQSDFTQMKDFVAKLMGQLASTSTSFSLQYSILKTHFT 203
QY 68 LTEDR-----EQIRQGLEIQLKVLPGSDTYMEGFERRASEQIYYENRGYRTA-SVIAL 121
DB 204 FTEFKSLSPQSLVDIVQLQ-----GLTYTAGIQLKVKELFHSKNGARKSAKILIVI 258
QY 122 TDEGLHEDLFFYSE--REANRSDLGAIYVCVGKD-FNE-TOLARI-----ADSKDHF 172
DB 259 TDQQRPRDPLEYHVIPEAKA---GIRYALVGDAFREPTALQELINTIGSAPSODHVF 315
QY 173 PVNDGFOALOGIHSILKSCIEILAEPSITCAGSFQVVRGNGFRHARNVD 226
DB 316 KVGN-FVALRSIQROIQEK-----IFALEGTESRSSSFQHEMSQEGFSSALSMD 364

RESULT 4
US-08-362-652-46
Sequence 46, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States


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ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-46
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Query Match 10.9%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
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QY 10 PACYG-GFDLYFILDKSGSV-LHHMNEIYFVEQLAHKFTSPQLRMSFIVSTRGTTLMK 67
DB 144 PECGQEMDIAPFLDGGSGSIDQSFQMKDFVAKLMQGLASTSTSFIMQYSNLTKHFT 203
QY 68 LTEDR-----EQIRGLIEIQKVLPGDITYMHGFEFASQIYYENRGKRTA-SVIAL 121
DB 204 FTEFKSLSPQSLVDALVQLQ-----GLTYASGIQKVVLELPHSKNGARKSAKKILIVI 258
QY 122 TDGELHEDLFFYSE--REARSRDLGAIYVCVKD-FNE-TOLARI-----ADSKDHVF 172
DB 259 TDGQKRPDPLEYRHVPEAKA---GIRVAIGVDAFREPTALQELNTIGSAPSQDHVF 315
QY 173 PVNDGFOALOGIHSILKSCIEILAEPTICAGESFOYVVRNGFRHARNVD 226
DB 316 KVGN-FVALMSIQRIQIEK---IFALGTSRSSSSSFQHEMGOEGFSALSMD 364
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RESULT 5
US-08-605-672-46
Sequence 46, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-46
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Query Match 10.9%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;
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QY 10 PACYG-GFDLYFILDKSGSV-LHHMNEIYFVEQLAHKFTSPQLRMSFIVSTRGTTLMK 67
DB 144 PECGQEMDIAPFLDGGSGSIDQSFQMKDFVAKLMQGLASTSTSFIMQYSNLTKHFT 203
QY 68 LTEDR-----EQIRGLIEIQKVLPGDITYMHGFEFASQIYYENRGKRTA-SVIAL 121
DB 204 FTEFKSLSPQSLVDALVQLQ-----GLTYASGIQKVVLELPHSKNGARKSAKKILIVI 258
QY 122 TDGELHEDLFFYSE--REARSRDLGAIYVCVKD-FNE-TOLARI-----ADSKDHVF 172
DB 259 TDGQKRPDPLEYRHVPEAKA---GIRVAIGVDAFREPTALQELNTIGSAPSQDHVF 315
QY 173 PVNDGFOALOGIHSILKSCIEILAEPTICAGESFOYVVRNGFRHARNVD 226
DB 316 KVGN-FVALMSIQRIQIEK---IFALGTSRSSSSSFQHEMGOEGFSALSMD 364
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RESULT 6
US-08-482-293A-46
Sequence 46, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-46

Query Match 10.9%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYG-GFDLYFLDKSGV-LHHNRIYFVEQLAKFTSPQLRMSFIVSTRGTTLMK 67
DB 144 PECPCGEMDIAFLIDSGSIDQSDFTQMKDFVAKLWGQLASTSTSLMYSNILKTHFT 203
QY 68 LTEDR-----EQIRGLIELQKVLPGSDTYMHGFEFASQIYENRGYRTA-SVIAL 121
DB 204 FTEFKSLSPQSLVDALVQLQ-----GLTYTASGIQKVKELPHSKNGAKSAKKILIVI 258
QY 122 TDELHEDLFFYSE--REANRSRLGAIYCVGVD-FNE-TQLARI-----ADSKDHVF 172
DB 259 TDGQKRDLPEYRHVHVAPEAKA---GIIRYALGVDAFREPFLAQELNTIGSAPSDHVF 315
QY 173 PVNDGFOALOGIHSILKSCIEIIAEPSTICAGSFQVYVRNGNFRHARND 226
DB 316 KVGN-FVALRSIORQIOEK-----IFAIEGTERSSSSSFQHEMGEQGFSSALSM 364

RESULT 7

US-08-943-363-46
Sequence 46, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seair Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:

CLASSIFICATION: 530
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-46

Query Match 10.9%; Score 166; DB 1; Length 1155;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYG-GFDLYFLDKSGV-LHHNRIYFVEQLAKFTSPQLRMSFIVSTRGTTLMK 67
DB 144 PECPCGEMDIAFLIDSGSIDQSDFTQMKDFVAKLWGQLASTSTSLMYSNILKTHFT 203
QY 68 LTEDR-----EQIRGLIELQKVLPGSDTYMHGFEFASQIYENRGYRTA-SVIAL 121
DB 204 FTEFKSLSPQSLVDALVQLQ-----GLTYTASGIQKVKELPHSKNGAKSAKKILIVI 258
QY 122 TDELHEDLFFYSE--REANRSRLGAIYCVGVD-FNE-TQLARI-----ADSKDHVF 172
DB 259 TDGQKRDLPEYRHVHVAPEAKA---GIIRYALGVDAFREPFLAQELNTIGSAPSDHVF 315
QY 173 PVNDGFOALOGIHSILKSCIEIIAEPSTICAGSFQVYVRNGNFRHARND 226
DB 316 KVGN-FVALRSIORQIOEK-----IFAIEGTERSSSSSFQHEMGEQGFSSALSM 364

RESULT 8

US-09-193-043-46
Sequence 46, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 46
LENGTH: 1155
TYPE: PRT
ORGANISM: Mus musculus
US-09-193-043-46

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Query Match      10.9%; Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYG-GFDLYFLIDKSGSV-LHHMNEIYFVEQLAHKFTISPOLRMSFIVSTRGTTLMK 67
DB 144 PECGQEMDIAFLIDGSGSIDQSDFTQMKDFVXALMQLASTSTSFIMQYSNLTKTHT 203
QY 68 LTER-----EQIRQGLEBLQKVLPGDDTYMHGFERASQIYENQGRTA-SVIAL 121
DB 204 FTERKSSLSPOSQSLVDALVQL-----GLTYTASGIQKVVELFHSKNGARKSARKIIVI 258
QY 122 TDGELHEDLFFYSE--REARSRDLGAIYVCVQKD-FNE-TOLARI-----ADSKDHF 172
DB 259 TDGQKRPDPLEYRIVPEAKA---GIIRAIIGVDAREPTLQELNTIGSAPSQDHF 315
QY 173 PVNDGFOALQGIHSILKKSCEIILAEPTICAGESFOVVVRNGFRHARNVD 226
DB 316 KVG-N-FVALRSIQROIQEK----IFAIEGTESRSSSFQHEMSQEGFSALSMD 364

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RESULT 9
US-09-688-307A-46
; Sequence 46, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688,307A
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-688-307A-46

```

```

Query Match      10.9%; Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYG-GFDLYFLIDKSGSV-LHHMNEIYFVEQLAHKFTISPOLRMSFIVSTRGTTLMK 67
DB 144 PECGQEMDIAFLIDGSGSIDQSDFTQMKDFVXALMQLASTSTSFIMQYSNLTKTHT 203
QY 68 LTER-----EQIRQGLEBLQKVLPGDDTYMHGFERASQIYENQGRTA-SVIAL 121
DB 204 FTERKSSLSPOSQSLVDALVQL-----GLTYTASGIQKVVELFHSKNGARKSARKIIVI 258
QY 122 TDGELHEDLFFYSE--REARSRDLGAIYVCVQKD-FNE-TOLARI-----ADSKDHF 172
DB 259 TDGQKRPDPLEYRIVPEAKA---GIIRAIIGVDAREPTLQELNTIGSAPSQDHF 315
QY 173 PVNDGFOALQGIHSILKKSCEIILAEPTICAGESFOVVVRNGFRHARNVD 226
DB 316 KVG-N-FVALRSIQROIQEK----IFAIEGTESRSSSFQHEMSQEGFSALSMD 364

```

```

RESULT 10
US-09-350-259-46
; Sequence 46, Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6620915el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-350-259-46

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Query Match      10.9%; Score 166; DB 2; Length 1155;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYG-GFDLYFLIDKSGSV-LHHMNEIYFVEQLAHKFTISPOLRMSFIVSTRGTTLMK 67
DB 144 PECGQEMDIAFLIDGSGSIDQSDFTQMKDFVXALMQLASTSTSFIMQYSNLTKTHT 203
QY 68 LTER-----EQIRQGLEBLQKVLPGDDTYMHGFERASQIYENQGRTA-SVIAL 121
DB 204 FTERKSSLSPOSQSLVDALVQL-----GLTYTASGIQKVVELFHSKNGARKSARKIIVI 258
QY 122 TDGELHEDLFFYSE--REARSRDLGAIYVCVQKD-FNE-TOLARI-----ADSKDHF 172
DB 259 TDGQKRPDPLEYRIVPEAKA---GIIRAIIGVDAREPTLQELNTIGSAPSQDHF 315
QY 173 PVNDGFOALQGIHSILKKSCEIILAEPTICAGESFOVVVRNGFRHARNVD 226
DB 316 KVG-N-FVALRSIQROIQEK----IFAIEGTESRSSSFQHEMSQEGFSALSMD 364

```

```

RESULT 11
US-08-485-618-53
; Sequence 53, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/08/485,618
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32797
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 53:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1161 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-485-618-53

Query Match          10.9%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYG-GPDLYFLDKSGSV-LHHMNEYFVEQLAHKFI SPQLRMSPFI VSTRGTTLMK 67
DB 144 PECPGEMDI AFIDSGSIDSGDFTQMDPFAALMGQLASTSTSLMYSLTLTHFT 203
QY 68 LTEDR-----EQIRGLLELOKVLPGGDTYMHGFERASEQIYENROGYRTA-SVYIAL 121
DB 204 FTEFSSLSPOSLVDAIVQLQ-----GLTYTASGIQKVVELPHSKNGAKSAKILLIYI 258
QY 122 TDGELHEDLFFYSE--REANRSRDLGAIYVCVVKD-FNE-TOLARI-----ADSKDHVF 172
DB 259 TDQKFRDPLEYRHVIPLEAKA---GIIRYAIGVGAFREPTALOELINTIGSAPSDHVF 315

QY 173 PVNDGFOALQGIHSLIKKSCIEILAAPSTICAGSFQVYVNGFRHARND 226
DB 316 KVGN-FVALKSTORQIOEK---IFAIGTESRSSSSFQHEMSQEGFSSALSMD 364

RESULT 12
US-08-362-652-53
/ Sequence 53, Application US/08362652
/ Patent No. 5766850
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 93
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/362,652
/ FILING DATE:
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/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32391
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 53:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1161 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-362-652-53

Query Match          10.9%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYG-GPDLYFLDKSGSV-LHHMNEYFVEQLAHKFI SPQLRMSPFI VSTRGTTLMK 67
DB 144 PECPGEMDI AFIDSGSIDSGDFTQMDPFAALMGQLASTSTSLMYSLTLTHFT 203
QY 68 LTEDR-----EQIRGLLELOKVLPGGDTYMHGFERASEQIYENROGYRTA-SVYIAL 121
DB 204 FTEFSSLSPOSLVDAIVQLQ-----GLTYTASGIQKVVELPHSKNGAKSAKILLIYI 258
QY 122 TDGELHEDLFFYSE--REANRSRDLGAIYVCVVKD-FNE-TOLARI-----ADSKDHVF 172
DB 259 TDQKFRDPLEYRHVIPLEAKA---GIIRYAIGVGAFREPTALOELINTIGSAPSDHVF 315

QY 173 PVNDGFOALQGIHSLIKKSCIEILAAPSTICAGSFQVYVNGFRHARND 226
DB 316 KVGN-FVALKSTORQIOEK---IFAIGTESRSSSSFQHEMSQEGFSSALSMD 364

RESULT 13
US-08-605-672-53
/ Sequence 53, Application US/08605672
/ Patent No. 5817515
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/605,672
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
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```

1 APPLICATION NUMBER: US 08/286,889
2
3 FILING DATE: 5-AUG-1994
4
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: US 08/362,652
7
8 FILING DATE: 21-DEC-1994
9
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Williams Jr., Joseph A.
12
13 REGISTRATION NUMBER: 38,659
14
15 REFERENCE/DOCKET NUMBER: 27866/32684
16
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: 312-474-6300
19
20 TELEFAX: 312-474-0448
21
22 TELEX: 25-3856
23
24 INFORMATION FOR SEQ ID NO: 53:
25
26 SEQUENCE CHARACTERISTICS:
27
28 LENGTH: 1161 amino acids
29
30 TYPE: amino acid
31
32 TOPOLOGY: linear
33
34 MOLECULE TYPE: protein
35
36 JS-08-605-672-53

```

Query Match	10.9%	Score 166;	DB 1;	Length 1161;
Best Local Similarity	28.2%;	Pred. No. 6.5e-09;		
Matches	66;	Conservative	42;	Mismatches 96;
			Indels	30;
			Gaps	12;

QY 10 PACAG-GDLEFIILDKSSV-LHHNLEYVFEOLAHFISPOLMSPIVSTRGTLMLK 67
Db 144 PECCEGQENDIAFLIDSGSIDOSDPTQMKDFYKALMGQLASTSTSFSLMYSNLKTIFT 203
QY 68 LTEDR-----EQIROGSEBELQKVLPGSDTYMHGEFERASEQIYYENROGVRTA-SVIAL 121
Db 204 FTEPRSLSPQSLVDALIVQL-----GLTYASGIGKVKVELFHSKNGARSAKKILLVI 258
QY 122 TDGELHEDLFFYSF--REANRSRDIGAIVYCYGVKD-FNE-TOLARI-----ADSKDHF 172
Db 259 TDGQKFRDPLEYRHVYIPEAKRA---GIRVAIGVDAREPFTALQELNTIGSPSQDHVF 315
QY 173 PVNDGFOALQGIHSHLLKSCIEILAAPSTTCAGESQVYVVRNGGFHANVD 226
Db 316 KVGK-PVALRRIQRIQK-----IFAIGTSRRSSSFQIHEMSOGFGFSALLMD 364

```

1      RESULT 14
2      US-08-482-293A-53
3      ; Sequence 53 Application US/08482293A
4      ; Patent No.5831029
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Gallatin, W. Michael
7      ; APPLICANT: Van der Vieren, Monica
8      ; TITLE OF INVENTION: No. 5831029e1 Human 2 Integrin Alpha Subunit
9      ; NUMBER OF SEQUENCES: 103
10     ; CORRESPONDENCE ADDRESSES:
11     ; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
12     ; STREET: 233 South Wacker Drive, 6300 Sear Tower
13     ; CITY: Chicago
14     ; STATE: Illinois
15     ; COUNTRY: United States
16     ; ZIP: 60606-6402
17     ;
18     ; COMPUTER READABLE FORM:
19     ; MEDIUM TYPE: Floppy disk
20     ; COMPUTER: IBM PC compatible
21     ; OPERATING SYSTEM: PC-DOS/MS-DOS
22     ; SOFTWARE: PatentIn Release #1.0, Version #1.25
23     ; CURRENT APPLICATION DATA:
24     ; APPLICATION NUMBER: US/08/482,293A
25     ; FILING DATE:
26     ; CLASSIFICATION: 530
27     ; PRIOR APPLICATION DATA:
28     ; APPLICATION NUMBER: US 08/173,497
29     ; FILING DATE: 23-DEC-1993
30     ; PRIOR APPLICATION DATA:
31     ; APPLICATION NUMBER: US 08/286,889
32     ; FILING DATE: 5-AUG-1994
33     ;

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1      PRIOR APPLICATION DATA:
2      APPLICATION NUMBER:  US 08/362,652
3      FILING DATE:  21-DEC-1994
4      ATTORNEY/AGENT INFORMATION:
5      NAME:  Williams Jr., Joseph A.
6      REGISTRATION NUMBER:  38,658
7      REFERENCE/DOCKET NUMBER:  27866/32684
8      TELECOMMUNICATION INFORMATION:
9      TELEPHONE:  312-474-6300
10     TELEFAX:  312-474-0448
11     TELEX:  25-3856
12     INFORMATION FOR SEQ ID NO:  53:
13     SEQUENCE CHARACTERISTICS:
14     LENGTH:  1161 amino acids
15     TYPE:  amino acid
16     TOPOLOGY:  linear
17     MOLECULE TYPE:  protein
18     US-08-462-293A-53

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Query Match	10.9%	Score 166;	DB 1;	Length 1161;
Best Local Similarity	28.2%	Pred. No. 6;	Se 09;	
Matches	66;	Conservative	42;	Mismatches 96;
			Indels	30;
			Gaps	12;

Qy 10 PACG-GFDIYFIIIDKSGSV-LHHMNIIYFVEEDLAKFTISPOLRMSFIFYSTGTTIMK 67
Db 144 PECGCGEMDIAFLIDSGSGSIDSGFTQMGDFVAKMQLASTSTSPBMLQMYNTLKTHTF 203
Qy 68 LTEDR-----EQIRQGLEELQKVLPGSDYTHHEGFERASQIYYENQGRYTA-SVIAL 121
Db 204 PTEKSKSLSPQSLVDALIVQL-----GLVTASQIQKVVKELFHSKNGARRSAKKILIVI 258
Qy 122 TDGELHEDLPFYSS--REARRSRDLGAIIVCVGYKD-FNE-TQLARI-----ADSKOHVF 172
Db 259 TDGCKFRPDPLEYRHVPIPEAKA---GIIRYAIAGDAREPPTLAQELNTIGSAPSODHVF 315
Qy 173 PVNDGFOALGIIHSLIKSCITELAAEPSTICAGESFOVYVNRGNGFRHARNVD 226
Db 316 KVNG-FALKSTIORIOEK-----FALEGTESRSSSFQHEMGOEGSSALSKMD 364

RESULT 15
 US-08-943-363-53
 Sequence 53 Application US/08943363
 Patent No. 5837478
 GENERAL INFORMATION:
 APPLICANT: Gallatin, W. Michael
 APPLICANT: Van der Vlieten, Monica
 TITLE OF INVENTION: No. 5837478e1 Human 2 Integrin Alpha Subunit
 NUMBER OF SEQUENCES: 114
 CORRESPONDENCE ADDRESS:
 ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 213 South Wacker Drive, 6300 Sear Tower
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/943,363
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/173,497
 FILING DATE: 23-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/286,889
 FILING DATE: 5-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-53

Query Match 10.9%; Score 166; DB 1; Length 1161;
Best Local Similarity 28.2%; Pred. No. 6.5e-09;

Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 10 PACYG-GFDLYPTLDKSGSV-LHANEIYFVEQLAHKFTSPQLRMSPIVSTRTTLMK 67
DB 144 PEPGQEMDIAPLIDSGSIDSDFTQMKDFVXALMGQLASTSTSPSLMQYSNLTHT 203
QY 68 LTEDR-----EQRQGLEELQKVLPGDDTYMHEGFERASEQIYYENRQGYRTA-SVIAL 121
DB 204 FTEFKSSLSPQSLVDALIVQLQ-----GLYTTASGIQKVKELPHSIQGAKSKAKILIVI 258
QY 122 TQELHEDLFFYSE--REANRSRLGAIYVCVVKD-FNE-TQLARI-----ADSKDHYF 172
DB 259 TQQKFRDPLEYHVIPEAKA---GIIRYALGVDAFREPTALQELNTIGSAPQDHVF 315
QY 173 PVNDGFQALQGIHSLTKKSCIEILAAEPSTICAGSFQYVVRGNGFRHARNVD 226
DB 316 KVGN-FVALRSIQRIQEK----IFAIEGTSSRSSSFQHEMSQEGFSSALSMD 364

Search completed: December 14, 2005, 11:21:06
Job time : 27.4228 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 11:18:07 ; Search time 88.2719 Seconds
(without alignments)
1386.897 Million cell updates/sec

Title: US-09-970-076-2_COPY_28_320

Perfect score: 1526

Sequence: 1 OQGRREDGACGACGFDLYF.....DGLSFSSSVITTTTCSDG 293

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417629326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodaca/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodaca/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodaca/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodaca/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodaca/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodaca/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1526	100.0	368	US-11-047-278-2	Sequence 2, Appli
2	1526	100.0	403	US-09-833-245-621	Sequence 621, App
3	1526	100.0	551	US-10-038-307-18	Sequence 18, Appl
4	1526	100.0	551	US-10-201-292-18	Sequence 18, Appl
5	1526	100.0	564	US-09-918-715-187	Sequence 187, App
6	1526	100.0	564	US-10-301-822-193	Sequence 232, App
7	1526	100.0	564	US-10-408-765A-1823	Sequence 1823, App
8	1526	100.0	564	US-10-474-794-187	Sequence 187, App
9	1526	100.0	564	US-10-474-794-187	Sequence 187, App
10	1526	100.0	564	US-10-979-159-187	Sequence 187, App
11	1526	100.0	564	US-10-979-159-187	Sequence 187, App
12	1526	100.0	564	US-10-979-159-232	Sequence 232, App
13	1526	100.0	564	US-11-047-278-6	Sequence 6, Appli
14	1515	99.3	403	US-09-833-245-620	Sequence 620, App
15	1514	99.2	333	US-09-796-753-12	Sequence 12, Appl
16	1514	99.2	333	US-10-038-307-2	Sequence 2, Appli
17	1514	99.2	333	US-10-201-292-2	Sequence 2, Appli
18	1514	99.2	333	US-11-047-278-8	Sequence 8, Appli
19	1514	99.2	345	US-10-038-307-24	Sequence 24, Appl
20	1514	99.2	345	US-10-201-292-24	Sequence 24, Appl
21	1514	99.2	564	US-10-038-307-20	Sequence 20, Appl
22	1514	99.2	564	US-10-201-292-20	Sequence 20, Appl
23	1509	98.9	562	US-09-918-715-194	Sequence 194, App
24	1509	98.9	562	US-09-918-715-301	Sequence 301, App
25	1509	98.9	562	US-10-474-794-194	Sequence 194, App
26	1509	98.9	562	US-10-474-794-301	Sequence 301, App
27	1509	98.9	562	US-10-979-159-194	Sequence 194, App

28	1509	98.9	562	US-10-979-159-301	Sequence 301, App
29	1501	98.4	328	US-10-038-307-26	Sequence 26, Appl
30	1501	98.4	328	US-10-201-292-26	Sequence 26, Appl
31	1499.5	98.3	342	US-10-038-307-22	Sequence 22, Appl
32	1499.5	98.3	342	US-10-201-292-22	Sequence 22, Appl
33	1493	97.8	543	US-10-038-307-14	Sequence 14, Appl
34	1493	97.8	543	US-10-038-307-16	Sequence 16, Appl
35	1493	97.8	543	US-10-201-292-16	Sequence 16, Appl
36	1493	97.8	543	US-10-201-292-16	Sequence 16, Appl
37	1483	97.2	543	US-10-038-307-10	Sequence 10, Appl
38	1483	97.2	543	US-10-201-292-10	Sequence 10, Appl
39	1478	96.9	534	US-10-038-307-12	Sequence 12, Appl
40	1478	96.9	534	US-10-201-292-12	Sequence 12, Appl
41	1413	92.6	529	US-10-201-292-36	Sequence 36, Appl
42	1299.5	85.2	504	US-10-201-292-34	Sequence 34, Appl
43	1172	76.8	479	US-10-201-292-32	Sequence 32, Appl
44	1058	69.3	460	US-10-201-292-28	Sequence 28, Appl
45	1048	68.7	460	US-10-201-292-30	Sequence 30, Appl

ALIGNMENTS

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RESULT 1
US-11-047-278-2
; Sequence 2, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047.278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970.076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; SOFTWARE: Patentin Ver. 2.1
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-047-278-2

Query Match      100.0%; Score 1526; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.1e-147;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 OQGRREDGACGACGFDLYFILDKSGSVLHNMNIYFYFQLAHKFISPOLRMSFIVFST 60
DB      28 OQGRREDGACGACGFDLYFILDKSGSVLHNMNIYFYFQLAHKFISPOLRMSFIVFST 87
      88 RGTTLKMLTDRDRIQRLGELQKVLPGGVTVHGEFRASBOIYYENRGYRTASYIA 147
QY      61 RGTTLKMLTDRDRIQRLGELQKVLPGGVTVHGEFRASBOIYYENRGYRTASYIA 120
DB      28 OQGRREDGACGACGFDLYFILDKSGSVLHNMNIYFYFQLAHKFISPOLRMSFIVFST 87
      88 RGTTLKMLTDRDRIQRLGELQKVLPGGVTVHGEFRASBOIYYENRGYRTASYIA 147
QY      121 LTGGLHEDEDFPFSBRBANSRDIGAIIVCVGKDFNEQTOLARIASKDHVPVNDGFOA 180
DB      148 LTGGLHEDEDFPFSBRBANSRDIGAIIVCVGKDFNEQTOLARIASKDHVPVNDGFOA 207
QY      181 LOGIHSILKSCIEILAAEPSTICAGESPQVVVNGGPFHARNVDRVLCSFKINDSVTL 240
DB      208 LOGIHSILKSCIEILAAEPSTICAGESPQVVVNGGPFHARNVDRVLCSFKINDSVTL 267
QY      241 NEKPFVSEYEDYLLCPAPILKEVGKALQVSNNDGJSFSSSVIITTTTCSDG 293
DB      268 NEKPFVSEYEDYLLCPAPILKEVGKALQVSNNDGJSFSSSVIITTTTCSDG 320
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RESULT 2
US-09-833-245-621
; Sequence 621, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albulmin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 621
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-621

Query Match          100.0%; Score 1526; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.2e-147;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  OGGRRDGGPACYGCGFDLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISQLRMSFIVFST 60
      |||
DB      28  OGGRRDGGPACYGCGFDLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISQLRMSFIVFST 87
      |||

QY      61  RGTTLMLKLTEDREQIQGLBELOKVLPGGDTYMHGFEFASQIYYENRQGYRTASVITA 120
      |||
DB      88  RGTTLMLKLTEDREQIQGLBELOKVLPGGDTYMHGFEFASQIYYENRQGYRTASVITA 147
      |||

QY      121 LTTDGLHEDLFFYSEREANRSRDLAGIYVCVGKDNENETOLARIADSKDHVPVNDGFOA 180
      |||
DB      148 LTTDGLHEDLFFYSEREANRSRDLAGIYVCVGKDNENETOLARIADSKDHVPVNDGFOA 207
      |||

QY      181 LOGIHSILKSCIEILAEPSITTCAGSFQVYVRNGRHRANVDRVLCSPKINDSVTL 240
      |||
DB      208 LOGIHSILKSCIEILAEPSITTCAGSFQVYVRNGRHRANVDRVLCSPKINDSVTL 267
      |||

QY      241 NEKPSVEDTYLLCPAPILKEVGKAAALQVSNMDGLSFISSVIITTHCSDG 293
      |||
DB      268 NEKPSVEDTYLLCPAPILKEVGKAAALQVSNMDGLSFISSVIITTHCSDG 320
      |||

RESULT 3
US-10-038-307-18
; Sequence 18, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-18

Query Match          100.0%; Score 1526; DB 4; Length 551;
Best Local Similarity 100.0%; Pred. No. 2e-147;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1  OGGRRDGGPACYGCGFDLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISQLRMSFIVFST 60
      |||
DB      28  OGGRRDGGPACYGCGFDLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISQLRMSFIVFST 87
      |||

QY      61  RGTTLMLKLTEDREQIQGLBELOKVLPGGDTYMHGFEFASQIYYENRQGYRTASVITA 120
      |||
DB      88  RGTTLMLKLTEDREQIQGLBELOKVLPGGDTYMHGFEFASQIYYENRQGYRTASVITA 147
      |||

QY      121 LTTDGLHEDLFFYSEREANRSRDLAGIYVCVGKDNENETOLARIADSKDHVPVNDGFOA 180
      |||
DB      148 LTTDGLHEDLFFYSEREANRSRDLAGIYVCVGKDNENETOLARIADSKDHVPVNDGFOA 207
      |||

QY      181 LOGIHSILKSCIEILAEPSITTCAGSFQVYVRNGRHRANVDRVLCSPKINDSVTL 240
      |||
DB      208 LOGIHSILKSCIEILAEPSITTCAGSFQVYVRNGRHRANVDRVLCSPKINDSVTL 267
      |||

QY      241 NEKPSVEDTYLLCPAPILKEVGKAAALQVSNMDGLSFISSVIITTHCSDG 293
      |||
DB      268 NEKPSVEDTYLLCPAPILKEVGKAAALQVSNMDGLSFISSVIITTHCSDG 320
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RESULT 4
US-10-201-292-18
; Sequence 18, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-18

Query Match          100.0%; Score 1526; DB 4; Length 551;
Best Local Similarity 100.0%; Pred. No. 2e-147;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  OGGRRDGGPACYGCGFDLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISQLRMSFIVFST 60
      |||
DB      28  OGGRRDGGPACYGCGFDLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISQLRMSFIVFST 87
      |||

QY      61  RGTTLMLKLTEDREQIQGLBELOKVLPGGDTYMHGFEFASQIYYENRQGYRTASVITA 120
      |||
DB      88  RGTTLMLKLTEDREQIQGLBELOKVLPGGDTYMHGFEFASQIYYENRQGYRTASVITA 147
      |||

QY      121 LTTDGLHEDLFFYSEREANRSRDLAGIYVCVGKDNENETOLARIADSKDHVPVNDGFOA 180
      |||
DB      148 LTTDGLHEDLFFYSEREANRSRDLAGIYVCVGKDNENETOLARIADSKDHVPVNDGFOA 207
      |||

QY      181 LOGIHSILKSCIEILAEPSITTCAGSFQVYVRNGRHRANVDRVLCSPKINDSVTL 240
      |||
DB      208 LOGIHSILKSCIEILAEPSITTCAGSFQVYVRNGRHRANVDRVLCSPKINDSVTL 267
      |||

QY      241 NEKPSVEDTYLLCPAPILKEVGKAAALQVSNMDGLSFISSVIITTHCSDG 293
      |||
DB      268 NEKPSVEDTYLLCPAPILKEVGKAAALQVSNMDGLSFISSVIITTHCSDG 320
      |||

RESULT 5
US-09-918-715-187
; Sequence 187, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
```



```

APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918.715
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 187
LTDGELHEDLFFYSERANRSDIGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOA
LENGTH: 564
TYPE: PRT
ORGANISM: Homo sapiens
US-09-918-715-187

Query Match      100.0%; Score 1526; DB 3; Length 564;
Best Local Similarity 100.0%; Pred. No. 2e-147;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGRRDGGPACGCGFPLYLFDKSGSVLHHNMEIYFVEQLAKFISPOLRMSFIYST 60
DB 28 OGGRRDGGPACGCGFPLYLFDKSGSVLHHNMEIYFVEQLAKFISPOLRMSFIYST 87

QY 61 RGTTLMLTDRDRIROGLELOKVLPGSDTYMHGEGERSAQIYENRQGYRTASVIA 120
DB 88 RGTTLMLTDRDRIROGLELOKVLPGSDTYMHGEGERSAQIYENRQGYRTASVIA 147

QY 121 LTDGELHEDLFFYSERANRSDIGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOA 180
DB 148 LTDGELHEDLFFYSERANRSDIGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOA 207

QY 181 LOGIHSILKKSCEIILAAEPSTICAGESFOVVRNGGFRHARVNDVLCSEFKINDSVTL 240
DB 208 LOGIHSILKKSCEIILAAEPSTICAGESFOVVRNGGFRHARVNDVLCSEFKINDSVTL 267

QY 241 NEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFISSVIITTHCSGD 293
DB 268 NEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFISSVIITTHCSGD 320

RESULT 6
US-09-918-715-232
Sequence 232, Application US/09918715
Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918.715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 232
LENGTH: 564
TYPE: PRT
ORGANISM: Homo sapiens
US-09-918-715-232

Query Match      100.0%; Score 1526; DB 3; Length 564;
Best Local Similarity 100.0%; Pred. No. 2e-147;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 2e-147;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGRRDGGPACGCGFPLYLFDKSGSVLHHNMEIYFVEQLAKFISPOLRMSFIYST 60
DB 28 OGGRRDGGPACGCGFPLYLFDKSGSVLHHNMEIYFVEQLAKFISPOLRMSFIYST 87

QY 61 RGTTLMLTDRDRIROGLELOKVLPGSDTYMHGEGERSAQIYENRQGYRTASVIA 120
DB 88 RGTTLMLTDRDRIROGLELOKVLPGSDTYMHGEGERSAQIYENRQGYRTASVIA 147

QY 121 LTDGELHEDLFFYSERANRSDIGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOA 180
DB 148 LTDGELHEDLFFYSERANRSDIGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOA 207

QY 181 LOGIHSILKKSCEIILAAEPSTICAGESFOVVRNGGFRHARVNDVLCSEFKINDSVTL 240
DB 208 LOGIHSILKKSCEIILAAEPSTICAGESFOVVRNGGFRHARVNDVLCSEFKINDSVTL 267

QY 241 NEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFISSVIITTHCSGD 293
DB 268 NEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFISSVIITTHCSGD 320

RESULT 7
US-10-301-822-199
Sequence 199, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MPM01-029P2RNM
CURRENT APPLICATION NUMBER: US/10/301.822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 199
LENGTH: 564
TYPE: PRT
ORGANISM: Homo sapiens
US-10-301-822-199

Query Match      100.0%; Score 1526; DB 4; Length 564;
Best Local Similarity 100.0%; Pred. No. 2e-147;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGGRRDGGPACGCGFPLYLFDKSGSVLHHNMEIYFVEQLAKFISPOLRMSFIYST 60
DB 28 OGGRRDGGPACGCGFPLYLFDKSGSVLHHNMEIYFVEQLAKFISPOLRMSFIYST 87

QY 61 RGTTLMLTDRDRIROGLELOKVLPGSDTYMHGEGERSAQIYENRQGYRTASVIA 120
DB 88 RGTTLMLTDRDRIROGLELOKVLPGSDTYMHGEGERSAQIYENRQGYRTASVIA 147

QY 121 LTDGELHEDLFFYSERANRSDIGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOA 180
DB 148 LTDGELHEDLFFYSERANRSDIGAIVYCVGVDFNETOLARIADSKDHVPVNDGFOA 207

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QY 121 LTDELHEDLFFYSEERANRSDGAIYVCVGDVFNETOIARIADSKDHFVPVNDGFOA 180
| | | | |
DB 148 LTDELHEDLFFYSEERANRSDGAIYVCVGDVFNETOIARIADSKDHFVPVNDGFOA 207
| | | | |
QY 181 LOGIHSILKKSCTEILAAEPSTICAGESFOVVVRNGGFRHARNDVLCSPKINDSVTL 240
| | | | |
DB 208 LOGIHSILKKSCTEILAAEPSTICAGESFOVVVRNGGFRHARNDVLCSPKINDSVTL 267
| | | | |
QY 241 NEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFISSVIITTHCSGD 293
| | | | |
DB 268 NEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFISSVIITTHCSGD 320
| | | | |
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RESULT 11

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US-10-979-159-187
; Sequence 187, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-979-159-187
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Query Match 100.0%; Score 1526; DB 5; Length 564;
Best Local Similarity 100.0%; Pred. No. 2e-147;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 QGGRREDGGPACYGFDLYFLDKSGSVLHNMNIYFVEQLAHKFTSPQLRMSFIVFST 60
| | | | |
DB 28 QGGRREDGGPACYGFDLYFLDKSGSVLHNMNIYFVEQLAHKFTSPQLRMSFIVFST 87
| | | | |
QY 61 RGTTLMLKLTEDRQIRQGLELOKVLPGGDTYHBEGERASEQIYYENRQGYRTASVITA 120
| | | | |
DB 88 RGTTLMLKLTEDRQIRQGLELOKVLPGGDTYHBEGERASEQIYYENRQGYRTASVITA 147
| | | | |
QY 121 LTDELHEDLFFYSEERANRSDGAIYVCVGDVFNETOIARIADSKDHFVPVNDGFOA 180
| | | | |
DB 148 LTDELHEDLFFYSEERANRSDGAIYVCVGDVFNETOIARIADSKDHFVPVNDGFOA 207
| | | | |
QY 181 LOGIHSILKKSCTEILAAEPSTICAGESFOVVVRNGGFRHARNDVLCSPKINDSVTL 240
| | | | |
DB 208 LOGIHSILKKSCTEILAAEPSTICAGESFOVVVRNGGFRHARNDVLCSPKINDSVTL 267
| | | | |
QY 241 NEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFISSVIITTHCSGD 293
| | | | |
DB 268 NEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFISSVIITTHCSGD 320
| | | | |
```

RESULT 12

```
US-10-979-159-232
; Sequence 232, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
```

```
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 232
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-979-159-232
```

```
Query Match 100.0%; Score 1526; DB 5; Length 564;
Best Local Similarity 100.0%; Pred. No. 2e-147;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 QGGRREDGGPACYGFDLYFLDKSGSVLHNMNIYFVEQLAHKFTSPQLRMSFIVFST 60
| | | | |
DB 28 QGGRREDGGPACYGFDLYFLDKSGSVLHNMNIYFVEQLAHKFTSPQLRMSFIVFST 87
| | | | |
QY 61 RGTTLMLKLTEDRQIRQGLELOKVLPGGDTYHBEGERASEQIYYENRQGYRTASVITA 120
| | | | |
DB 88 RGTTLMLKLTEDRQIRQGLELOKVLPGGDTYHBEGERASEQIYYENRQGYRTASVITA 147
| | | | |
QY 121 LTDELHEDLFFYSEERANRSDGAIYVCVGDVFNETOIARIADSKDHFVPVNDGFOA 180
| | | | |
DB 148 LTDELHEDLFFYSEERANRSDGAIYVCVGDVFNETOIARIADSKDHFVPVNDGFOA 207
| | | | |
QY 181 LOGIHSILKKSCTEILAAEPSTICAGESFOVVVRNGGFRHARNDVLCSPKINDSVTL 240
| | | | |
DB 208 LOGIHSILKKSCTEILAAEPSTICAGESFOVVVRNGGFRHARNDVLCSPKINDSVTL 267
| | | | |
QY 241 NEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFISSVIITTHCSGD 293
| | | | |
DB 268 NEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFISSVIITTHCSGD 320
| | | | |
```

RESULT 13

```
US-11-047-278-6
; Sequence 6, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; PRIOR FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-047-278-6
```

```
Query Match 100.0%; Score 1526; DB 6; Length 564;
Best Local Similarity 100.0%; Pred. No. 2e-147;
```

	Matches	293; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
QY	1	OGGRREDGPACGCGFDLYFLIDKSGSVLHNNETYYFEQALAHKFPISQLMSTIVST	60			
Db	28	OGGRREDGPACGCGFDLYFLIDKSGSVLHNNETYYFEQALAHKFPISQLMSTIVST	87			
QY	61	RGTTLMKLTEDREQIRQGLBELQKVLPGGDIYMHGFEFASQIYYENKQYRTASVILIA	120			
Db	88	RGTTLMKLTEDREQIRQGLBELQKVLPGGDIYMHGFEFASQIYYENKQYRTASVILIA	147			
QY	121	LTDGELHDLFPYSSREANRSRDLCIAYCVCVKQENFRQLARINDSKDHVPVNDGFOA	180			
Db	148	LTDGELHDLFPYSSREANRSRDLCIAYCVCVKQENFRQLARINDSKDHVPVNDGFOA	207			
QY	161	LOGIHSILIKSCIEIILAAPESTICAGESFOVYVGVNGFRHARANDVRLCSEKINDSVTL	240			
Db	208	LOGIHSILIKSCIEIILAAPESTICAGESFOVYVGVNGFRHARANDVRLCSEKINDSVTL	267			
QY	241	NEKPSVBDTYLLCAPILIKVGMKRAALQVSNNDGLSFSSVILITTHHCSPG	293			
Db	268	NEKPSVBDTYLLCAPILIKVGMKRAALQVSNNDGLSFSSVILITTHHCSPG	320			

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US-09-833-245-620
; Sequence 620, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 620
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (320)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (331)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (368)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-620

Query Match          99.3%; Score 1515; DB 3; Length 403;
Best Local Similarity 99.7%; Pred. No. 1,7e-146;
Matches 291; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY      1  QGGRREDGDPACGGGDLVFIIDKSSSVLHNMWEIYFFVEQLAKHFIPLRLMSFIYFST 60
DB      28  QGGRREDGDPACGGGDLVFIIDKSSSVLHNMWEIYFFVEQLAKHFIPLRLMSFIYFST 87
QY      61  RGTTLMLKLTEDREQIQGLLELOKVLPGGDTYMHGEGFERASEQIYYENRGYRTASYIIA 120
DB      68  RGTTLMLKLTEDREQIQGLLELOKVLPGGDTYMHGEGFERASEQIYYENRGYRTASYIIA 147
QY      121 LTDEGLHEDLFFYSEERANRSRDGLAIYVCVGVDENETQLARIADSKDHVPVNDGFOA 180

```

Accession	Sequence	Length
D6	LTDTGELHEDLFFSSEENARSDLCATYCVGVDDPNTQLARLNDSDHVFNPNDGFA	207
OY	LOGIHSILKSKCIEILAAEPSTCAGESFOVYVRGNGFRRARVDRVLCSEFKINDSVTL	240
D6	LOGIHSILKSKCIEILAAEPSTCAGESFOVYVRGNGFRRARVDRVLCSEFKINDSVTL	267
OY	NEKPEFVEDPYYLCPAPILKEVGKMAALQVSNQDLSITSSVITITTHGSD	292
D6	NEKPEFVEDPYYLCPAPILKEVGKMAALQVSNQDLSITSSVITITTHGSD	319

```

RESULT 15
US-09-796-753-12
; Sequence 12, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751

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; PRIOR FILING DATE: 2000-09-30
 ; NUMBER OF SEQ ID NOS: 162
 ; SEQ ID NO 12
 ; LENGTH: 333
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-796-753-12

Query Match 99.2%; Score 1514; DB 3; Length 333;
 Best Local Similarity 100.0%; Pred. No. 1.6e-146;
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	QGGRRDGGPACGPGDLYFILDKSGSVLHHMNEIYYFVEQLAHKFIISPOLRMSFIYFST	60
DB	28	QGGRRDGGPACGPGDLYFILDKSGSVLHHMNEIYYFVEQLAHKFIISPOLRMSFIYFST	87
QY	61	RGTTLMKLTEDREQIROGLEELQKVLPGDVTYMHGFERASEQIYYENRQGYRTASVIA	120
DB	88	RGTTLMKLTEDREQIROGLEELQKVLPGDVTYMHGFERASEQIYYENRQGYRTASVIA	147
QY	121	LTDGELHBDLFFYSEERANRSRDIGAIYVCVGVDFNETQLARIADSKDHFPPVNDGFOA	180
DB	148	LTDGELHBDLFFYSEERANRSRDIGAIYVCVGVDFNETQLARIADSKDHFPPVNDGFOA	207
QY	181	LOGIHSILKKSCTEILAAEPSTICAGBSFOVVVRGNGFRHARVDRVLCSEFKINDSVTL	240
DB	208	LOGIHSILKKSCTEILAAEPSTICAGBSFOVVVRGNGFRHARVDRVLCSEFKINDSVTL	267
QY	241	NEKPFVSDTYLLCPAPILKEVGKKAALQVSMNDGLSFISSVIITTHCS	291
DB	268	NEKPFVSDTYLLCPAPILKEVGKKAALQVSMNDGLSFISSVIITTHCS	318

Search completed: December 14, 2005, 11:59:00
 Job time : 89.4385 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 14, 2005, 11:18:48 ; Search time 4.30595 Seconds

(without alignments)
458.218 Million cell updates/sec

Title: US-09-970-076-2_COPY_28_320

Perfect score: 1526
Sequence: 1 QGGRREDGCGACGCGFDLYF.....DGLSFSSSVITTHCSDC 293

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 51441 seqs, 6734002 residues

Total number of hits satisfying chosen parameters: 51441

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

Published Applications AA New:
1: /cgn2_6/p/codata/1/pubpaa/US09_NEW_PUB.pep:*
2: /cgn2_6/p/codata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/p/codata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/p/codata/1/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/p/codata/1/pubpaa/PCr_NEW_PUB.pep:*
6: /cgn2_6/p/codata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/p/codata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/p/codata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1526	100.0	564	US-11-186-284-199	Sequence 199, App
2	145.5	9.5	1152	US-11-080-026-4	Sequence 4, Appl
3	131	8.6	3063	US-11-186-284-26	Sequence 26, Appl
4	113.5	7.4	739	US-11-057-047-2	Sequence 2, Appl
5	113.5	7.4	764	US-11-057-047-1	Sequence 1, Appl
6	113.5	7.4	798	US-10-821-234-1034	Sequence 1034, App
7	113.5	7.4	915	US-10-131-826A-294	Sequence 294, App
8	113.5	7.4	956	US-11-113-424-39	Sequence 39, Appl
9	111	7.3	1141	US-10-601-368-24	Sequence 24, Appl
10	111	7.3	1166	US-10-601-368-22	Sequence 22, Appl
11	111	7.3	1188	US-10-601-368-21	Sequence 21, Appl
12	110.5	7.2	761	US-11-057-047-6	Sequence 6, Appl
13	107	7.0	1141	US-10-601-368-6	Sequence 6, Appl
14	107	7.0	1166	US-10-601-368-4	Sequence 4, Appl
15	107	7.0	1188	US-10-601-368-3	Sequence 3, Appl
16	107	7.0	1188	US-11-000-463-338	Sequence 338, App
17	107	7.0	1188	US-11-000-463-810	Sequence 810, App
18	104.5	6.8	828	US-10-995-561-983	Sequence 983, App
19	104.5	6.8	918	US-10-995-561-981	Sequence 981, App
20	104.5	6.8	1019	US-10-995-561-982	Sequence 982, App
21	103.5	6.8	182	US-10-601-368-25	Sequence 25, Appl
22	100	6.6	678	US-11-102-240-34	Sequence 34, Appl
23	99.5	6.5	182	US-10-601-368-7	Sequence 7, Appl
24	95.5	6.3	1179	US-11-097-125-1	Sequence 1, Appl
25	95.5	6.3	1196	US-10-995-561-921	Sequence 921, App

26	95	6.2	1167	US-11-097-125-2	Sequence 2, Appl
27	94	6.2	353	US-11-137-465-44	Sequence 44, Appl
28	94	6.2	448	US-11-137-465-45	Sequence 45, Appl
29	91.5	6.0	627	US-10-467-657-5432	Sequence 5432, App
30	91	6.0	1167	US-10-601-368-18	Sequence 18, Appl
31	82	5.4	1062	US-11-137-465-43	Sequence 43, Appl
32	81	5.3	1804	US-10-513-786-2	Sequence 2, Appl
33	81	5.3	3704	US-10-513-786-1	Sequence 1, Appl
34	79.5	5.2	904	US-10-510-386-158	Sequence 5, Appl
35	77.5	5.1	319	US-10-793-626-1040	Sequence 1040, App
36	77.5	5.1	415	US-10-763-712A-25	Sequence 25, Appl
37	77.5	5.1	426	US-10-763-712A-5	Sequence 5, Appl
38	76	5.0	469	US-10-467-657-4370	Sequence 4370, App
39	75.5	4.9	1933	US-10-523-912-2	Sequence 2, Appl
40	74	4.8	384	US-10-510-386-158	Sequence 158, App
41	74	4.8	509	US-10-793-626-2880	Sequence 2880, App
42	74	4.8	619	US-10-999-886-3	Sequence 3, Appl
43	74	4.8	640	US-10-999-886-4	Sequence 4, Appl
44	73.5	4.8	5935	US-10-595-561-776	Sequence 776, App
45	73	4.8	264	US-10-793-626-388	Sequence 388, App

ALIGNMENTS

RESULT 1
US-11-186-284-199
; Sequence 199, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangt
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John B.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MEMO1-029P2RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-199

Query Match 100.0%; Score 1526; DB 7; Length 564;
Best Local Similarity 100.0%; Pred. No. 6.8e-135;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGGRREDGCGACGCGFDLYFILDKSGSVLHNMNIYYFVEQLAKFTISPOLRMSFIVFST 60
DB 28 QGGRREDGCGACGCGFDLYFILDKSGSVLHNMNIYYFVEQLAKFTISPOLRMSFIVFST 87
QY 61 RGTTLMLKLTDRDROIQGLBELQKLPFGGTTYHBSGFEARSQIYYENRGYTTASVITA 120
DB 88 RGTTLMLKLTDRDROIQGLBELQKLPFGGTTYHBSGFEARSQIYYENRGYTTASVITA 147
QY 121 LTTGELHEDLFFYSEREARNSRDLGAIYVCVGVKDFNETQTLARIADSKDHVPVNDGFOA 180


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: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: SeqSrv for Windows Version 3.0
: SEQ ID NO 24
: LENGTH: 1141
: TYPE: prt
: ORGANISM: Mus musculus
: OS-10-601-368-24

```

Query Match	7.3%	Score 111;	DB 6;	Length 1141;
Best Local Similarity	24.1%;	Pred. No. 0.018;		
Matches 49;	Conservative 28;	Mismatches 88;	Indels 36;	Gaps 9;

OY 12 CYGAFDLKFLDKSGSVLHHNMEYYFVQLANRE-ISP-QLRNSPIVSTRGTMLMKT 69
 | || | | | | | | | | |
DB 159 CQRTMDIYVLDDGSNST-YRWVEQHFLNLILKKFYIGEGQIQVGIVQXGEDAVHNEPIL- 216

OY 70 EDEEQIGCLEELQKLVFGSDTYMHGFE--RASEQIYYENRGQRATSVIIILTDGEL 126
:::|::|:
Db 217 NDVRSVKQVEADSHIEGRGTERTAFGLGFARSEAFQGGKRGAQ--KVMIYITDGS 274

OY 127 HED-----LPFXSEREARRSRDLGAIYVCVGD----FNEHQ 160
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 275 HDSPDLEKIVROSEKDNTRYAVAVLGYNNRRGINPETLINEIKTIAASPDDDKGFENNVD 334

Oy	161LARIADSKDHVFVNDFGALOG	183
	: : : :	
Dd	335 EAAL---KDVIDALGDRIFSLEG	354

[illegible]

```

; Sequence 22 Application US/10601368
; Publication No. US20050260702A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Pan, Yang
;
; ADDRESSEE: TONG M

```

FILE REFERENCE: 0734-275001
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/601,368
CURRENT FILING DATE: 2003-05-21

PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRTING DATE: 2000-05-26

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; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PairedSeq for Windows Version 3.0
; SEQ ID NO. 22
; LENGTH 1166

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!      TYPE: PRT
!      ORGANISM: Mus musculus
US-10-601-368-22

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Query Match 7.3%; Score 111; DB 6; Length 1166;
Best Local Similarity 24.1%; Pred. No. 0.019;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

QY 12 CYG GFDL F E I L D S G S V L H M N E I Y Y F E A O L A H R F - I S P - Q L R S S F I V S T R G T L M K Y T 69
Db 137 C Q Y M D I Y I V L D S G S N S I - Y P W E V Q H F L N I L K K F Y I G G Q I Q V G I V Q X G E D A V H E F H L - 194

Cy 70 EDEQIRGLEEEQKVLFGSDTVNHEGFE--RASEQIYVENYNGQRTASVIALTDGEL 126
 :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
 Db 195 NDYRSVKDVEAASHIEQRGCTERTRTAFGIEFARSEAFQCGRRGAK--KVMILVITDDGS 252

QY 127 HED-----LFFSERENRSRLGAIYCVGVKD-----FNEEQ 160
 Db 253 HSDPDLKAVIRSEKDNVTRYAVAVLGYYNRGIRNPEFTLNEIKYIASPDDKHFFNVTD 312

Oy	161 LARIADSKDHVPVNDGFOALOG	183
	: :	
	: :	
Db	313 BAAL--KDVIDALGDRIEFLSLEG	332

RESULT 11
US-10-601-368-21
; Sequence 21, Application US/10601368
; Publication No. US20050260702A1
: GENERAL INFORMATION:

; APPLICANT: Pan, yang
 ; APPLICANT: Lora, Jose M.
 ; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
 ; FILE REFERENCE: 07334-275001

;; CURRENT APPLICATION NUMBER: US/10/601,368
;; CURRENT FILING DATE: 2003-06-23
;; PRIOR APPLICATION NUMBER: US/09/561,263A
;; PRIOR FILING DATE: 2000-04-27

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;
; PRIOR APPLICATION NUMBER: US 09/322,790
;
; PRIOR FILING DATE: 1999-05-28
;
; NUMBER OF SEQ ID NOS: 40
;
; SOFTWARE: FastSeq for Windows Version 3.0

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: SEQ ID NO 21
:
: LENGTH: 1188
:
: TYPE: PRT
:
: ORGANISM: Mus musculus
:

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; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1) ... (22)
US-10-601-368-21

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Query Match	7.3%	Score 111	DB 6	Length 1168
Best Local Similarity	24.1%	Pred. No. 0.019		
Matches 49:	Conservative	28	Mismatches	88
			Indels	38
			Gaps	9

QY 12 CYGGFDLYFLDCKSGSVLHMHNEIYYFVEQLAHKE-1SD-QLRMSPIVESTGRTTLMKLT 69

DB 159 CQRYMDIVVLDCGNSI-YPVMEVOHFLNLTKKFYIGGGQIOVGIVOGEDAVAHFHL-216

Qy 70 EDDEQIROGLLELOKVLPEGGDTYHGEFE--RASEQIYYENRGQRTASVIALTDGEL 126
 ::: -:-
Db 217 NDYRSVKUVEASHIEORGTETRTAFGLEPASEAFOGKRGAOK--KVMIVTLDGES 274

QY 127 HED-----LFPYSEREANRRSDLGAIYVCVQVD-----ENETQ 160

Db 275 HSDPDLKIVROSEKDNTRYAVAVLVGYNRRGINPETFNEIKIASDPDDKHFNTD 334

QY 161 LARIADSKDHVPVNDGFQALQG 183
| : ||| : : ||
Db 335 EAAL--KDIVDALGDRIFSLEG 354

RESULT 12
US-11-057-047-6

```

; sequence 6, Application US/1105/04/
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon

```

APPLICANT: Inurman, Jossaba
APPLICANT: Taube, Christian
APPLICANT: Gelfand, Erwin
APPLICANT: Gilkeson, Gary

FILE REFERENCE: 2848-66
CURRENT APPLICATION NUMBER: US/11/057,047
TITLE OF INVENTION: Methods Related Thereto
TITLE OF INVENTION: Immunoblot of Factor B, the Alternative Complement Pathway and
TITLE OF INVENTION: Immunoblot of Factor B, the Alternative Complement Pathway and

```

; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239

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; PRIOR FILING DATE: 2004-12-14
 ; PRIOR APPLICATION NUMBER: US04/015040
 ; PRIOR FILING DATE: 2004-05-13
 ; NUMBER OF SEQ ID NOS: 6

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; SOFTWARE: PARENCHIM VERSION 3.3
; SEQ ID NO 6
; LENGTH: 761
; TYPE: PRT

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: ORGANISM: Mus musculus
US-11-057-047-6

Query Match      7.2%; Score 110.5; DB 7; Length 761;
Best Local Similarity 20.5%; Pred. No. 0.011;
Matches 71; Conservative 59; Mismatches 99; Indels 117; Gaps 20

QY      1  QGGRREDG-----GPACYGCDLYFILDKSGSV-----LHHNNEY 36
DB      240  EGADAEDEHSPGEOQKRKIVLDPS--GSMNIIYLVLDGSDISSNFTGAKRCITN-----292

QY      37  YFVEOLAKHFISPOLRMSRIVPSTGTTLMKLTDR-----EQIQGLELOKVLRG 88
DB      293  -LIEKVAIYGVNR--RYGLITVATPKVLVRSDESSADADWTEKLNISYEDHKLKSG 349

QY      89  GDTVAHGESFERASEQIYY-----ENRQY-RTASVIALTLDGELH-----EDL 130
DB      350  TNT-----KRLQAVYSMMWSAGADARPFGGMKRTIRVILIIMTDG-LHNNGNPVYIYDI 402

QY      131  FFYSB-REANRSRD-LGAIYCYG--VKDENETOLARIADSKOHFVPVNDGFOALGI 184
DB      403  RALLDIGRDKNPRREDYLDVVYFGVGLPVDVSNINNALASKDNENHVFVKD-MEDLENY 461

QY      185  IHSIIKSCIEFLAABPSTTCAGESEQVYVVRKNGGFHAAVNDRVLSFKINDSVTLANEP 244
DB      462  FYQMIDET-----KSLSLC-----GWVEHKKGNDYHKQPOAKISVT---RP 501

QY      245  FSVEDTYLLCPAPILKEVGMKALQVSNMNDGSLFISSVYIITTHC 290
DB      502  LKHET---CMGAV-----VSEYFVLTAHC 524

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RESULT 13
US-10-601-368-6
/ Sequence 6, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 6
/ LENGTH: 1141
/ TYPE: prt
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: (1)...(22)
US-10-601-368-6

Query Match          7.0%; Score 107; DB 6; Length 1141;
Best Local Similarity 24.1%; Pred. No. 0.043;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9

QY      12  CYGGEFLVYILDKSGSVLHMHNEIYVFEQLAHKF-ISP-QLRMSFVETRGTTMLKLT 69
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB      159  CQYWDIVDIVLQGSNSI-YPMVEVQHFILNLIKFFITGPGQIQVGVOGEDVHEFHL- 216
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY      70  EDREQIRQLEELQKVLPGGDIYMHGFE---RASQIYYENKQGYRTASVIALTDEL 126
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB      217  NDYRSKDVVEASHIEQGGTETRTAFGIEFARSEAFQGRKGAK--KVMIVTDGES 274
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY      127  HED-----LFFYSERLANSRDGLAIVYCVGVKD---FNETQ 160
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB      275  HOSPDLKVIQOOSERDNTYRAVAVLGYNNRGINETETLNELKYLASDPDDKHFFNVTD 334

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Oy      161 LARIADSKOHVFPVNGFOALOG 163
Db      335 EAPL--KDIVDALGDRIFSLEG 354

RESULT 14
US-10-601-368-4
Sequence 4, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lora, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-215001
CURRENT APPLICATION NUMBER: US/10/601,368
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 1166
TYPE: PRT
ORGANISM: Homo sapiens
US-10-601-368-4

```

```

Query March 7.0%; Score 107; DB 6; Length 1166;
Best Local Similarity 24.1%; Pred. No. 0.044;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

Oy 12 CYGFFDLVFLIDKSGSLVHMHNEIYYVEQLAKRF-ISP-QLRMSFVFSRGTITMLKT 69
Db 137 CQYIMDIIVLIDGSSNI-YPMVEVQHLINILKKFYIGPGIIGVGVGGEDVVEHFLL- 194
Oy 70 EDREQIQSGLELQKVPFGCDTYVHGSEFE---RASEQIYYENRQGYRTASVIALTDGEL 126
Db 195 NDYNSVDDVYEAASHIQRGSTERTRTAFGLEPANSFAFGKGRGAK--KMIIVITDGES 252
Oy 127 HED-----LFFYSERANRSDLCATYYCVGKD---FNETQ 160
Db 253 HDSPLDKVIOQSERDNYTRVAVALGYNRRGINPETFLINEIKYIASDPDDKGFENVTD 312
Oy 161 LARIADSKDHVPVNDGFOALOG 183
Db 313 EAL---KDIYDALGDRIFFSLGG 332

RESULT 15
US-10-601-368-3
; Sequence 3, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 0734-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1188
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL

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LOCATION: (1) ... (22)
US-10-601-368-3

Query Match 7.0%; Score 107; DB 6; Length 1188;
Best Local Similarity 24.1%; Pred. No. 0.045;
Matches 49; Conservative 28; Mismatches 88; Indels 38; Gaps 9;

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QY 12 CYGGEFDLYFTIDKSGSVLHMHNEIYYFVEOLAHKF-ISP-QLRMSPFVFSRGTTLMKLT 69
    |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 159 CQYMDIVIVLDGNSI-YFWVEVQHFLINILKKFYIGPGQIQGVVQYGEDVVEHFL- 216
    |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 70 EDREQIRQGLEBELQKVLPGSDTYMHGFE--RASEQIYYENROGYRTASVYIALTDGEL 126
    |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 217 NDYRSVNDVVEAASHIEQRGETETRTAFGIEPARSEAFQKGRKAK--KMIIVITDGS 274
    |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 127 HED-----LFFYSERANRSDLGAIYVCVKD---FNETQ 160
    |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 275 HDSPDLKVIQOQSERDNTRYAVAVLGYNNRGINPETFLNEIKYIASDPDDKHFFVTTD 334
    |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 161 LARIADSKDHVPVNDGFOALQG 183
    |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 335 EAL--KDIYDALGDRIFSLDG 354
    |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

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Search completed: December 14, 2005, 11:59:28
Job time : 5.30595 secg

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_pgm model

Run on: December 18, 2005, 07:01:37 ; Search time 205.707 Seconds
(without alignments)
2531.884 Million cell updates/sec

Title: US-09-970-076-2_COPY_28_320

Perfect score: 1526
Sequence: 1 OGGRRRDGPGACGCGFDLYF.....DGLSFSSVITTHCSDG 293

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/usftp0.epool/US09970076/runat_14122005_111850_20999/app_query.fasta_1.2410
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-LOOEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=pc -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTMT=pc -NOEM=ext -HEAPSIZE=500 -MTLEN=0 -MAXLEN=200000000
-USR=US09970076.QCGN_1.1535.runtat_14122005_111850_20999 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/68.COMB.seq:*
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7: /cgn2_6/ptodata/1/ina/PP.COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE.COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1257	82.4	1609	3	US-09-620-312D-8
2	786	51.5	2234	3	US-10-104-047-669
3	709	46.5	1492	3	US-09-774-528-297
4	709	46.5	1492	3	US-10-120-988-297
5	658	43.1	3981	3	US-09-789-451-250
6	166	10.9	3519	2	US-08-286-889-45
7	166	10.9	3519	2	US-08-485-618-45
8	166	10.9	3519	2	US-08-362-652-45
9	166	10.9	3519	2	US-08-605-672-45

10	166	10.9	3519	2	US-08-482-293A-45	Sequence 45, Appl
11	166	10.9	3519	2	US-08-943-363-45	Sequence 45, Appl
12	166	10.9	3519	3	US-09-193-043-45	Sequence 45, Appl
13	166	10.9	3519	3	US-09-688-307A-45	Sequence 45, Appl
14	166	10.9	3519	3	US-09-350-259-45	Sequence 45, Appl
15	166	10.9	3803	2	US-08-485-618-52	Sequence 52, Appl
16	166	10.9	3803	2	US-08-362-652-52	Sequence 52, Appl
17	166	10.9	3803	2	US-08-605-672-52	Sequence 52, Appl
18	166	10.9	3803	2	US-08-482-293A-52	Sequence 52, Appl
19	166	10.9	3803	2	US-08-943-363-52	Sequence 52, Appl
20	166	10.9	3803	3	US-09-193-043-52	Sequence 52, Appl
21	166	10.9	3803	3	US-09-688-307A-52	Sequence 52, Appl
22	166	10.9	3803	3	US-09-350-259-52	Sequence 52, Appl
23	159.5	10.5	3528	2	US-08-286-889-36	Sequence 36, Appl
24	159.5	10.5	3528	2	US-08-485-618-36	Sequence 36, Appl
25	159.5	10.5	3528	2	US-08-362-652-36	Sequence 36, Appl
26	159.5	10.5	3528	2	US-08-605-672-36	Sequence 36, Appl
27	159.5	10.5	3528	2	US-08-482-293A-36	Sequence 36, Appl
28	159.5	10.5	3528	2	US-08-943-363-36	Sequence 36, Appl
29	159.5	10.5	3528	3	US-09-193-043-36	Sequence 36, Appl
30	159.5	10.5	3528	3	US-09-688-307A-36	Sequence 36, Appl
31	159.5	10.5	3528	3	US-09-350-259-36	Sequence 36, Appl
32	159.5	10.5	3528	2	US-08-485-618-54	Sequence 54, Appl
33	159.5	10.5	3528	2	US-08-362-652-54	Sequence 54, Appl
34	159.5	10.5	3528	2	US-08-605-672-54	Sequence 54, Appl
35	159.5	10.5	3528	2	US-08-482-293A-54	Sequence 54, Appl
36	159.5	10.5	3528	2	US-08-943-363-54	Sequence 54, Appl
37	159.5	10.5	3528	3	US-09-193-043-54	Sequence 54, Appl
38	159.5	10.5	3528	3	US-09-688-307A-54	Sequence 54, Appl
39	159.5	10.5	3528	3	US-09-350-259-54	Sequence 54, Appl
40	156	10.2	2499	2	US-08-485-618-96	Sequence 96, Appl
41	156	10.2	2499	2	US-08-605-672-96	Sequence 96, Appl
42	156	10.2	2499	2	US-08-482-293A-96	Sequence 96, Appl
43	156	10.2	2499	2	US-08-943-363-96	Sequence 96, Appl
44	156	10.2	2499	3	US-09-193-043-96	Sequence 96, Appl
45	156	10.2	2499	3	US-09-688-307A-96	Sequence 96, Appl

ALIGNMENTS

RESULT 1
US-09-620-312D-8
; Sequence 8, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungang
; APPLICANT: Wang, Duntui
; APPLICANT: Wang, Zhilwei
; APPLICANT: John Thilghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic acids and
; POLYPEPTIDES
; FILE REFERENCE: 784CIP28
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_fl_genes Version 1.0

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/ SEQ ID NO 8
/ LENGTH: 1609
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (309)..(1202)
US-09-620-312D-8
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Alignment Scores:

Pred. No.:	5.03e-153	Length:	1609
Score:	125.90	Matches:	240
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	99.17%	Mismatches:	0
Query Match:	82.37%	Indels:	0
DB:	3	Gaps:	0

US-09-970-076-2_COPY_28_320 (1-293) x US-09-620-312D-8 (1-1609)

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QY 1 GlnGlyArgArgGluAspGlyGlyProAlaCysTyrGlyGlyPheAspLeuTyrPhe 20
DB 390 CAAAGGGGACGCGAGGAGATGGGGGTCCAGCTGCTACGGCGGATTGACCTGACTTC 449
QY 21 IleLeuAspLysSerGlySerValIleuHisTyrAsnGluIleTyrTyrPheValGlu 40
DB 450 ATTTGGACAAATCAGAAAGTGTGCTSCACCACTGGAAATGAAATCTATTCTTTGGAA 509
QY 41 GlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSerPheIleValPheSerThr 60
DB 510 CAGTTGGCTCACAATTGATCAGCCCAAGTTGAGAAATGCTTTATTTGTTTCTCCACC 569
QY 61 ArgGlyThrThrLeuMetLysLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGlu 80
DB 570 CGAGGAACAACCTTAAGAACTGACAGAAACAGAAACAAATCCCTCAGGCTTAGAA 629
QY 81 GlnLeuGlnLysValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgAla 100
DB 630 GAACCTCAGAAAGTTCTGCAGAGGAGACACTTACATGATGAAAGATTGAAAGGGCC 689
QY 101 SerGlnGlnIleTyrTyrGluAspArgGlnGlyTyrArgThrPheValIleIleAla 120
DB 690 AGTGAAGAGATTTATTTATGAAAACAGCAAGGGTACAGACAGCCAGCTCATCTGCT 749
QY 121 LeuThrAspGlyGluLeuHisGluAspLeuPheTyrSerGluArgGluAlaAspArg 140
DB 750 TTGACTGATGAGAACTCCATGAAGATCTTTTTCATTACAGAGGAGGCTTAATAG 809
QY 141 SerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAspPheAsnGluThrGln 160
DB 810 TCTCGAGATCTTGCGAATTTGTTTACTGTGTGTGTGAAGATTTCATATGAGACACAG 869
QY 161 LeuAlaArgGluIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAla 180
DB 870 CTGGCCCGGATTTGGAGCAAGTAAAGATCATGTGTTTCCCTGAATGACGGCTTTCAGGCT 929
QY 181 LeuGlnGlyIleIleHisSerIleLeuLysSerCysIleGluIleLeuAlaAlaGlu 200
DB 930 CTGCAAGGCATCATCTCCATATTTTGAAGAAGCTCTGCATCGAAATTTCTAGCAGCTGAA 989
QY 201 ProSerThrIleCysAlaGlyGlySerPheGlnValValAlaArgGlyAsnGlyPheArg 220
DB 990 CCATCCACCATATGTGACAGAGAGTCAATTCAGATTGTCTGAGAGAGAAACGGCTTCGGA 1049
QY 221 HisAlaArgPheAspValAspArgValLeuCysSerPheLysIleAsnAspSerValThrLeu 240
DB 1050 CATGCGCGCAATGTGGAAGAGGCTCTCTGACGTTCAAGATCAATGACTGCTCACATC 1109
QY 241 AsnGlu 242
DB 1110 AGTAAAG 1118
RESULT 2
US-10-104-047-669
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/ Sequence 669, Application US/10104047
/ Patent No. 6943241
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: NO. 6943241el full length cDNA
/ FILE REFERENCE: H1-A0105
/ CURRENT APPLICATION NUMBER: US/10/104,047
/ PRIOR FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER:
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 669
/ LENGTH: 2234
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-104-047-669
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Alignment Scores:

Pred. No.:	1.61e-91	Length:	2234
Score:	786.00	Matches:	153
Percent Similarity:	72.89%	Conservative:	54
Best Local Similarity:	53.87%	Mismatches:	75
Query Match:	51.51%	Indels:	2
DB:	3	Gaps:	1

US-09-970-076-2_COPY_28_320 (1-293) x US-10-104-047-669 (1-2234)

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QY 10 ProAlaCysTyrGlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeu 29
DB 637 CCTCCTCGAAGAAAGCCCTTGAATCTTACTTCTGCTGAGACAACTGGAGCTGTGGCA 696
QY 30 HisHisTyrAsnGluIleTyrTyrPheValGlnLeuAlaHisLysPheIleSerPro 49
DB 697 AATACTGATGTAATTAATTTATATTTCTGACACAACTTCGAGAGAGATTGTGACCCCT 756
QY 50 GlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThr 69
DB 757 GAATGAGATTTATCTTTCATATGTTGTTTCTCTCAAGCAATATATTTTGGCCATTAAT 816
QY 70 GluAspArgGlnGlnIleArgGlnGlyLeuGlnGlnLysValLeuProGlyGly 89
DB 817 GGAGACAGAGGCAAAATCAGTAAAGGCTTGAGGATTAAACGTTGATGTCAGTAGGA 876
QY 90 AspThrTyrMetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAspArg 109
DB 877 GAGACATATATCTCATAGAGACTAAAGCTAGCGCAATGAACTAATTT-----CAGAAAGCA 930
QY 110 GlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp 129
DB 931 GGAGCTTGAAAACTCCAGATATCATATATTTGCTCTGACAGATGGCAAGTTGACGGCTTG 990
QY 130 LeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeuGlnValIleValTyr 149
DB 991 GTGGCATCATATGACAGAAAGAGCAAGATATCCAGGTCACTTGAGGCTCATGTATTAT 1050
QY 150 CysValGlyValLysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAsp 169
DB 1051 TGTGTGTGTCTCTTATATTTTGAACAACAGCAGCTTGAAGAAATTCGATTTCCAAAGAG 1110
QY 170 HisValPheProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu 189
DB 1111 CAAATTTCCTCTGCAAGGTGATTTCAAGGCTCTTAAGAAATTAATTAATCTATATCTA 1170
QY 190 LysLysSerCysIleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGlySer 209
DB 1171 GCTCAGTCAATGTACTAATAATCCTAGAATTCAGGCTCAAGTGTCTGTGTGGGGAGGAA 1230
QY 210 PheGlnValValAlaArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeu 229
DB 1231 TTTCAGATTTGCTTAATGAGAGAGATTCATGCTGGCAGCTGGAATGCAAGTGTCTTC 1290
QY 230 CysSerPheLysIleAsnAspSerValThrLeuAsnGlnLysBProPheSerValGluAsp 249
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Db      1291 TGCACCTTACACTGTAATGMAACATATATCAACAGACTGTAAACACAGTAAGTACAGCTT 1350
Oy      250 ThTYrTLeuLeuCyAProAlaProIleLeuYsgIValGlyMetLysAlaAlaLeuGln 269
Db      1351 AATTCTAGCTTTGTGCTGCACACTTCTCGTAATAAAGCTGGAGAAACCTTGATGTTTCA 1410
Oy      270 ValSerMetAsnAspGlyLeuSerPheIleSerSerValIleIleThrThrHis 289
Db      1411 GTGAGCTTTAATGGAGAAATCTGTCTATTCAGGATCATTAATGTGCACGCCACAGAA 1470
Oy      290 CysSerAspGly 293
Db      1471 TGTTCAAAGG 1482

RESULT 3
US-09-774-528-297
; Sequence 297, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619e1 Nucleic Acids and
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pc_fl_genes Version 2.0
; SEQ ID NO 297
; LENGTH: 1492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79)..(1434)
US-09-774-528-297

Alignment Scores:
Pred. No.:      8,77e-82      Length:      1492
Score:          709.00      Matches:      139
Percent Similarity: 72.35%      Conservative: 52
Best Local Similarity: 52.65%      Mismatches: 71
Query Match:      46.46%      Indels:      2
DB:              3          Gaps:      1

US-09-970-076-2_COPY_28_320 (1-293) x US-09-774-528-297 (1-1492)

Oy      30 HnHtATPRAngGlnIleTYrTYrPheValGlnGlnLeuAlaHnLysPheIleSerPro 49
Db      16 AATACTGATGTAATTAATTATTAATTCGTACAGCAACTTCGCGAGAGATTTGTGAGCCCT 75
Oy      50 GlnLysArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetCysLeuThr 69
Db      76 GAAATGAGATTAATCTTCATGTCGTGTTCTTCTCAAGCAACATATTATTTTGCATTAACT 135
Oy      70 GlnAPRATsGlnGlnIleArgGlnGlyLeuGlnGlnLeuGlnLysValLeuProGlyGly 89
Db      136 GGAGACAGAGCGAAATATCAGTAAGGCTTGGAGGATTTTAAACCGTTAGTCCAGTACGA 195
Oy      90 AApThrTYrMetCnIGlnGlyPheGlnIArgAlaSerGlnGlnIleTYrTYrGlnuAnArg 109

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Db	196	GAACATATATTCATTAAGCACTAAAGCCTAGGAGTAAAGCAAAATT-----CAGAAAGCA	249
QY	110	gncgllytatrgrthralaservalllellaaleuthraerglygluleuניהגלואר	1299
Db	250	GGAGGCTTGAAACCTCCAGTATCATTAATTGCTGTGACAGATGGCAAGTTGGACGCTGTG	3099
QY	130	leupherheylseretlurgtlulalavnaugserlaryarlsuylalallevaltyt	1499
Db	310	GTGCATCATATTCAGAAAGAAAGGCAAGATATCTACAGTCACTTGGGGCTAAGTGTAT	3699
QY	150	CyevalglYalIyAsrPheanngluThrglnleulalagrlleaAspSerlyAsp	1699
Db	370	TGtGTtGGGCTCTTAATTTTGAACAAGCAGCAGCTTGAAGATTTGCTGATCCAAAGAG	4299
QY	170	HlaValPheProValAsnAspGlyPheGlnalaleugnglyllelhenlserlleu	1899
Db	430	CAAGTTTTCCTGTCAAAAGTGGATTTGAGGCTTTAAAGATTAATTAATTCATACTA	4899
QY	190	lyslAspSerCyglleuulleulalagluP-roserThrlleCyAlaGlyGluSer	2099
Db	490	GCTCAGTCAGTACTGTAATTCCTAGAAATTCAGCCCTCAATGTCTGTGGGGAGGAA	5499
QY	210	PheGlnValValAlaIrgGlyAsnGlyPheArgHlsAlaGsnValAspArgValIeu	2299
Db	550	TTTCAGATTTCTTAACTGAGAAAGAGATTCATGCTGGCAGTCCGAATGCGAGTGTCTC	6099
QY	230	CyAspSerPheValIleaAspSerValThrlleuAnngluY-ProPheSerValGluAsp	2499
Db	610	TGCACTTACACGTAAATGAACATATCAACAGATGTAACAGTAAACAGTAAAGTACAGCTT	6699
QY	250	ThrTyrlleuLeuCyAsProAlaProlleuylvgGluValGlyMetlyValAlaLeuGln	2699
Db	670	AATTCATGCTTTTGCTCCTCAGCTATCCGTGATTAAGCTGGAAGAACTTTGATGTTCA	7299
QY	270	ValSerMetAsnAspGlyLeuSerPheIleSerSerValIleIleThrThrHis	2899
Db	730	GTGAGCTTTAATGAGAGAAATGTGTCAITTTGAGATCAITTAATTTGTACAGCCACAGAA	7899
QY	290	CyAspSerAspGly 293	
Db	790	TGTTCTTAACGG 801	
RESULT 4			
US-10-120-988-297			
; Sequence 297, Application US/10120988			
; Patent No. 6919193			
GENERAL INFORMATION:			
; APPLICANT: Tang, Y. Tom			
; APPLICANT: Goodrich, Ryle			
; APPLICANT: Liu, Chenghua			
; APPLICANT: Ren, Feiyan			
; APPLICANT: Wang, Dunru			
; APPLICANT: Demanac, Radoje T			
; TITLE OF INVENTION: No. 6919193el Nucleic Acids and			
; FILE REFERENCE: 802CON			
; CURRENT APPLICATION NUMBER: US/10/120,988			
; PRIOR FILING DATE: 2002-04-11			
; PRIOR APPLICATION NUMBER: 09/774,528			
; NUMBER OF SEQ ID NOS: 441			
; SOFTWARE: pc_Fl_genes Version 2.0			
; SEQ ID NO 297_			
; LENGTH: 1492			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (79) .. (1434)			
US-10-120-988-297			
Alignment Scores:			

Pred. No.:	8.77e-82	Length:	1492
Score:	709.00	Matches:	139
Percent Similarity:	72.35%	Conservative:	52
Best Local Similarity:	52.65%	Mismatches:	71
Query Match:	46.46%	Indels:	2
DB:	3	Gaps:	1

US-09-970-076-2_COPY_28_320 (1-293) X US-10-120-988-297 (1-1492)

[illegible]

```

APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Xue, Aidong J.
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Ma, Yunding
APPLICANT: Yamazaki, Victoria
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Dunrui
APPLICANT: Yang, Yonghong
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Dmanac, Radoje T.
TITLE OF INVENTION: No. 678369e1 Nucleic Acids and
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pc_fl_genes Version 2.0
SEQ ID NO 250
LENGTH: 3981
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (297)..(1118)
US-09-799-451-250

Alignment Scores:
Pred. No.: 1,84e-74 Length: 3981
Score: 658.00 Matches: 128
Percent Similarity: 100.00% Conserved: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 43.12% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-2_COPY_28_320 (1-293) x US-09-799-451-250 (1-3981)

Oy 166 AppSerLyAspHisValPheProValAspGlyPheGlnAlaLeuGlnGlyLeIle 185
Db 3 GAGAGTAAGATCACTGTCTTCCCGTAATACCGCTTCAGCGCTCGCAAGCATATC 62
Oy 186 HisSerIleLeuLysLysSerCysIleGlnIleLeuAlaGlnProSerThrIleCys 205
Db 63 CACTCAATTTTGAAGAGCTCGCATCGAAATTTCTAGACGTGAACCATCCACCATATGT 122
Oy 206 AlGlyGlnSerPheGlnValValAlaArgGlyAsnGlyPheAsnGlnAlaArgAsnVal 225
Db 123 GCGAGAGATCATTTTCAGTTGTCGTGAGAGGAAACGGCTTCCAGCATGCCCGAACGTG 182
Oy 226 AspArgValLeuCysSerPheLysIleAsnAspSerValThrLeuAsnGlnLysPProPhe 245
Db 183 GAGAGGATCTCTCGACGCTTCAAGATCAATGACTCGTCACATCAATGAGAGCCCTTT 242
Oy 246 SerValGlnAspThrTyIleLeuLeuCysAspProAlaProIleLeuLysGlnValGlyMetLys 265
Db 243 TCTGTGGAAGATACCTATTATTACTGTGTCGAGGCTTATTAAGAAAGTTGGCATGAAA 302
Oy 266 AlAlAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIleSerSerSerValIleIle 285
Db 303 GCTGCACTCCAGGTGAGCATGAACATGAGCCCTCTTTATCTCCAGTTCGTGTCATCATC 362
Oy 286 ThrThrThrHisCysSerAspGly 293
Db 363 ACCACCAACACACTGTTCTGACGCT 386

RESULT 6
US-08-286-889-45
; Sequence 45: Application US/08286889
; Patent No. 5470953

```

```

: GENERAL INFORMATION:
: APPLICANT: Gallatin, W. Mich
: APPLICANT: Van der Vlieten, Monica
: TITLE OF INVENTION: No. 5470935el Human 2 Integrin Alpha Subunit
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Garstein, Murray & Borum
: STREET: 233 South Wacker Drive, 6300 Seear Tower
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/286,889
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/173,497
: FILING DATE: 23-DEC-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Williams Jr., Joseph A.
: REGISTRATION NUMBER: P38,659
: REFERENCE/DOCKET NUMBER: 27866/32168
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-474-6300
: TELEFAX: 312-474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3519 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 52..3519
: US-08-286-889-45

Alignment Scores:
Pred. No.: 1,54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.88% Indels: 30
DB: 2 Gaps: 12

US-09-970-076-2_COPY_28_320 (1-293) x US-08-286-889-45 (1-3519)
QY 10 ProAlaCyATrGly---GlyPheAPLeuTYrPheLeuAPLeuSerySerVal 28
Db 481 CCAAGAGTGTCCAGAGACAAAGATGACATTGCTTCTCTGATGATGAGCTCCGGACAGATT 540
QY 29 ---LeuHstHstPheHngLuiLeTYrTYrPheValGluInLeuAlHLePheLe 47
Db 541 GATCAAAAGTACTTTTCCCAAGATGAAGAGACTTCCTCAAGCTTTGATGGCCAGTTGGCG 600
QY 48 SerProGlnLeuArygMetSerPheLeValPheSerThrArgLYrThrThLeuMetLys 67
Db 601 AGCAGCCAGCACTTCGTTCTCCCGATGCAATACTCAAACTCTGAAGACTCATTTTACC 660
QY 68 LeuThrGluAphArg-----GluGlnIleArgGlnGlyLeuGluGluLeu 82
Db 661 TTCACGGAAATTCAAGAGACAGACCTGAGCCCTCAGAGAGCTGGATGATGCATGTCACGCTC 720
QY 83 GlnIlyValLeuProGlyGlyAphTrTYrMetHsIsgIuGlyPheGluArgAlaSerGlu 1020
Db 721 CAA-----GGCTGAGAGTACACAGAGCTGGGGATCCAGAAAGTGATGAA 765

```

```

OY      103  GlnIleTyrTyrGluAsnArgGlnGlyTyrXrghrNla-----SerValIleIleAlaLeu 121
Db      766  GAGCTATTTCCTACCAAGATGCGGCGCCGAAAAGTGCACAAAGATACTATTGTCTATC 825
OY      122  ThrAspGlyGluLeuHISgluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsn 139
Db      826  ACAGATGGCGAGAAATTCAGAGACCCCTCGAGTATGACATGTCATCCCTGAAGCAGAG 885
OY      140  ArgSerArgAspLeuGlyAlaIleValIleTyrCysValGlyValIlyAsp---PheAsnGlu 158
Db      886  AAACCT-----GGGATCATTCGCTATGCTATTAGAGGGGGGAGATGCTTCGGGAA 936
OY      159  ---ThrgluAlaArgIle-----AlaAspSerIlyAspHisValPhe 172
Db      937  CCCATGCGCTACAGAGACTGTAACAACCATTCGCTCACTCCCTCGCAGACCATGTTTC 996
OY      173  ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIlySer 192
Db      997  AAGGTGGGCAAT---TTGTGTGCACTTCGACGATCCAGCGGCAAAATTCAGAGAA--- 1050
OY      193  CysIleGluIleLeuAlaAlaGluPProSerThrIleCysAlaGlyGluSerPheGlnVal 212
Db      1051  -----ACCTTTCGCATTGGAAGAACCAACATCAAGATCAAGTACTCTTCCTTACAGCAC 1101
OY      213  ValValaArgGlyAsnGlyPheArgHisAlaAlaGAsnValaAsp 226
Db      1102  GAGATGTCACAAAGGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 7
US-08-485-618-45
; Sequence 45, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vaeren, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,618
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32797
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:

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Db 721 CAA-----GGCCACGCTACACAGCTCGGGCATCCAGAAAGTGTAA 765
Qy 103 GlnleTyTgTgUaAaTgGnglyTyArgThraA---SerVallelleAlaLeu 121
Db 766 GAGCTATTTCACCAAGAAATGGGCCCCGAAAGTGTCAAGAAAGTCAATTCATC 825
Qy 122 ThrAspGlyGluLeuHlsGluAspLeuPhePheTySerGlu-----ArgGluAlaAsn 139
Db 826 ACAGATGGCGAAGAAATTCAGAGACCCCTGGAGTATAGCATTCATCCCTGAAGCGAG 885
Qy 140 ArgSerArgAspLeuGlyAlaAlaValTyTyCyValGlyValysAsp---PheAsnGlu 158
Db 886 AAAGCT-----GGGATCATTCGCTATGCTATAGGGGGGAGATGCTCCGGGAA 936
Qy 159 ---ThrGlnLeuAlaArgIle-----AlaAspSerTyAspPheValPhe 172
Db 937 CCCACTGCCCTACAGAGCTGACACCATTCGCTCAGCTCCCTCCGACGACCATGTTTC 996
Qy 173 ProValAsnAspGlyPheGlnAlaLeuGnglyIleIleHisSerIleLeuTyAspSer 192
Db 997 AAGTGGGCAAT---TTTGATGACCTTCGACATCCAGCGGCAAAATTCAGAGAAA--- 1050
Qy 193 CysIleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 212
Db 1051 -----ATCTTGCCATTGAAAGAAACCAAGTCAAGTCAAGTCTCTTTCAGACAC 1101
Qy 213 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 226
Db 1102 GAGATGTACAGAAAGTTTCAGCTCAGCTCTCAATGAT 1143

RESULT 9
US-08-605-672-45
; Sequence 45, Application US/08605672
; Patent No. 5817515
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Seair Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,672
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856

```

```

; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3519 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 52..3519
; US-08-605-672-45

Alignment Scores:
Pred. No.: 1,54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.88% Indels: 30
DB: 2 Gaps: 12

US-09-970-076-2_COPY_28_320 (1-293) x US-08-605-672-45 (1-3519)

Qy 10 ProAlaCyAspTyGly---GlyPheAspLeuTyPheIleLeuAspTySerGlySerVal 28
Db 481 CCAAGATGTCCAGAGCAAGAGATGACATTCCTTCTGATGATGAGCTCCGGCAGCAT 540
Qy 29 ---LeuHisIleStrPheGnglyIleTyTyPheValGluGlnLeuAlaHisPheIle 47
Db 541 GATCAAGATGACCTTCCAGATGAAAGACCTTGTCMAAGCTTGTATGGCGAGTTGGCG 600
Qy 48 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 67
Db 601 AGCACAGACACCTCGTTCTCTCCATGATCAATCTCAACACTCTGAAGACTCTTTTACC 660
Qy 68 LeuThrGluAspArg-----GluGlnIleArgGnglyLeuGnglyLeu 82
Db 661 TTCACGGAATTCAGAGACAGCTGAGCCCTCAGAGCTGAGTGCATGCTGCAGCTC 720
Qy 83 GlnIleValLeuProGlyGlyAspThrTyTyMetHisGluGlyPheGluAlaSerGlu 102
Db 721 CAA-----GGCCCTGACGTACACAGCTCGGCAATCCAGAAAGTGTAA 765
Qy 103 GlnIleTyTgTgUaAaTgGnglyTyArgThraA---SerVallelleAlaLeu 121
Db 766 GAGCTATTTCACCAAGAAATGGGCCCCGAAAGTGTCAAGAAAGTCAATTCATC 825
Qy 122 ThrAspGlyGluLeuHlsGluAspLeuPhePheTySerGlu-----ArgGluAlaAsn 139
Db 826 ACAGATGGCGAAGAAATTCAGAGACCCCTGGAGTATAGCATTCATCCCTGAAGCGAG 885
Qy 140 ArgSerArgAspLeuGlyAlaAlaValTyTyCyValGlyValysAsp---PheAsnGlu 158
Db 886 AAAGCT-----GGGATCATTCGCTATGCTATAGGGGGGAGATGCTCCGGGAA 936
Qy 159 ---ThrGlnLeuAlaArgIle-----AlaAspSerTyAspPheValPhe 172
Db 937 CCCACTGCCCTACAGAGCTGAAACCATTCGCTCAGCTCCCTCCGACGACCATGTTTC 996
Qy 173 ProValAsnAspGlyPheGlnAlaLeuGnglyIleIleHisSerIleLeuTyAspSer 192
Db 997 AAGTGGGCAAT---TTTGATGACCTTCGACATCCAGCGGCAAAATTCAGAGAAA--- 1050
Qy 193 CysIleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 212
Db 1051 -----ATCTTGCCATTGAAAGAAACCAAGTCAAGTCAAGTCTCTTTCAGACAC 1101
Qy 213 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 226
Db 1102 GAGATGTACAGAAAGTTTCAGCTCAGCTCTCAATGAT 1143

RESULT 10
US-08-482-293A-45
; Sequence 45, Application US/08482293A

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Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-482-293A-45
Alignment Scores:
Pred. No.: 1.54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Beet Local Similarity: 28.21% Mismatches: 96
Query Match: 10.88% Indels: 30
DB: 2 Gaps: 12
US-09-970-076-2_copy_28_320 (1-293) x US-08-482-293A-45 (1-3519)
QY 10 ProalaGlyTyrGly---GlyPheAPLeuTyrPheIleuAPLeuTyrSerGlySerVal 28
DB 481 CCAAGAGTCCAGGACAGAGATGACATGCTTCTCTGATGATGCTCCGCGCAGATT 540
QY 29 ---LeuThiIshIstrPaengIuIleTyrTyrPheValGluInleuAlaHISlySPheIle 47
DB 541 GATCAAGTAGACTTATCCAGATCAAGAGCTTGCTCAAGCTTGATGGCGCAGTTGGC 600
QY 48 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrIleuMetLys 67
DB 601 AGCACAGACACCTGCTTCTCCGTGATGCAATCAACTCAACATCTCGAAGACTCATTTTACC 660

QY 68 LeuThrgIuAspArg-----GluGlnIleArgGlnGlyLeuGlnGluLeu 82
DB 661 TTCACGGAATTCAGAGCAGCTGAGCCCTGAGAGCTGGATGATGCCATCGTCCAGCTC 720
QY 83 GlnLysValLeuProGlyGlyAspThrTyrMetCnISgluGlyPheGluArgLysSerGlu 102
DB 721 CAA-----GGCTGACGTACACAGAGCTCGGGCATCCAGAAAGTGTGTGAA 765
QY 103 GlnIleTyrGluAsnArgGlnGlyTyrArgThrAla---SerValIleIleAlaLeu 121
DB 766 GAGCTATTTCATAGCAAGAAATGGGCGCCGAAAGAGTCCCAAGAAATCTATTGTGCATC 825
QY 122 ThrAspGlyGluLeuThiIshIleuAspLeuPhePheTyrSerGlu-----ArgGluAlaAsn 139
DB 826 ACAGATGGGCGAGAAATTCAGAGACCCCTGAGATGATGACATGTATCCCTGTAAGCAGAG 885
QY 140 ArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAsp---PheAsnGlu 158
DB 886 AAGAGCT-----GGATCATTCGCTATGCTATAGGGGTGGAGATGCTTCCGGGAA 936
QY 159 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 172
DB 937 CCCACTGCCCTTACAGAGAGCTGAACACATGGCTGACGCTCCCTCCGAGACACAGTGTTC 996
QY 173 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHiserIleLeuLysSer 192
DB 997 AAGGTGGCGCAAT---TTGTAGCAGCTTCCGACATCCAGCGGCAATTCAGAGAA--- 1050
QY 193 CysIleGluIleuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 212
DB 1051 -----ATCTTGGCCATTGAAGAACCGAATCAAGGTCAAGTAGTTCCTTCAGCAC 1101
QY 213 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 226
DB 1102 GAGATGTCAAGAAAGTTCAGCTCAGCTCTCTCAATGAT 1143
RESULT 11
US-08-943-363-45
Sequence 45, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659

```

REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-943-363-45

Alignment Scores:
Pred. No.: 1,54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.88% Indels: 30
DB: Gaps: 12

US-09-970-076-2_COPY_28_320 (1-293) x US-08-943-363-45 (1-3519)

QY 10 ProAlaCyArgTgLy--GlyPheAerLeuTyRheIleLeuAerLySergLyServal 28
DB 481 CCAGAGGTCCAGAGCAAGATGACATTCCTTCTGATGATGAGCTCCGCGAGCAT 540

QY 29 ---LeuHtHtHtRpaNgLiLeTyTyRheValGluGlnLeuAlaHtLyRheIle 47
DB 541 GATCAAGTGACTTACCCAGATGAAGACTTCTCAAACTTGATGGCCAGTTGGCG 600

QY 48 SerProGlnLeuAerGmetSerPheIleValPheSerThxArgLyThrThleuMetLy 67
DB 601 AGCACCAGCAACCTGTTCTCCGATGACATTAACAACCTCGAAGACTCATTTTACC 660

QY 68 LeuThrGluAerArg-----GluGlnIleArgGlnGlyLeuGluGluLeu 82
DB 661 TTCACGGATTCAGAGCAGCAGCTGAGCCCTGAGAGCTGGATGATCGATCGCCAGCTC 720

QY 83 GlnIleValLeuProGlyAerThyRheThyMetHtGlnGlyRheGlnAglAserGlu 102
DB 721 CAA-----GGCCTGACGTACAGACCTCGGAGCATCCGAAAGTGGTGAA 765

QY 103 GlnIleTyRgIuAerAerGlnGlyTyRArgThAla---SerValIleIleAlaLeu 121
DB 766 GAGCTATTTCATGCAAGAAATGGGGCCGAAAGTCCCAAGAAATTAATTTGTCATC 825

QY 122 ThrAerGlyGluLeuHtHtAerLeuAerPheRheTySergLy-----ArgGluAlaAer 139
DB 826 ACAAGATGGGCAAAATTCAGAGACCCCTCGAGATATGACATGTCATCCCTGAAGCAGAG 885

QY 140 ArgSerAerAerLeuGlyAlaIleValTyRcyValGlyValAer---PheAerGlu 158
DB 886 AAAGCT-----GGGATCATTCGCTATGCTATAGGGGTGGAGATGCTTCGGGAA 936

QY 159 ---ThrGlnLeuAlaArgLyLe-----AlaAerSerLyAerPheIleServalPhe 172
DB 937 CCCAGTCCCTTACAGAGAGTGAACATTCGCTGAGCTCCCTCGCAGAGCAGCTGTC 996

QY 173 ProValAerAerLeuPheGlnAlaLeuGlnGlyIleIleHtSerIleLeuLyAerSerg 192
DB 997 AAGGTGGGCAAT---TTTGTAGCACTTCGACAGCATCAGAGCGCAAAATTCAGAGAA--- 1050

QY 193 CyeIleGluIleLeuAlaAglProSerThrIleCyeAlaGlyGlySerPheGlnVal 212
DB 1051 -----ATCTTGGCATTTGAAGAAACCAATCAAGGTCAAGTACTCTTCACAGCAC 1101

QY 213 ValIleAerGlyAerGlyPheAerGlnIleAlaAerAerValAer---PheAerGlu 226
DB 226

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DB 1102 GAGATGTCAAGAAAGTTTCAGCTCAGCTCTCTCATGAT 1143

RESULT 12
US-09-193-043-45
Sequence 45, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
EARLIER FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 45
LENGTH: 3519
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (52)..(3516)
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-193-043-45

Alignment Scores:
Pred. No.: 1,54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.88% Indels: 30
DB: Gaps: 12

US-09-970-076-2_COPY_28_320 (1-293) x US-09-193-043-45 (1-3519)

QY 10 ProAlaCyArgTgLy--GlyPheAerLeuTyRheIleLeuAerLySergLyServal 28
DB 481 CCAGAGGTCCAGAGCAAGATGACATTCCTTCTGATGATGAGCTCCGCGAGCAT 540

QY 29 ---LeuHtHtHtRpaNgLiLeTyTyRheValGluGlnLeuAlaHtLyRheIle 47
DB 541 GATCAAGTGACTTACCCAGATGAAGACTTCTCAAACTTGATGGCCAGTTGGCG 600

QY 48 SerProGlnLeuAerGmetSerPheIleValPheSerThxArgLyThrThleuMetLy 67
DB 601 AGCACCAGCAACCTGTTCTCCGATGACATTAACAACCTCGAAGACTCATTTTACC 660

QY 68 LeuThrGluAerArg-----GluGlnIleArgGlnGlyLeuGluGluLeu 82
DB 661 TTCACGGATTCAGAGCAGCAGCTGAGCCCTGAGAGCTGGATGATCGATCGCCAGCTC 720

QY 83 GlnIleValLeuProGlyAerThyRheThyMetHtGlnGlyRheGlnAglAserGlu 102
DB 721 CAA-----GGCCTGACGTACAGACCTCGGAGCATCCGAAAGTGGTGAA 765

QY 103 GlnIleTyRgIuAerAerGlnGlyTyRArgThAla---SerValIleIleAlaLeu 121
DB 766 GAGCTATTTCATGCAAGAAATGGGGCCGAAAGTCCCAAGAAATTAATTTGTCATC 825

QY 122 ThrAerGlyGluLeuHtHtAerLeuAerPheRheTySergLy-----ArgGluAlaAer 139
DB 826 ACAAGATGGGCAAAATTCAGAGACCCCTCGAGATATGACATGTCATCCCTGAAGCAGAG 885

QY 140 ArgSerAerAerLeuGlyAlaIleValTyRcyValGlyValAer---PheAerGlu 158
DB 158

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DB 886 AAGCT-----GGGATCATTCGCTATGCTATAGGGGTGGAGATGCTTCGCGGAA 936
QY 159 ---ThrgInLeuAlaArgIle-----AlaAspSerIleAspHisValPhe 172
DB 937 CCCACTGCCCTCAGAGAGTGAACACCATTTGGCTGCTCCCTCGGAGACACGCGTTC 996
QY 173 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIleValSer 192
DB 997 AAGGTGGGCAAT---TTTGTAGCACTTCGACAGATTCACGGCAATTCAGAGAAA--- 1050
QY 193 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 212
DB 1051 -----ATCTTGCCCATTTGAGAGACCGAATCAAGGTCAAGTAGTTCCTTCAGCAC 1101
QY 213 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 226
DB 1102 GAGATGTCAAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 13
US-09-688-307A-45
/ Sequence 45, Application US/09688307A
/ Patent No. 6432404
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 6432404el Human Beta-2
/ FILE REFERENCE: 27866/36646
/ CURRENT APPLICATION NUMBER: US/09/688,307A
/ PRIOR FILING DATE: 2000-10-13
/ PRIOR APPLICATION NUMBER: 09/193,043
/ PRIOR FILING DATE: 1998-11-16
/ PRIOR APPLICATION NUMBER: 08/605,672
/ PRIOR FILING DATE: 1996-02-22
/ PRIOR APPLICATION NUMBER: 08/173,497
/ PRIOR FILING DATE: 1993-12-23
/ PRIOR APPLICATION NUMBER: 08/286,889
/ PRIOR FILING DATE: 1994-08-05
/ PRIOR APPLICATION NUMBER: 08/362,652
/ PRIOR FILING DATE: 1994-12-21
/ PRIOR APPLICATION NUMBER: 08/943,363
/ PRIOR FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 45
/ LENGTH: 3519
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (52)..(3516)
/ OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-688-307A-45

Alignment Scores:
Pred. No.: 1,54e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 10.88% Indels: 30
DB: 3 Gaps: 12

US-09-970-076-2_COPY_28_320 (1-293) x US-09-688-307A-45 (1-3519)
QY 10 ProAlaCysArgGly---GlyPheAspLeuValPheIleLeuAspIleValSerVal 28
DB 481 CCAGAGTGTCCAGAGACAGATGACATTCCTTCTGATGATGAGCTCCGCGAGCAT 540
QY 29 ---LeuHisHisThrAsnGluIleValPheValGluIleLeuAlaHisValPheIle 47
DB 541 GATCAAGATGATTTTACCCGAGATGAGGACCTTGATGAGGCGGCGGATGGCG 600
QY 48 SerProGluIleValArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetIle 67
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DB 601 AGCAGCAGACACTCTGCTTCCTCGATGCAATCTCAAAATCTGAAAGCTATTTTACC 660
QY 68 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGluIleVal 82
DB 661 TTCACGGAATTTCAAGACAGACGCTTACGCTTACAGACCTGTGTGATGCCATCTCCACGTC 720
QY 83 GlnIleValLeuProGluIleValAspThrIleValGluIleGluIlePheGluArgAlaSerGlu 102
DB 721 CAA-----GGCTGACGTACACAGCCTCGGGGATCCAGAAAGTGTGAA 765
QY 103 GlnIleValPheGluAsnArgGlnGlyValArgThrAla---SerValIleIleAlaVal 121
DB 766 GAGCATATTTCAATAGCAAGAAATGGGGCCGAAAGTGCAGAGATTAATTTGTCAATC 825
QY 122 ThrAspGlyLeuLeuHisGluIleValLeuPhePheValPheValPheValPheValPhe 139
DB 826 ACAGATGGGCAAAATTCAGAGACCCCTGGAGTATGACATGTATCCCTTAAGCAGAG 885
QY 140 ArgSerArgAspLeuGlyAlaIleValIleValIleValIleValIleValIleValIleVal 158
DB 886 AAGCT-----GGGATCATTCGCTATGCTATAGGGGTGGAGATGCTTCGCGGAA 936
QY 159 ---ThrgInLeuAlaArgIle-----AlaAspSerIleAspHisValPhe 172
DB 937 CCCACTGCCCTCAGAGAGTGAACACCATTTGGCTGCTCCCTCGGAGACACGCGTTC 996
QY 173 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIleValSer 192
DB 997 AAGGTGGGCAAT---TTTGTAGCACTTCGACAGATTCACGGCAATTCAGAGAAA--- 1050
QY 193 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 212
DB 1051 -----ATCTTGCCCATTTGAGAGACCGAATCAAGGTCAAGTAGTTCCTTCAGCAC 1101
QY 213 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 226
DB 1102 GAGATGTCAAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 14
US-09-350-259-45
/ Sequence 45, Application US/09350259
/ Patent No. 6620915
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 6620915el Human 2
/ FILE REFERENCE: 27866/35004
/ CURRENT APPLICATION NUMBER: US/09/350,259
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: 09/193,043
/ PRIOR FILING DATE: 1998-11-16
/ PRIOR APPLICATION NUMBER: 08/173,497
/ PRIOR FILING DATE: 1993-12-23
/ PRIOR APPLICATION NUMBER: 08/286,889
/ PRIOR FILING DATE: 1994-08-05
/ PRIOR APPLICATION NUMBER: 08/362,652
/ PRIOR FILING DATE: 1994-12-21
/ PRIOR APPLICATION NUMBER: 08/943,363
/ PRIOR FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 45
/ LENGTH: 3519
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (52)..(3516)
/ OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-350-259-45
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Alignment Scores:

Pred. No.:	1,54e-10	Length:	3519
Score:	166.00	Matches:	66
Percent Similarity:	46.15%	Conservative:	42
Best Local Similarity:	28.21%	Mismatches:	96
Query Match:	10.88%	Indels:	30
DB:	3	Gaps:	12

US-09-970-076-2_COPY_28_320 (1-293) x US-09-350-259-45 (1-3519)

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QY 10 ProAlaCyETrgLy---GlyPheAapLeuTyrrPheIleuAapLySergLySerVal 28
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 481 CCAGAGTGTCCAGAGCAAGAGATGACATGCTTCTCTGATGATGCTCGGACGATT 540
QY 29 ---LeuHieHieTrpAengLuiLeTyrrTyrrPheValGluGlnLeuAlaHieLySPhile 47
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 541 GATCAAGATGACTTTACCCAGATGAAGACTTCTCAAGCTTTGATGGCCAGATTGGCG 600
QY 48 SerProGlnLeuAArgMetSerPheIleValPheSerThrAArgLyThrThrLeuMetLyS 67
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 601 AGCACCGACGACCTGCTTCTCCCTGATGATCAATCAACATCCGAAAGACTCATTTTACC 660
QY 68 LeuThrGluAapArg-----GluGlnIleAArgGlnLyLeuGlnGluLeu 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 661 TTCACGGAATTCAGACGACGCTGAGCCCTCAGAGCTGGTGATGCTCATGCTCAGACTC 720
QY 83 GlnLyValLeuProGlyGlyAapTrhTyrrMetHieGlnLyPheGlnAArgLySergLy 102
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 721 CAA-----GGCTGACGTACACAGCCCTCGGACATCCAGAAAGTGTGAAA 765
QY 103 GlnIleTyrrGlnAenAArgGlnLyTyrrAArgThraIa---SerValIleIleAlaen 121
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 766 GACATATTTCATGACCAAGAAATGGGGCCCGAAAGTCCCAAGAAAGATCTAATTGTTCATC 825
QY 122 ThrAapLyGluLeuHieGlnAapLeuPhePheTyrrSergLy-----AArgLyAlaen 139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 826 ACAGATGGGCAAAATTCAGAGACCCCTGAGATATGACATGTCATCCCTGAAGACAG 885
QY 140 ArgSerAArgAapLeuGlyAlaIleValTyrrCyValGlyValLyAap---PheAengLy 158
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 886 AAGGCT-----GGGATCATTCGCTATGAGGGGTGGAGATGCTTCGCGGAA 936
QY 159 ---ThrGlnLeuAlaArgIle-----AlaAapSerLySapAphIleValPhe 172
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 937 CCCACTGCTTACAGAGCTGAACACCATTTGGCTCAGCTCCCTGCGAGCACAGTGTTC 996
QY 173 ProValAapAapLyPheGlnAlaLeuGlnLyIleIleHieSerIleLeuLySerg 192
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 997 AAGGTGGGCAAT---TTGTAGCACTTCGAGCATCCAGCGGCAAAATTCAGAGAAA--- 1050
QY 193 CysIleGlnIleLeuAlaGluProSerThrIleCyAlaGlyGluSerPheGlnVal 212
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1051 -----ATCTTTGTCATTGAAGAACCAATCAAGTCAAGTACTCTTTCAGACAC 1101
QY 213 ValIleAArgLyAengLyPheAArgHieAlaAArgAValAap 226
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1102 GAGATGTCAAGAAAGGTTTCAGCTCAGCTCTCTCTCAATGGAT 1143

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RESULT 15

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US-08-485-618-52
; Sequence 52, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vliet, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States

```

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,618

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994

TEL/COMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:

LENGTH: 3803 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..3486

US-08-485-618-52

Alignment Scores:

Pred. No.:	1.74e-10	Length:	3803
Score:	166.00	Matches:	66
Percent Similarity:	46.15%	Conservative:	42
Best Local Similarity:	28.21%	Mismatches:	96
Query Match:	10.88%	Indels:	30
DB:	2	Gaps:	12

US-09-970-076-2_COPY_28_320 (1-293) x US-08-485-618-52 (1-3803)

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QY 10 ProAlaCyETrgLy---GlyPheAapLeuTyrrPheIleuAapLySergLySerVal 28
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 430 CCAGAGTGTCCAGAGCAAGAGATGACATGCTTCTCTGATGATGCTCGGACGATT 489
QY 29 ---LeuHieHieTrpAengLuiLeTyrrTyrrPheValGluGlnLeuAlaHieLySPhile 47
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 490 GATCAAGATGACTTTACCCAGATGAAGACTTGTCAAGCTTTGATGGCCAGATTGGCG 549
QY 48 SerProGlnLeuAArgMetSerPheIleValPheSerThrAArgLyThrThrLeuMetLyS 67
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 550 AGCACCGACGACCTGCTTCTCCCTGATGATCAATCAACATCCGAAAGACTCATTTTACC 609
QY 68 LeuThrGluAapArg-----GluGlnIleAArgGlnLyLeuGlnGluLeu 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 670 CAA-----GGCTGACGTACACAGCCCTCGGACATCCAGAAAGTGTGAAA 714
QY 103 GlnIleTyrrGlnAenAArgGlnLyTyrrAArgThraIa---SerValIleIleAlaen 121
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 715 GACATATTTCATGACCAAGAAATGGGGCCCGAAAGTCCCAAGAAAGATCTAATTGTTCATC 774

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:35:12 ; Search time 938.696 Seconds
(without alignments)
2581.163 Million cell updates/sec

Title: US-09-970-076-2_COPY_28_320

Perfect score: 1526
Sequence: 1 CGCRREDGCGACGFDLYF.....DGLSFSSVITTTTCSDG 293

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Published.Applications.NA.Main -QFMT=fastcap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09970076.ecgn_1_2715_@runac.14122005_11852_21035
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-Fgapop=6 -Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database: Published.Applications.NA.Main.*

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2: /cg2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
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4: /cg2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
5: /cg2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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9: /cg2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cg2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1526	100.0	1414	10	US-11-047-278-1
2	1526	100.0	1454	6	US-10-133-937-58
3	1526	100.0	1454	6	US-10-159-563-58
4	1526	100.0	1674	6	US-10-038-307-17
5	1526	100.0	1674	6	US-10-201-292-17
6	1526	100.0	5540	3	US-09-918-715-176
7	1526	100.0	5540	3	US-09-918-715-231
8	1526	100.0	5540	6	US-10-301-822-198

9	1526	100.0	5540	8	US-10-474-794-176	Sequence 176, App
10	1526	100.0	5540	8	US-10-474-794-231	Sequence 231, App
11	1526	100.0	5540	9	US-10-979-159-176	Sequence 176, App
12	1526	100.0	5540	9	US-10-979-159-231	Sequence 231, App
13	1526	100.0	5540	10	US-11-047-278-5	Sequence 5, Appl1
14	1514	99.2	1056	6	US-10-038-307-23	Sequence 23, Appl1
15	1514	99.2	1056	6	US-10-201-292-23	Sequence 23, Appl1
16	1514	99.2	1650	6	US-10-038-307-13	Sequence 13, Appl1
17	1514	99.2	1650	6	US-10-038-307-15	Sequence 15, Appl1
18	1514	99.2	1650	6	US-10-201-292-13	Sequence 13, Appl1
19	1514	99.2	1650	6	US-10-201-292-15	Sequence 15, Appl1
20	1514	99.2	1713	6	US-10-038-307-19	Sequence 19, Appl1
21	1514	99.2	1713	6	US-10-201-292-19	Sequence 19, Appl1
22	1514	99.2	2112	10	US-11-047-278-7	Sequence 7, Appl1
23	1514	99.2	2272	3	US-09-796-753-11	Sequence 11, Appl1
24	1514	99.2	2272	6	US-10-038-307-1	Sequence 1, Appl1
25	1514	99.2	2272	6	US-10-201-292-1	Sequence 1, Appl1
26	1514	99.2	2353	5	US-10-198-846-9957	Sequence 9957, Ap
27	1509	98.9	5220	3	US-09-918-715-186	Sequence 186, App
28	1509	98.9	5220	3	US-09-918-715-300	Sequence 300, App
29	1509	98.9	5220	8	US-10-474-794-186	Sequence 186, App
30	1509	98.9	5220	8	US-10-474-794-300	Sequence 300, App
31	1509	98.9	5220	9	US-10-979-159-186	Sequence 186, App
32	1509	98.9	5220	9	US-10-979-159-300	Sequence 300, App
33	1504	98.6	1650	6	US-10-038-307-9	Sequence 9, Appl1
34	1504	98.6	1650	6	US-10-201-292-9	Sequence 25, Appl1
35	1501	98.4	1008	6	US-10-038-307-25	Sequence 25, Appl1
36	1501	98.4	1008	6	US-10-201-292-25	Sequence 25, Appl1
37	1499.5	98.3	1047	6	US-10-038-307-21	Sequence 21, Appl1
38	1499.5	98.3	1047	6	US-10-201-292-21	Sequence 21, Appl1
39	1499	98.2	1623	6	US-10-038-307-11	Sequence 11, Appl1
40	1499	98.2	1623	6	US-10-201-292-11	Sequence 11, Appl1
41	1413	92.6	1608	6	US-10-062-674-35	Sequence 35, Appl1
42	1385	90.8	2397	6	US-10-062-674-1757	Sequence 1757, Ap
43	1288	84.4	1534	6	US-10-201-292-33	Sequence 33, Appl1
44	1257	82.4	1436	10	US-11-047-278-9	Sequence 9, Appl1
45	1257	82.4	1609	5	US-10-037-270-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-11-047-278-1
; Sequence 1, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Antitoxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (104)..(1207)
US-11-047-278-1
Alignment Scores: 6.33e-185
Pred. No.: 1526.00
Score: 100.00%
Length: 1414
Matches: 293
Percent Similarity: 100.00%
Conservative: 0

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-970-076-2_COPY_28_320 (1-293) x US-11-047-278-1 (1-1414)

QY 1 GINGLYGAYARGGLUAPGLYGLYProAlaCyTYrGLYpHeaPLeuTYrPhe
DB 185 CAAGGGGAGCGCAGGAGATGGGGGTCCAGCTGTACGGCGGATTTGACCTGACTTC 244
QY 21 ILEUAAPLYSeRGLYSeRValleuHISHTPaNGluILETYrPheValGlu 40
DB 245 ATTTTGACAAATACAGAAAGTGTGCACCACTGGAATGAATCTTAATCTTGTGGAA 304
QY 41 GINleuAlaHISlyrPheHISerProGlnleuAArgMetSerPheIleValPheSerThr 60
DB 305 CAGTTGGCTCACAAATTCATCCACCCACAGTTGAGAAATGCTTTTATTTGTTTCTCCACC 364
QY 61 ARGGLYThrThreumetLySLeuThrgLUaSPARGluGlnIleArgGlnIleuGlu 80
DB 365 CAGAGAACAACTTAATGAACAGACAGAAAGACAGAAACAAATCCGTCAAGGCTTAGAA 424
QY 81 GIUleuGlnLYeValleuProGlyGLYaSPThrTYrMechISGLIuGLYPheGluAAla 100
DB 425 GAACTCCAGAAAGTTCTGCAGAGAGAGACATTAATGATGATGAAGATTGAAAGGCC 484
QY 101 SerGluGlnIleTYrTYrGluAaARGGlnIlyTYrAArgThraJaservaIleIleAla 120
DB 485 AGTGAACAGATTATTAATGAACAGCAAGGTTACAGGACACCGCTCATCATTTGCT 544
QY 121 LeuThraSPGLYGLIuLeuHISGLIuAPLeuPhePheTYrSerGluArgGluAaAARG 140
DB 545 TTGACATGATGAGAAATCCATGAAGATCTTTTCTATTCAGAGGGAGGCTTAATAG 604
QY 141 SerARGaSPLeuGlnYAlaIleValTYrCySValGlyValIyASPheAengluThrgln 160
DB 605 TCTCGAGATCTTGTCGAATTTGTTTACTGTGTGTGTAAGATTTCATATGAGACACAG 664
QY 161 LeuAlaARGIleAlaSPSerLySaSPHISValPheProValaSPGLYPheGlnAla 180
DB 665 CTGGCCCGGATTCGGACAGTAAGATCATGTGTTCCCTGAATGACGGCTTTCAGGCT 724
QY 181 LeuGlnGlyIleIleHISerIleLeuLYaLYeSerCySIIeGluIleleuAlaAlaGlu 200
DB 725 CTGCAGAGCATCATCCACTCAATTTTGAAGAAGCTCGATCGAAATTTAGACAGCTGAA 764
QY 201 ProSerThrIleCYaAlaGlyGluSerPheGlnValValIyARGIyaengIyPheARG 220
DB 785 CCATCCACCATATGTGACAGAGATCATTTCAAGTTGTCTGTGAGAGAAACGGCTTCGA 844
QY 221 HISAlaARGaNVAlaSPARGValleuCYeSerPheLySIIeAaSPSerValThreU 240
DB 845 CAGTCCCGCAACGTGACAGGGGTCTGTGAGCTTCAAGATCATGATCTGGATCACTC 904
QY 241 AaNGluLYeProPheSerValGluAaSPThrTYrleuLeuCYeProAlaProIleLeuLYs 260
DB 905 AAGAGAAAGCCCTTTCTGTGAAAGACATTAATTAATGATGACAGGCTATCTTAATAA 964
QY 261 GluValGlyMeLYeValaAlaLeuGlnValSerMetAaSPGLYLeuSerPheIleSer 280
DB 965 GAAGTTGGCATGAAGCTGCACCTCCAGTCAAGTCAAGTGAACATGAGCTCTTATATCTCC 1024
QY 281 SerSerValIleIleThrThraHISCySeSerAPGLY 293
DB 1025 AGTTCTGTATCATCACACACACACACTGTTGTGACGCT 1063

RESULT 2
US-10-133-937-58
; Sequence 58, Application US/10133937
; Publication No. US20030207278A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
```

```
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; TITLE OF INVENTION: OTHER BIOLOGICAL STATES
; FILE REFERENCE: 11613.56US01
; CURRENT APPLICATION NUMBER: US/10/133, 937
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-937-58

Alignment Scores:
Pred. No.: 6,61e-185 Length: 1454
Score: 1526.00 Matches: 293
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-970-076-2_COPY_28_320 (1-293) x US-10-133-937-58 (1-1454)

QY 1 GINGLYGAYARGGLUAPGLYGLYProAlaCyTYrGLYpHeaPLeuTYrPhe 20
DB 225 CAAGGGGAGCGCAGGAGATGGGGGTCCAGCTGTACGGCGGATTTGACCTGACTTC 284
QY 21 ILEUAAPLYSeRGLYSeRValleuHISHTPaNGluILETYrPheValGlu 40
DB 285 ATTTTGACAAATACAGAAAGTGTGTGCACCACTGGAATGAATCTTAATCTTGTGGAA 344
QY 41 GINleuAlaHISlyrPheHISerProGlnleuAArgMetSerPheIleValPheSerThr 60
DB 345 CAGTTGGCTCACAAATTCATCCACCCACAGTTGAGAAATGCTTTTATTTGTTTCTCCACC 404
QY 61 ARGGLYThrThreumetLySLeuThrgLUaSPARGluGlnIleArgGlnIleuGlu 80
DB 405 CAGAGAACAACTTAATGAACAGCAAGGTTACAGGACACCGCTCATCATTTGCT 464
QY 81 GIUleuGlnLYeValleuProGlyGLYaSPThrTYrMechISGLIuGLYPheGluAAla 100
DB 465 GAACTCCAGAAAGTTCTGCAGAGAGAGACATTAATGATGATGAAGATTGAAAGGCC 524
QY 101 SerGluGlnIleTYrTYrGluAaARGGlnIlyTYrAArgThraJaservaIleIleAla 120
DB 525 AGTGAACAGATTATTAATGAACAGCAAGGTTACAGGACACCGCTCATCATTTGCT 584
QY 121 LeuThraSPGLYGLIuLeuHISGLIuAPLeuPhePheTYrSerGluArgGluAaAARG 140
DB 585 TTGACATGATGAGAAATCCATGAAGATCTTTTCTATTCAGAGGGAGGCTTAATAG 644
QY 141 SerARGaSPLeuGlnYAlaIleValTYrCySValGlyValIyASPheAengluThrgln 160
DB 645 TCTCGAGATCTTGTCGAATTTGTTTACTGTGTGTGTAAGATTTCATATGAGACACAG 704
QY 161 LeuAlaARGIleAlaSPSerLySaSPHISValPheProValaSPGLYPheGlnAla 180
DB 705 CTGGCCCGGATTCGGACAGTAAGATCATGTGTTCCCTGAATGACGGCTTTCAGGCT 764
QY 181 LeuGlnGlyIleIleHISerIleLeuLYaLYeSerCySIIeGluIleleuAlaAlaGlu 200
DB 765 CTGCAGAGCATCATCCACTCAATTTTGAAGAAGTCTGTCAATCGAAATTTAGACAGCTGAA 824
QY 201 ProSerThrIleCYaAlaGlyGluSerPheGlnValValIyARGIyaengIyPheARG 220
DB 825 CCATCCACCATATGTGACAGAGAGTCAATTTCAAGTTGTGTGAGAGAAACGGCTTCGA 884
QY 221 HISAlaARGaNVAlaSPARGValleuCYeSerPheLySIIeAaSPSerValThreU 240
DB 885 CAGTCCCGCAACGTGACAGGGGTCTGTGACCTTCAAGATCAATGATGCTGTGTCACACTC 944
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Qy 241 AsnGluYsEProPheSerValGluAspThrTyrLeuLeuCyProAlaProIleLeuLys 260
Db 945 AATGAGAAAGCCCTTTCTGTGGAGACACTTATTACTGTCTCAAGGCCCTATTGAAAA 1004
Qy 261 GluValGlyMetCysAlaAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIleSer 280
Db 1005 GAAGTTGGCATGAAAGCTGCACCTCCAGGTGACATGAGATGGCCCTCTTTATCTCC 1064
Qy 281 SerSerValIleIleThrThrThrHisCysSerAspGly 293
Db 1065 AGTTCTGTCAATCAACACCACTGTTCTGACGCT 1103

RESULT 3

US-10-159-563-58
Sequence 58, Application US/10159563
Publication No. US20040009154A1
GENERAL INFORMATION:
APPLICANT: Khan, Javed
APPLICANT: Rinsner, Markus
APPLICANT: Peterson, Carsten
APPLICANT: Metzger, Paul
TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
FILE REFERENCE: 11613.56US11
CURRENT APPLICATION NUMBER: US/10/159,563
PRIOR FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 10/133,937
NUMBER OF SEQ ID NOS: 444
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58
LENGTH: 1454
TYPE: DNA
ORGANISM: Homo sapiens
US-10-159-563-58

Alignment Scores:

Pred. No.: 6 61e-185 Length: 1454
Score: 1526.00 Matches: 293
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-970-076-2_COPY_28_320 (1-293) x US-10-159-563-58 (1-1454)

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Db 225 CAAGGGGAGCGAGGAGATGGGGGCTCCAGCCGCTACGGCGATTGACCTGTACTTC 284
Qy 21 IleLeuAspIysSerGlySerValLeuHisIleThrAsnGluIleTyrTyrPheValGlu 40
Db 285 ATTTGGACAATCAGAGAGTGTCTGCACCACTGAGATGAATCTATTACTTTGTGGA 344
Qy 41 GlnLeuAlaHisIleSerPheIleSerProGlnLeuArgSerPheIleValPheSerThr 60
Db 345 CAGTGGCTCAAAATTCATCAGCCCAAGTGAAGATGCTTTATTTGTTCTCCACC 404
Qy 61 ArgGlyThrThrLeuMetCysLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGlu 80
Db 405 CGAGGAACAACTTAATGAACTGACAGAGACAGAGAACAAATCCCTCAAGGCTTGAA 464
Qy 81 GluLeuGlnIlyValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgAla 100
Db 465 GAACCTCAGAAAGTTCGACAGAGAGAGACATTACATGATGAAAGATTGAAAGGCC 524
Qy 101 SerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyrTrpArgTrpAlaSerValIleIleAla 120
Db 525 AGTGAAGCATTTATTTATGAAACAGACAGAGGACAGGACAGCCGCTCATCATTTGCT 584
Qy 121 LeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGluArgGluAlaAsnArg 140

Db 585 TTGACTAGTGAAGAACTCCATGAAGATCTTTTCTATTTCAGAGAGGAGCTAATAG 644
Qy 141 SerArgAspLeuGlyAlaIleValTyrCysValGlyValIysAspPheAsnGluThrGln 160
Db 645 TCTCGAATCTGTGTGCAATTTGTTACTGTGTGTGTGTGAAGATTTCAATGAACACAG 704
Qy 161 LeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAla 180
Db 705 CTGGCCCGGATGGGACAGTAAAGATCATGTGTTCCTCCGTAATGACGGCTTCAGGCT 764
Qy 181 LeuGlnGlyIleIleHisSerIleLeuAllySerCysIleGluIleLeuAlaGlu 200
Db 765 CTGCAAGGCATCATCCACTCAATTTTGAAGAAGCTCGATCGAAATTTAGACAGCTGA 824
Qy 201 ProSerThrIleCysAlaGlyGlySerPheGlnValValAlaArgGlyAsnGlyPheArg 220
Db 825 CCATCCACCATATGTGAGAGAGAGTCACTTTCAATGTTCTCGAAGAGAAACGGCTTCGA 884
Qy 221 HisAlaArgAsnValAspArgValLeuCysSerPheIleAsnAspSerValThrLeu 240
Db 885 CATCCCGCAACGTGGACAGGGTCTTGCAGCTTCAAGATCAATGACTCGGTACACTC 944
Qy 241 AsnGluYsEProPheSerValGluAspThrTyrLeuLeuCyProAlaProIleLeuLys 260
Db 945 AATGAGAAAGCCCTTTCTGTGGAGACACTTATTACTGTGTCCAGGCCCTATTGAAAA 1004
Qy 261 GluValGlyMetCysAlaAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIleSer 280
Db 1005 GAAGTTGGCATGAAAGCTGCACCTCCAGGTGACATGAGATGGCCCTCTTTATCTCC 1064
Qy 281 SerSerValIleIleThrThrThrHisCysSerAspGly 293
Db 1065 AGTTCTGTCAATCAACACCACTGTTCTGACGCT 1103

RESULT 4

US-10-038-307-17
Sequence 17, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Englin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 1674
TYPE: DNA
ORGANISM: Homo sapiens
US-10-038-307-17

Alignment Scores:

Pred. No.: 8 28e-185 Length: 1674
Score: 1526.00 Matches: 293
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-970-076-2_COPY_28_320 (1-293) x US-10-038-307-17 (1-1674)

Qy 1 GlnGlyGlyArgArgGluAspGlyGlyProAlaCysEtyrGlyGlyPheAspLeuTyrPhe 20
Db 94 CAAGGGGAGCGAGGAGATGGGGGCTCCAGCCGCTACGGCGATTGACCTGTACTTC 153
Qy 21 IleLeuAspIysSerGlySerValLeuHisIleThrAsnGluIleTyrTyrPheValGlu 40
Db 154 ATTTGGACAATCAGAGAGTGTCTGCACCACTGAGATGAATCTATTACTTTGTGGA 213

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QY 41 GlnLeuAlaHisIleuPheIleSerProGlnLeuArgMetSerPheIleValPheSerThr 60
Db 214 CAGTTGGCTCACAATTCATTCAGCCCACTTGAGAAATGCTCTTATTTGTTTCTCCACC 273
QY 61 ArgGlyThrThrLeuMetLeuSerLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGlu 80
Db 274 CGAGGAAACAACCTTATGAACTGACAGAAACAGAGAAACAATCCGTCAGAGCCCTAGAA 333
QY 81 GluLeuGlnIleValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgAla 100
Db 334 GAATCTCCAGAAAGTTCTGCGAGAGAGACACTTATCATGATGAAAGATTTGAAAGGGCC 393
QY 101 SerGluGlnIleTyrTyrGlnAsnArgGlnGlyTyrArgThrAlaSerValIleIleAla 120
Db 394 AGTGACCAATTTATTTATGAAAACAGACAGGGTACAGAGCCAGCGCTCATCTGCT 453
QY 121 LeuThrAspGlyGlyLeuHisGlyAspLeuPhePheTyrSerGluArgGluAlaAsnArg 140
Db 454 TTGACTGATGGAGAACTCCATGAAAGATCTTTTCTATTCAAGAGAGGAGGCTAATAG 513
QY 141 SerArgAspLeuGlyValIleValTyrCybValGlyValIleAspPheAsnGluThrGln 160
Db 514 TCTCGAGATCTTGCTCAATGTTTACTGTGTGTGTAAGATTTCATAGAGACAG 573
QY 161 LeuAlaArgIleAlaAspSerLeuAspHisValPheProValAsnAspGlyPheGlnAla 180
Db 574 CTGGCCCGGATTCGGACAGTAAAGATCATGTGTTCCCGTAATGACGGCTTCAAGCT 633
QY 181 LeuGlnGlyIleIleHisSerIleLeuValLeuSerCybIleGluIleLeuAlaIleGlu 200
Db 634 CTGCAGAGCATCATCCACTCAATTTGAGAGAGCTCGCATGAAATTCAGACAGCTGAA 693
QY 201 ProSerThrIleCybAlaGlyGlyLeuSerPheGlnValValArgGlyAsnGlyPheArg 220
Db 694 CCATCCACCACTATGTCAGAGAGAGTCAATTCAGAGTGTCTGAGAGAGAAACGGCTTCCGA 753
QY 221 HisAlaArgAsnValAspArgValLeuCybSerPheIleValIleAsnAspSerValThrLeu 240
Db 754 CATGCCCGCACTGACAGAGGCTCTCTGACCTTCAGATCATGACTCGGTCAACACTC 813
QY 241 AsnGluIleAspProPheSerValGluAspThrTyrLeuLeuCybProAlaProIleLeuVal 260
Db 814 AATGAGAGAGCCCTTTCTGTGAAGATCTTATTACTGTGTCCAGGCGCTATCTTAAAA 873
QY 261 GluValGlyMetLeuValAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIleSer 280
Db 874 GAAGTTGGCATGAAGCTGCACTCCAGTGACATGACATGAAAGCGCTCTCTTTATCTCC 933
QY 281 SerSerValIleIleThrThrThrHisCybSerAspGly 293
Db 934 AGTTCTGTCTATCATCACCAACACACTGTTCTGACGGT 972
RESULT 5
US-10-201-292-17
; Sequence 17, Application US/10201292
; Publication No US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-17
```

```
Alignment Scores:
Pred. No.: 8,286-185 Length: 1674
Score: 1526.00 Matches: 293
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_copy_28_320 (1-293) x US-10-201-292-17 (1-1674)
QY 1 GlnGlyValArgArgGluAspGlyGlyProAlaCybTyrGlyGlyPheAspLeuTyrPhe 20
Db 94 CAAGGGGAGCGCAGGAGAGATGGGGTCCAGCTGCTAGGAGATTTACCTGACTTC 153
QY 21 IleuAspLeuSerGlySerValIleuHisIleTyrAsnGluIleTyrTyrPheValGlu 40
Db 154 ATTTTGACAAATTCAGAAAGTGTCTGCACTGGAATGAAATCTTATCTTGTGGAA 213
QY 41 GlnLeuAlaHisIleuPheIleSerProGlnLeuArgMetSerPheIleValPheSerThr 60
Db 214 CAGTTGGCTCACAATTCATTCAGCCCACTTGAGAAATGCTCTTATTTGTTTCTCCACC 273
QY 61 ArgGlyThrThrLeuMetLeuSerLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGlu 80
Db 274 CGAGGAAACAACCTTATGAACTGACAGAAACAGAGAAACAATCCGTCAGAGCCCTAGAA 333
QY 81 GluLeuGlnIleValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgAla 100
Db 334 GAATCTCCAGAAAGTTCTGCGAGAGAGACACTTATCATGATGAAAGATTTGAAAGGGCC 393
QY 101 SerGluGlnIleTyrTyrGlnAsnArgGlnGlyTyrArgThrAlaSerValIleIleAla 120
Db 394 AGTGACCAATTTATTTATGAAAACAGACAGGGTACAGAGCCAGCGCTCATCTGCT 453
QY 121 LeuThrAspGlyGlyLeuHisGlyAspLeuPhePheTyrSerGluArgGluAlaAsnArg 140
Db 454 TTGACTGATGGAGAACTCCATGAAAGATCTTTTCTATTCAAGAGGAGGCTAATAGG 513
QY 141 SerArgAspLeuGlyValIleValTyrCybValGlyValIleAspPheAsnGluThrGln 160
Db 514 TCTCGAGATCTTGCTCAATGTTTACTGTGTGTGTAAGATTTCATAGAGACAG 573
QY 161 LeuAlaArgIleAlaAspSerLeuAspHisValPheProValAsnAspGlyPheGlnAla 180
Db 574 CTGGCCCGGATTCGGACAGTAAAGATCATGTGTTCCCGTAATGACGGCTTCAAGCT 633
QY 181 LeuGlnGlyIleIleHisSerIleLeuValLeuSerCybIleGluIleLeuAlaIleGlu 200
Db 634 CTGCAGAGCATCATCCACTCAATTTGAGAGAGTCTGCAATGCAAAATTCAGACAGCTGAA 693
QY 201 ProSerThrIleCybAlaGlyGlyLeuSerPheGlnValValArgGlyAsnGlyPheArg 220
Db 694 CCATCCACCACTATGTCAGAGAGGATCTTCAAGTGTCTGTAAGAGAAACGGCTTCCGA 753
QY 221 HisAlaArgAsnValAspArgValLeuCybSerPheIleValIleAsnAspSerValThrLeu 240
Db 754 CATGCCCGCACTGACAGAGGCTCTCTGACCTTCAGATCATGACTCGGTCAACACTC 813
QY 241 AsnGluIleAspProPheSerValGluAspThrTyrLeuLeuCybProAlaProIleLeuVal 260
Db 814 AATGAGAGAGCCCTTTCTGTGAAGATCTTATTACTGTGTCCAGGCGCTATCTTAAAA 873
QY 261 GluValGlyMetLeuValAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIleSer 280
Db 874 GAAGTTGGCATGAAGCTGCACTCCAGTGACATGACATGAAAGCGCTCTCTTTATCTCC 933
QY 281 SerSerValIleIleThrThrThrHisCybSerAspGly 293
Db 934 AGTTCTGTCTATCATCACCAACACACTGTTCTGACGGT 972
RESULT 6
US-09-918-715-176
; Sequence 176, Application US/09918715
```

```
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107, 00134
; CURRENT APPLICATION NUMBER: US/09/918, 715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FaestSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-176
```

```
Alignment Scores:
Pred. No.: 5,57e-184 Length: 5540
Score: 1526.00 Matches: 293
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
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US-09-970-076-2_COPY_28_320 (1-293) x US-09-918-715-176 (1-5540)

```
QY 1 GlnGlyGlyArgArgGluAspGlyGlyProAlaCysTrpGlyGlyPheAspLeuTrpPhe 20
DB 225 CAAGGGGGAGCGCAGGAGGATGGGGGTCACCGCTGACGCGGATTTGACCTGTACTTC 284
QY 21 IleLeuAspLysSerGlySerValLeuHisTrpAsnGluIleTrpTrpPheValGlu 40
DB 285 ATTTTGACAAATCAGAAAGTGCTGACCACTGGAATGAAATCTATTACTTTGTGAA 344
QY 41 GlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSerPheIleValPheSerThr 60
DB 345 CAGTTGGCTCACAATTCATCAGCCCAAGTTGAGATGTCCTTATTTGTTTCTCACC 404
QY 61 ArgGlyThrThrLeuMetLysLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGlu 80
DB 405 CGAGGAACAACCTTAATGAAACTGACAGAAACAGAAACAAATCCGTCAAGGCTAGAA 464
QY 81 GlnLeuGlnLysValLeuProGlyGlyAspThrTrpMetHisGluGluPheGluArgAla 100
DB 465 GAACTCCAGAAAGTTCTGCGCAGGAGGACACTTAACATGCAATGAAAGATTGAAAGGCC 524
QY 101 SerGlnGlnIleTrpTrpGluAsnArgGlnGlyTrpArgThrAlaSerValIleIleAla 120
DB 525 AGTGAAGACAGTTTATTTGAAAACAGACAGAGGACAGACAGCCGTCATATTGCT 584
QY 121 LeuThrAspGlyGlyLeuHisGluAspLeuPhePheTrpSerGluArgGluAlaAsnArg 140
DB 585 TTGACTGATGAGAACTCCATGAAGATCTCTTTTCTATTCAAGAGAGGAGGCTTAATAG 644
QY 141 SerArgAspLeuGlyAlaIleValTrpCysValGlyValLysAspPheAsnGluThrGln 160
DB 645 TCTCGAATCTTGTTGTCAAATGTTTACTGTGTGTGTGAAAGATTTCAATGAAACAG 704
QY 161 LeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAla 180
DB 705 CTGGCCCGGATTTGGGCAAGTAAAGATCATGTGTTCCGTGAATGACGGCTTTACGGCT 764
QY 181 LeuGlnGlyTrpIleHisSerIleLeuLysLysSerCysIleGluIleLeuAlaIleGlu 200
DB 765 CTCGAAGGATCATCTCACTCAATTTTGAAGAAGTCTGCATCGAAATTTCTAGCAGCTGAA 824
```

```
QY 201 ProSerThrIleCysAlaGlyGluSerPheGlnValValArgGlyAsnGlyPheArg 220
DB 825 CCATCCACCATATATGACGAGAGTCAATTTCAATGTTCCGGAAGAGAAACGGCTTCCGA 884
QY 221 HisAlaArgAsnValAspArgValLeuCysSerPheLysIleAsnAspSerValThrLeu 240
DB 885 CATCCCGCAACGTGACAGGGTCTCTGACGCTTCAAGATCATGATGATCGGTCAACTC 944
QY 241 AsnGluLysProPheSerValGluAspThrTrpLeuLeuCysProAlaProIleLeuLys 260
DB 945 AATGAGAAGCCCTTTTGTGAAAGATCTTAATTTACTGTGTCCAGCGCTATCTTAA 1004
QY 261 GluValGlyMetLysAlaAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIleSer 280
DB 1005 GAATTTGGCATGAAGCTGCACTCCAGGTACGATGAACATGAGCTCTCTTTATCTCC 1064
QY 281 SerSerValIleIleThrTrpThrHisCysSerAspGly 293
DB 1065 AGTTCTCATCATCATCACACACACACTGTTCTGACCGT 1103
```

RESULT 7

```
US-09-918-715-231
; Sequence 231, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107, 00134
; CURRENT APPLICATION NUMBER: US/09/918, 715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FaestSeq for Windows Version 3.0
; SEQ ID NO 231
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-231
```

```
Alignment Scores:
Pred. No.: 5,57e-184 Length: 5540
Score: 1526.00 Matches: 293
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
```

US-09-970-076-2_COPY_28_320 (1-293) x US-09-918-715-231 (1-5540)

```
QY 1 GlnGlyGlyArgArgGluAspGlyGlyProAlaCysTrpGlyGlyPheAspLeuTrpPhe 20
DB 225 CAAGGGGGAGCGCAGGAGGATGGGGGTCACCGCTGACGCGGATTTGACCTGTACTTC 284
QY 21 IleLeuAspLysSerGlySerValLeuHisTrpAsnGluIleTrpTrpPheValGlu 40
DB 285 ATTTTGACAAATCAGAAAGTGCTGACCACTGGAATGAAATCTATTACTTTGTGAA 344
QY 41 GlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSerPheIleValPheSerThr 60
DB 345 CAGTTGGCTCACAATTCATCAGCCCAAGTTGAGATGTCCTTATTTGTTTCTCACC 404
QY 61 ArgGlyThrThrLeuMetLysLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGlu 80
DB 405 CGAGGAACAACCTTAATGAAACTGACAGAAACAGAAACAAATCCGTCAAGGCTAGAA 464
QY 81 GlnLeuGlnLysValLeuProGlyGlyAspThrTrpMetHisGluGluPheGluArgAla 100
```

```
DB 465 GAACTCCGAAAGTTCTGCCAGAGGAGACATTACATGAGAGATTGGAAGGCC 524
QY 101 SerGluGlnIleTyTyrGluAanArgInGlyTyrArgThrAlaSerValIleIleAla 120
DB 525 AGTGAGCAGATTATATGAAAAACAGACAAAGGTAACAGACGCCCTCATTCATTGCT 584
QY 121 LeuThrAspGlyGluLeuHISGluAAspLeuPhePheTyrSerGluArgGlnAlaAanArg 140
DB 585 TTGACTGATGAGAACTCCATGAAAGATCTTTTCTTATTCAGAGGAGGCTAATAG 644
QY 141 SerArgAspLeuGlyAlaIleValTyrCySValGlyValIleAspPheAsnGluThrGln 160
DB 645 TCTCGAGATCTTGTCGCAATTGTTTACTGTGTGGTGAAGATTTCATGAGACAG 704
QY 161 LeuAlaArgIleAlaAspSerIleAspPheHISValPheProValAanAspGlyPheGlnAla 180
DB 705 CTGGCCCGGATTCGGAGAGTAAGATCATGTGTTCCCGTGAATGACGGCTTTCAGGCT 764
QY 181 LeuGlnGlyIleIleHISerIleLeuIleuIleuIleuIleuIleuIleuIleuIleuIleu 200
DB 765 CTGCAGAGCATCATCCACTCAATTGTAAGAGTCTTCGATCCAAATTCCTAGCAGCTGAA 824
QY 201 ProSerThrIleCySAlaGlyIleSerPheGlnValValValArgGlyAsnGlyPheArg 220
DB 825 CCATCCACCATATGTCAGAGAGAGTCAATTCAAGTTGTGTGAGAGAAACGGCTTCCGA 884
QY 221 HIsAlaArgAanValAspArgValLeuCySAspPheIleuIleuIleuIleuIleuIleu 240
DB 885 CATGCCCGCAACGTGAGACAGGGTCTCTGACGCTTCAAGATCATGACGTGCTCAACATC 944
QY 241 AsnGluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 260
DB 945 AATGAGAAAGCCCTTCTTCTGGAAGATCTTATTTACTGTGTCCAGGCTTATCTTAAAA 1004
QY 261 GluValGlyMetIleValAlaIleuGlnValSerMetAanAspGlyLeuSerPheIleSer 280
DB 1005 GAAGTTGGCATGAAGCTGACCTCCAGTCAGCATGAAGATGGCCCTCTTTTATCTTCC 1064
QY 281 SerSerValIleIleThrThrThrHisCySAspGly 293
DB 1065 AGTTCTGTCTCATCATCACACACACACTGTTCTGACGGT 1103

RESULT 8
US-10-301-822-198
; Sequence 198, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, ShubhangI
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: BURGART, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RMM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 5540
; TYPE: DNA
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; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144)...(1838)
US-10-301-822-198

Alignment Scores:
Pred. No.: 5,576-184 Length: 5540
Score: 1526.00 Matches: 293
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_copy_28_320 (1-293) x US-10-301-822-198 (1-5540)
QY 1 GlnGlyValArgValArgGluAspGlyGlyProAlaCySValGlyValPheAspLeuTyrPhe 20
DB 225 CAAGGGGAGCGCAGAGAGATGGGGGTCCAGCTGTCTACGGCGGATTTGACCTGTACTTC 284
QY 21 IleuAspIleSerGlySerValLeuHISValIleuIleuIleuIleuIleuIleuIleuIleu 40
DB 285 ATTGTGACAAATCAGAGAGTGTCTGACCACTGGAATGAAATCTATTACTTTGTGGAA 344
QY 41 GlnLeuAlaHISValPheIleSerProGlnLeuArgMetSerPheIleValPheSerThr 60
DB 345 CAGTGGCTCACAAATTCATCAGCCACAGTTGAGAATGTCTTTATTGTTTCTCCACC 404
QY 61 ArgGlyThrThrLeuMetIleuThrGlnAAspArgGlnIleArgGlnGlyLeuGlu 80
DB 405 CGAGGAACAACCTTAATGAAGCTGACAGAAACAGAGAACCAAAATCCGTCAAGGCTTAGAA 464
QY 81 GluLeuGlnIleuValLeuProGlyIleAspThrTyrMetHISGluGlyPheGlnArgAla 100
DB 465 GAACTCCGAAAGTTCTGCCAGAGAGACACTTACATGATGAAGATTGAAAGGCC 524
QY 101 SerGluGlnIleTyTyrGluAanArgInGlyTyrArgThrAlaSerValIleIleAla 120
DB 525 AGTGAGCAGATTATATGAAAAACAGACAAAGGTAACAGACGCCCTCATTCATTGCT 584
QY 121 LeuThrAspGlyGluLeuHISGluAAspLeuPhePheTyrSerGluArgGlnAlaAanArg 140
DB 585 TTGACTGATGAGAACTCCATGAAAGATCTTTTCTTATTCAGAGGAGGCTAATAG 644
QY 141 SerArgAspLeuGlyAlaIleValTyrCySValGlyValIleAspPheAsnGluThrGln 160
DB 645 TCTCGAGATCTTGTCGCAATTGTTTACTGTGTGGTGAAGATTTCATGAGACAG 704
QY 161 LeuAlaArgIleAlaAspSerIleAspPheHISValPheProValAanAspGlyPheGlnAla 180
DB 705 CTGGCCCGGATTCGGAGAGTAAGATCATGTGTTCCCGTGAATGACGGCTTTCAGGCT 764
QY 181 LeuGlnGlyIleIleHISerIleLeuIleuIleuIleuIleuIleuIleuIleuIleuIleu 200
DB 765 CTGCAGAGCATCATCCACTCAATTGTAAGAGTCTTCGATCCAAATTCCTAGCAGCTGAA 824
QY 201 ProSerThrIleCySAlaGlyIleSerPheGlnValValValArgGlyAsnGlyPheArg 220
DB 825 CCATCCACCATATGTCAGAGAGAGTCAATTCAAGTTGTGTGAGAGAAACGGCTTCCGA 884
QY 221 HIsAlaArgAanValAspArgValLeuCySAspPheIleuIleuIleuIleuIleuIleuIleu 240
DB 885 CATGCCCGCAACGTGAGACAGGGTCTCTGACGCTTCAAGATCATGACGTGCTCAACATC 944
QY 241 AsnGluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 260
DB 945 AATGAGAAAGCCCTTCTTCTGGAAGATCTTATTTACTGTGTCCAGGCTTATCTTAAAA 1004
QY 261 GluValGlyMetIleValAlaIleuGlnValSerMetAanAspGlyLeuSerPheIleSer 280
DB 1005 GAAGTTGGCATGAAGCTGACCTCCAGTCAGCATGAAGATGGCCCTCTTTTATCTTCC 1064
QY 281 SerSerValIleIleThrThrThrHisCySAspGly 293
```


DB 405 CGAGGAACTTATGAACTGACAGAGACAGAACCAATCCGTCAAGGCTTAGAA 464
QY 81 GILUEGLINLYSVALLEUPROGLYGLYASPTHTYRMEHISGLUGLYPHEGLUARGLA 100
DB 465 GAACCTCCAGAAAGTTCTGCGAGAGAGACACTTACATCAAGAGATTGAAAGGGCC 524
QY 101 SERGLUGNILETYRTYRGLUBSNARGINGLYTYRARGTHRLASERVALILEILEA 120
DB 525 AGTGACGATTTATTTATGAAAACAGACAAGGTCACGACCGCTCATCTGCT 584
QY 121 LEUTHASPGILGLUEUHSGLUEPLEUPHEPHETYRSEGLUARGLUAAENARG 140
DB 589 TTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTATTACAGAGAGGAGCTAATAG 644
QY 141 SERHARGAPLEUGLYVALAILEVALTYRCYSEVALGLYVALLYASPHASPHENGLU 160
DB 645 TCTCGAGATCTTGCGCAATGTTTACTGTGTGTGTAAGATTTCATGACACAG 704
QY 161 LEUALAARGILEALASPSERLYSAPHSVALPHEPROVALASNAPGLYPHEGLNLA 180
DB 705 CTGGCCCGAATTCGGACAGTAAGATCATGTGTTCCCGTGAATGACGGCTTTCAGGCT 764
QY 181 LEUGINGLYILEIHEISERILEUPLYSESCYSEILEGUILLEUALAAGLU 200
DB 765 CTGCAAGGCATCATCACTCAATTTTGAAGAAGTCTCGCATCGAAATTCAGACGCTGAA 824
QY 201 PROSETHRLIECYVALAAGLYGUSERPHEGLNVALVALARGLYLENGLYPHEARG 220
DB 825 CCATCCACATATGTCAGAGAGAGTCAATTCAGGTGCGTGAAGAGAAACGGCTTCCGA 884
QY 221 HISALARGASNAVALASPARGVALLIUCYSESPHELYLEASNAPSERVALTHRL 240
DB 885 CATGCCCGAAGCTGACAGGGCTCTCTGACGTTCAAGATCATATACCTGGCACACATC 944
QY 241 AENGLIYSPROBSESERVALGUASPTHRYRLEULEUCYSPROILAPOILLEULYS 260
DB 945 AATGAGAAAGCCCTTTCTGGAAGATCTTATTATCTGTCTCAAGCCTATCTTAAAA 1004
QY 261 GILVALIGLYMETLYSVALAILEUGINVALSERMEASNAPGLYLEUSERPHEILESE 280
DB 1005 GAAGTTGGCATGAAGCTGACCTCCAGGTCAGCATGAACGATGGCCTCTTTTATCTCC 1064
QY 281 SERSEVALILEIETHRTHRLHSYSESEASPGLY 293
DB 1065 AGTTCTGTCTATCTACACCAACACACTGTCTGACGCT 1103
RESULT 11
US-10-979-159-176
; Sequence 176, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107 00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-979-159-176
Alignment Scores:
Pred. No.: 5,576-184 Length: 5540
Score: 1526.00 Matches: 293
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-970-076-2_COPY_28_320 (1-293) x US-10-979-159-176 (1-5540)
QY 1 GINGLYGYARGXGILUASPGLYGLYPROALAICYRTYRGLYGLYPHEASPLEUTHRY 20
DB 225 CAAGGGGAGCGAGAGAGATGGGGGTCCAGCTGCTACGGCGGATTTGACCTGTCTTC 284
QY 21 ILEUASPLYSERGLYSERVALLEUHSISTPANSGLIILETYRTPHEVALIGLU 40
DB 285 ATTTTGGACAAATCGAAGAGTGTGTCACCACTGGAATGAATCTTACTTTGTGGA 344
QY 41 GINLEUALHILEYSPHEILESERPROGLNLEUARGMETSERPHEILEVALPHESETH 60
DB 345 CAGTTGGCTCAAAATTCATCAAGCCACAGTTGAGAAATGCTTTATGTTTCTCCACC 404
QY 61 ARGGLYTHRLTHLEUMETLYSLEUTHRGUASPARGLUGNILEARGINGLYLEUGLU 80
DB 405 CGAGGAACTTAAATGAAGTGAACAGAGAGACAGAAACAAATCCGTCAAGGCTTAGAA 464
QY 81 GILUEGLINLYSVALLEUPROGLYGLYASPTHTYRMEHISGLUGLYPHEGLUARGLA 100
DB 465 GAACCTCCAGAAAGTTCTGCGAGAGAGACACTTACATCAAGAGATTGAAAGGGCC 524
QY 101 SERGLUGNILETYRTYRGLUBSNARGINGLYTYRARGTHRLASERVALILEILEA 120
DB 525 AGTGACGATTTATTTATGAAAACAGACAAGGTCACGACAGACCGCATCTGCT 584
QY 121 LEUTHASPGILGLUEUHSGLUEPLEUPHEPHETYRSEGLUARGLUAAENARG 140
DB 589 TTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTATTACAGAGAGGAGCTAATAG 644
QY 141 SERHARGAPLEUGLYVALAILEVALTYRCYSEVALGLYVALLYASPHASPHENGLU 160
DB 645 TCTCGAGATCTTGCGCAATGTTTACTGTGTGTGTAAGATTTCATGACACAG 704
QY 161 LEUALAARGILEALASPSERLYSAPHSVALPHEPROVALASNAPGLYPHEGLNLA 180
DB 705 CTGGCCCGAATTCGGACAGTAAGATCATGTGTTCCCGTGAATGACGGCTTTCAGGCT 764
QY 181 LEUGINGLYILEIHEISERILEUPLYSESCYSEILEGUILLEUALAAGLU 200
DB 765 CTGCAAGGCATCATCACTCAATTTTGAAGAAGTCTCGCATCGAAATTCAGACGCTGAA 824
QY 201 PROSETHRLIECYVALAAGLYGUSERPHEGLNVALVALARGLYAENGLYPHEARG 220
DB 825 CCATCCACATATGTCAGAGAGAGTCAATTCAGGTGCGTGAAGAGAAACGGCTTCCGA 884
QY 221 HISALARGASNAVALASPARGVALLIUCYSESPHELYLEASNAPSERVALTHRL 240
DB 885 CATGCCCGAAGCTGACAGGGCTCTCTGACGTTCAAGATCATATGCTGGCACACATC 944
QY 241 AENGLIYSPROBSESERVALGUASPTHRYRLEULEUCYSPROILAPOILLEULYS 260
DB 945 AATGAGAAAGCCCTTTCTGGAAGATCTTATTATCTGTCTCAAGCCTATCTTAAAA 1004
QY 261 GILVALIGLYMETLYSVALAILEUGINVALSERMEASNAPGLYLEUSERPHEILESE 280
DB 1005 GAAGTTGGCATGAAGCTGACCTCCAGGTCAGCATGAACGATGGCCTCTTTTATCTCC 1064
QY 281 SERSEVALILEIETHRTHRLHSYSESEASPGLY 293
DB 1065 AGTTCTGTCTATCTACACCAACACACTGTCTGACGCT 1103
RESULT 12

QY 61 ArgGlyThrThreumetylserleuthrgluaspargluGlnlleargGlnlyleuGln 80
DB 405 CAGAGAACAACTTATGAACTGACAGAAACAGAAACAAATCCGTCAAGGCTTAGAA 464
QY 81 GluLeuGlnlyValleuProGlyIAspThrTYrmeChisGlnGlyPheGluArgAla 100
DB 465 GAACCTCAGAAAGTTCTGCAGAGAGAGACATTACATGATGAAAGATTGAAAGGCGC 524
QY 101 SerGluGlnlleTYrGluAenargGlnlyTYrArgThrAlaSerValilleleAla 120
DB 525 AGGAGACAGATTATATGAAACAGACAAAGGATACAGACAGCCAGCGTCATCATTTGCT 584
QY 121 LeuThrAspGlyGluLeuuhisGluAspLeuPhePheTYrSerGluArgGlnAlaAenArg 140
DB 585 TTGACGTGATGAGAACTCCATGAAAGATCTTTTCTATTCAAGAGAGGAGCTTAATAG 644
QY 141 SerArgAspLeuGlyAlaIleValTYrCyseValGlyValIysAspPheAenGluThrGln 160
DB 645 TCTCGAGATCTTGTCATTTGTTACTGTGTGTGTAAGATTTCATATGAGACACAG 704
QY 161 LeuAlaArgGlnleAlaSerSerlysaAspHisValPheProValAsnAspGlyPheGlnAla 180
DB 705 CTGGCCCGAGATGCGAGACAGTAAGATCATGTGTCCGTGATAGACGCTTTCAGGCT 764
QY 181 LeuGlnGlyIleIleHisSerIleLeuLysLysSerCyseIleGluIleLeuAlaIleGln 200
DB 765 CTGCAGAGCATCTCCATCTCAATTGGAAGAACTCTCGATCGAATTCAGACAGCTGAA 824
QY 201 ProSerThrIleCyseAlaGlyIuserPheGlnValIaValIArgGlyAenGlyPheArg 220
DB 825 CCATCCACCATATGTGCAGAGAGTCATTTCAAGTTGTCGTGAGAGAAACGCGCTTCCGA 884
QY 221 HisAlaArgAsnValAspArgValLeuCysePheLysIleAsnAspSerValThrLeu 240
DB 885 CATGCCCGACACGTGACAGGGGTCTCTGCAGCTTCAGATCATGACTGGACACACTC 944
QY 241 AsnGlyLysProPheSerValGluAspThrTYrLeuLeuCyseProIaProIleLeuLys 260
DB 945 AATGAGAAAGCCCTTTCTGTGGAAGATCTTATTACTGTCTCAAGCGCTTATCTTAA 1004
QY 261 GluValGlyMetLysAlaIleGlnValIserMetAsnAspGlyLeuSerPheIleSer 280
DB 1005 GAAGTTGGCATGAAGCTGCACCTCCAGTCCAGCATGAACGATGCGCTCTTTATCTCC 1064
QY 281 SerSerValIleIleThrThrThrHisCyseSerAspGly 293
DB 1065 AGTTCTGTCAATCAACCAACCACTGTTCTGACGCT 1103
RESULT 14
US-10-038-307-23
; Sequence 23, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038.307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ. ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-23
Alignment Scores: 1.39e-183 Length: 1056
Pred. No.: 1514.00 Matches: 291

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.21% Indels: 0
DB: 6 Gaps: 0
US-09-970-076-2_COPY_28_320 (1-293) x US-10-038-307-23 (1-1056)
QY 1 GlnGlyIArgArgGluAspGlyGlyProAlaCyseTYrGlyIysPheAspLeuTYrPhe 20
DB 94 CAAAGGGAGCGCAGAGGAGATGGGGGTCCAGGCTGCTACGGGGGATTTGACTGTACTTC 153
QY 21 IleLeuAspLysSerGlySerValLeuuhisIleIlePheAenGluIleTYrTYrPheValGlu 40
DB 154 ATTTTGGCAAAATTCAGAAAGTGTGTGCACTGGAATGAAATCTATTACTTTGTGGAA 213
QY 41 GlnLeuAlaHisLysPheIleSerProGlnLeuAArgMetSerPheIleValPheSerThr 60
DB 214 CAGTTGGCTCACAATAATTCATGACCACGTTTGAAGATGCTCTTATTGTGTTTCTCCACC 273
QY 61 ArgGlyThrThreumetylserleuthrgluaspargluGlnlleargGlnlyleuGln 80
DB 274 CAGAGAACAACTTATGAACTGACAGAAACAGAAACAAATCCGTCAAGGCTTAGAA 333
QY 81 GluLeuGlnlyValleuProGlyIAspThrTYrmeChisGlnGlyPheGluArgAla 100
DB 334 GAACCTCCAGAAAGTTCTGCAGAGAGACACTTACATGATGAAAGATTGAAAGGCGC 393
QY 101 SerGluGlnlleTYrGluAenargGlnlyTYrArgThrAlaSerValilleleAla 120
DB 394 AGTGAACAGATTATATGAAACAGACAAAGGATCAGGACAGCCGCTCATCTTGTCT 453
QY 121 LeuThrAspGlyGluLeuuhisGluAspLeuPhePheTYrSerGluArgGlnAlaAenArg 140
DB 454 TTGACGTGATGAGAACTCCATGAAGATCTTTTCTATTACAGAGGAGGAGCTTAATAG 513
QY 141 SerArgAspLeuGlyAlaIleValTYrCyseValGlyValIysAspPheAenGluThrGln 160
DB 514 TCTCAGATCTTGTCGCAATTTTACTGTGTGTGTAAGATTTCATATGAGACACAG 573
QY 161 LeuAlaArgIleAlaAspSerlysaAspHisValPheProValAsnAspGlyPheGlnAla 180
DB 574 CTGGCCCGAGTCCGACAGTAAGATCATGTGTTCCGTGATAGACGCGCTTTCAGGCT 633
QY 181 LeuGlnGlyIleIleHisSerIleLeuLysLysSerCyseIleGluIleLeuAlaIleGln 200
DB 634 CTGCAGAGCATCATCACTCAATTTTGAAGAGTCTGATCGAATTCAGACAGCTGAA 693
QY 201 ProSerThrIleCyseAlaGlyIuserPheGlnValIaValIArgGlyAenGlyPheArg 220
DB 694 CCATCCACCATATGTGCAGAGAGTCATTTCAAGTTGTGTGTAAGAGAAACGCGCTTCCGA 753
QY 221 HisAlaArgAsnValAspArgValLeuCyseSerPheLysIleAsnAspSerValThrLeu 240
DB 754 CATGCCCGACACGTGACAGGGGTCTCTGCAGCTTCAAAATGATGATCTCGTCAACACTC 813
QY 241 AsnGlyLysProPheSerValGluAspThrTYrLeuLeuCyseProIaProIleLeuLys 260
DB 814 AATGAGAAAGCCCTTTCTGTGGAAGATCTTATTACTGTGTCCAGCGCTTATCTTAA 873
QY 261 GluValGlyMetLysAlaIleGlnValIserMetAsnAspGlyLeuSerPheIleSer 280
DB 874 GAAGTTGGCATGAAGCTGCACCTCCAGTCCAGACATGAAGATGCGCTCTTTATCTCC 933
QY 281 SerSerValIleIleThrThrThrHisCyseSer 291
DB 934 AGTTCTGTCAATCAACCAACCACTGTTCTGACGCT 966
RESULT 15
US-10-201-292-23
; Sequence 23, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 1056
TYPE: DNA
ORGANISM: Homo sapiens
US-10-201-292-23

Alignment Scores:
Pred. No.: 1,396-183 Length: 1056
Score: 1514.00 Matches: 291
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.21% Indels: 0
DB: Gaps: 0

US-09-970-076-2_copy_28_320 (1-293) x US-10-201-292-23 (1-1056)

QY 1 GlnGlyGlyArgGlyArgGlyProAlaCysTyrGlyGlyPheAspLeuTyrPhe 20
DB 94 CAGGGGGAGCGCAGAGAGAGGGGGGCTCAGCCCTGCTACGGCGGATTTGACCTGTACTTC 153
QY 21 LLeuAspLysSerGlySerValLeuHisIleTrrPheGlnIleTyrTyrPheValGlu 40
DB 154 ATTTTGACCAATCAGGAGAGTGTCTGCACACCTGGAATGAATCTTACTTTGTGAA 213
QY 41 GlnLeuAlaHisIleLysPheIleSerProGlnLeuArgLysSerPheIleValPheSerThr 60
DB 214 CAGTTGGCTCACAATTCATCAGCCCAAGTTGAGAAATGCTTTATTTGTTCTCCACC 273
QY 61 ArgGlyThrThrLeuMetLysLeuThrGluAspArgGlnIleArgGlnIleLeuGlu 80
DB 274 CGAGGAACACCTTAATGAACCTGACAGACAGACAAATCCGTCAGAGGCTTGA 333
QY 81 GluLeuGlnLysValLeuProGlyLysPheThrTyrMetHisGlnGlyPheGluArgAla 100
DB 334 GAATCTCCAGAAAGTCTGCGCAGAGAGACCTTACATGCAATGAAGATTTGAAGGGCC 393
QY 101 SerGlnGlnIleTyrTyrGluAsnArgGlnIleTyrArgThrAlaSerValIleIleAla 120
DB 394 AGTAGAGAGATTTATATGAAACAGACAGAGGTACAGACAGCCAGCTCATCATGCT 453
QY 121 LeuThrArgGlyGluLeuHisGlnAspLeuPheThrTyrSerGluArgGluAlaAsnArg 140
DB 454 TTGACTGATGAGAACTCCATGAAGATCTTTTTCATTCAGAGAGGAGGCTAATAGG 513
QY 141 SerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAspPheAsnGluThrGln 160
DB 514 TCTGAGATCTTGATGCAATGTTACTGTGTGTGTGAAAGATTTCAATGAGACACAG 573
QY 161 LeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAla 180
DB 574 CTGGCCCGGATTCGCGACAGTAAGATCATGTGTTCCCGTAATGACGGCTTCAGGCT 633
QY 181 LeuGlnGlyIleIleHisSerIleLeuLysLysSerCysIleGluIleLeuAlaAlaGlu 200
DB 634 CTGCAGGCAATCATCTCAATTTTGAAGAGCTGCGATCGAAATTTAGCAGCTGAA 693
QY 201 ProSerThrIleCysAlaGlyGlySerPheGlnValValAlaArgGlyAsnGlyPheArg 220
DB 694 CCAATCCACCATATGTGACGAGAGATCATTTCAAGTTGTGCGAGAGAAACGGCTTCGA 753
QY 221 HisAlaArgAsnValAspArgValLeuCysSerPheLysIleAsnAspSerValThrLeu 240
DB 754 CATGCCCGCAACGTGACAGGGGTCTCTGACGCTTCAAGATCAATGACTCGGTCACTC 813

QY 241 AsnGluLysProPheSerValGluAspThrTyrLeuLeuCysProAlaProIleLeuLys 260
DB 814 AATGAGAGCCCTTTCTGTGAGAAATCTTATTACTGTGTCAGCGCTTACTTAA 873
QY 261 GluValGlyMetLysAlaAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIleSer 280
DB 874 GAAGTTGGCATGAAAGCTGCACTCCAGTCAGCATGACATGAGATGCTCTTTATCTCC 933
QY 281 SerSerValIleIleThrThrThrHisCysSer 291
DB 934 AGTTCTGTCAATCAACACACACTGTAGC 966

Search completed: December 19, 2005, 02:10:15
Job time : 959.696 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:41:36 / Search time 236.436 Seconds
(without alignments)
607.449 Million cell updates/sec

Title: US-09-970-076-2_COPY_28_320

Perfect score: 1526
Sequence: 1 OCGRRDGCAGCYGDFLYF.....DGLSFSSVITTHCSDG 293

Scoring table: BLOSUM62

Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5
Delpop 6.0	Delext 7.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cg2_1/USPTO.epool/US09970076/runac_14122005_111853_21065/app_query.fasta.1.2410
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=imbn -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=tblsune62
-TRANS=human40.cdt -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076 -CGC_1_1_675 -runac_14122005_111853_21065
-NCPU=6 -ICPU=3 -NO MAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA New:*

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2:	/cg2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3:	/cg2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4:	/cg2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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7:	/cg2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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9:	/cg2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
10:	/cg2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1526	100.0	5540	7	US-11-186-284-198
2	145.5	9.5	4740	7	US-11-080-026-3
3	131	8.6	11447	7	US-11-186-284-25
4	122	8.0	2834	6	US-10-750-185-39040
5	113.5	7.4	1325	6	US-10-750-185-36394
6	113.5	7.4	2501	6	US-10-821-234-182
7	113.5	7.4	3449	6	US-10-131-826A-293
8	111	7.3	3564	6	US-10-601-368-20

9	111	7.3	4858	6	US-10-601-368-19	Sequence 19, Appl
10	107.5	7.0	3175	6	US-10-995-561-464	Sequence 464, Appl
11	107.5	7.0	3464	6	US-10-995-561-465	Sequence 465, Appl
12	107.5	7.0	3468	6	US-10-995-561-466	Sequence 466, Appl
13	107	7.0	3564	6	US-10-601-368-2	Sequence 2, Appl1
14	107	7.0	3967	7	US-11-000-463-574	Sequence 574, Appl
15	107	7.0	3969	7	US-11-000-463-102	Sequence 102, Appl
16	107	7.0	5042	6	US-10-601-368-1	Sequence 1, Appl1
17	103.5	6.8	2765	6	US-10-750-185-25775	Sequence 25775, A
18	101.5	6.7	3868	6	US-10-995-561-404	Sequence 404, Appl
19	101.5	6.7	47572	6	US-10-995-561-13356	Sequence 13356, A
20	100	6.6	2773	7	US-11-102-240-33	Sequence 33, Appl1
21	96	6.3	3884	6	US-10-601-368-17	Sequence 17, Appl1
22	94	6.2	1062	7	US-11-137-465-11	Sequence 11, Appl1
23	94	6.2	1347	7	US-11-137-465-12	Sequence 12, Appl1
24	91.5	6.0	1881	6	US-10-467-657-5431	Sequence 5431, Appl
25	84.5	5.5	2715	6	US-10-507-275-4	Sequence 4, Appl1
26	82	5.4	3189	7	US-11-137-465-10	Sequence 10, Appl1
27	81.5	5.3	1688	6	US-10-510-386-157	Sequence 157, Appl
28	81	5.3	11115	6	US-10-513-786-6	Sequence 6, Appl1
29	81	5.3	11115	6	US-10-513-786-8	Sequence 8, Appl1
30	79.5	5.2	2317	6	US-10-793-626-4357	Sequence 4357, Appl
31	79.5	5.2	2987	6	US-10-793-626-3398	Sequence 3398, Appl
32	79.5	5.2	3366	6	US-10-467-657-6111	Sequence 6111, Appl
33	78.5	5.1	1895	6	US-10-750-185-42451	Sequence 42451, A
34	78	5.1	1329	6	US-10-467-657-3293	Sequence 3293, Appl
35	78	5.1	1443	6	US-10-467-657-7037	Sequence 7037, Appl
36	77.5	5.1	960	6	US-10-793-626-1039	Sequence 1039, Appl
37	77.5	5.1	1311	6	US-10-763-712A-118	Sequence 178, Appl
38	77.5	5.1	20600	6	US-10-829-826B-91	Sequence 91, Appl1
39	77.5	5.1	28586	6	US-10-829-826B-89	Sequence 89, Appl1
40	77.5	5.1	28586	6	US-10-829-826B-90	Sequence 90, Appl1
41	76.5	5.0	1548	6	US-10-467-657-7037	Sequence 7037, Appl
42	76	5.0	1407	6	US-10-467-657-4369	Sequence 4369, Appl
43	75.5	4.9	8157	6	US-10-523-912-1	Sequence 1, Appl1
44	75	4.9	3445	6	US-10-793-626-3648	Sequence 3648, Appl
45	74.5	4.9	2361	6	US-10-467-962B-102	Sequence 102, Appl

ALIGNMENTS

RESULT 1
US-11-186-284-198
Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kametkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF COLON CANCER
FILE REFERENCE: MP01-029P2RM
CURRENT APPLICATION NUMBER: US/11/186,284
PRIOR FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 198
LENGTH: 5540
TYPE: DNA

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/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (144)...(1838)
US-11-186-284-198

Alignment Scores:
Pred. No.: 3.8e-179 Length: 5540
Score: 1526.00 Matches: 293
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-970-076-2_COPY_28_320 (1-293) x US-11-186-284-198 (1-5540)

QY 1 GINGLYGIVARGRGIGUABRGIGYIPROALCYETRGIGYIPHEAPLEUTYRPHIE 20
DB 225 CAAGGGGGAGCGGAGGAGTGGGGGTCCAGCTGCTACGGCGGATTTGACCTGTACTTC 284
QY 21 ILEUABRPLYSERGLYSERVALLEUHISETYRABRGUULETYRTYRPHIEVALIGU 40
DB 285 ATTTTGACAAATCAGAAAGTGCTGTCGACCTGGAATGAATCTATTACTTGTGTGGA 344
QY 41 GINLEUALHISETYRPHIESETPROGINLEUARGMESERPHIELEVALPHESERTHR 60
DB 345 CAGTTGGCTCACAATTCATCAGCCACAGTTGAGATGCTCTTATTGTTTTCTCACG 404
QY 61 ARGGLYTHRTYRLEUWETLYSEUPTHYRGIUABRARGIGUINILEARGGINIGLEUGIU 80
DB 405 CGAGGAAACAACCTTAATGAAACTGACAGAGAACAGAACTCCGTCAAGGCGCTAGAA 464
QY 81 GIULEUGIULYVALLEUPROGIGIYABRTHRTYRMECHISGLIGIUPHEGIUARGIA 100
DB 465 GAACCTCAGAAATTTCTGCGAGAGAGACCTTACATGATGATGAAGATTTGAAAGGGCC 524
QY 101 SERGIUGINILETYRTYRGIUABRARGINGLYTYRARGTHRLASERVALILEALEA 120
DB 525 AGTGACACAAATTTATATGAAAACAGCAAGGATACAGACCCGCTCATCATTTGCT 584
QY 121 LEUTHRABRGIGIULUWHISGLIABRLEUPHERPHETYSERGIUARGIUALAANARG 140
DB 585 TTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTATTACAGAGAGGCGCTTAATAG 644
QY 141 SERARGABRLEUVALILEVALTYRCYVALGIVALLYABRPHIEANRGUININ 160
DB 645 TCTCGAGATCTGTGCAATTTGTTACTGTGTGGTGTGAAAGATTTCAATGAGACACAG 704
QY 161 LEUALARGILEALIAABRSETRLYABRPHIEVALPHERVOYALANBRGIPHEGINALA 180
DB 705 CTGGCCCGGATTCGCGACATTAAGATCATGTGTTCCCGTAATGACGGCTTTCAAGGCT 764
QY 181 LEUGINGIYILEIHEISERTILEUUYLYSERCYAILEGUILLEUALAALIGU 200
DB 765 CTCGAAAGGCATCATCTCAATTTTGAAAGAGCTCGCATCGAAATTTCTAGACAGCTGAA 824
QY 201 PROSETRTHRTYRLECYAALIGIUSERPHEGINVALIYALARGIYAANRGIPHEARG 220
DB 825 CCATCCACCAATATGTGAGAGAGATCTTTCAAGTTGTCGTGAGAGGAAAGCGCTTCGGA 884
QY 221 HIALAARGABVALAABRARGVALLEUCYSESRPHELYSILEANBRSETRVALTHNLEU 240
DB 885 CATGCCCGCAACGTGGACAGGGTCTCTGACGCTTCAAGATCAATGACTGGCTCACACTC 944
QY 241 AARGIULYABRPHESERVALIGUABRTHRTYRLEUENCYSPROIALPROIILEUUY 260
DB 945 AATGAGAAAGCCCTTTCTGTGAAAGATCTTATTATTACTGTCCAGGCGCTATCTTAAAA 1004
QY 261 GIUVALIGIUMETLYSALIALALEUGINVALISERTHEANBRGILYLEUSERTPHIESE 280
DB 1005 GAAGTTGGCATGAAAGCTGCACTCCAGTGACGATGAACATAGGCTCTCTTTATCTCC 1064
QY 281 SERSERVALILEIETHRTYRTHRTYRHIACYSERABRGILY 293
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DB 1065 AGTTCTGATCATCATCACACACGACATGTTCTGACGGT 1103

RESULT 2
US-11-080-026-3
/ Sequence 3, Application US/11080026
/ Publication No. US20050260192A1
/ GENERAL INFORMATION:
/ APPLICANT: Springer, Timothy A.
/ APPLICANT: Shinmoka, Motomu
/ APPLICANT: Lu, Chafen
/ TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
/ FILE OF INVENTION: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME
/ FILE REFERENCE: CPER-P02-021
/ CURRENT APPLICATION NUMBER: US/11/080,026
/ PRIOR FILING DATE: 2005-03-15
/ PRIOR APPLICATION NUMBER: 09/945,265
/ PRIOR FILING DATE: 2001-08-31
/ PRIOR APPLICATION NUMBER: US 60/229,700
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 4740
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-080-026-3

Alignment Scores:
Pred. No.: 1.15e-06 Length: 4740
Score: 145.50 Matches: 60
Percent Similarity: 45.85% Conservative: 45
Best Local Similarity: 25.20% Mismatches: 81
Query Match: 9.53% Indels: 43
DB: 7 Gaps: 12

US-09-970-076-2_COPY_28_320 (1-293) x US-11-080-026-3 (1-4740)

QY 17 ABPLUETHYRPHIILEUABRPLYSERGLYSERVALLEU---HIETRPHANGLIUE 35
DB 520 GACATTCGCTTTGATTTATGCTGTGTGATGATCATCTCCACATACCTTTGGCGGAG 579
QY 36 TYTYRPHIEVALIGUINLEUALHISLYRPHIESETPROGINLEUARGMESERPHIE 55
DB 580 AAGGAGTTTGTCTCAACT-----GTGATGAGCAATTAATAAAGTCCAA 624
QY 56 ILEVALPHESERTHRARGGLYTHRTYRLEUWETLYSEUPTHYRGIUABR----- 71
DB 625 ACCTGTCTCT-----TTGATGCACTACTCTGAAAGATTCGCGATTCAC 669
QY 72 -----ARGGIUGINILEARGGINIYLEUGIULYLEUGIULYLEUGIN 83
DB 670 TTTAACCTTAAGAGATTCCAGAAACAACCTTAACCCAAAGATCTGTGAAAGCCAAATAG 729
QY 84 LYVALLEUPROGIGIYABRTHRTYRMECHISGLIYRPHIEGIUARGIASERGIUGIN 103
DB 730 CAGCTGCTT-----GGGGGACACACACGGCCACGGGATCGCAAGAGTGAAGAGAG 783
QY 104 ILETYRTYRGIUABRARGGINIYTYRARGTHRLA---SERVALILEIHEIETHRT 122
DB 784 CTGTTTACATCAACCAACGAGGCCGAAAGATGCTTTAAGATCTTACTAGTTGATCACG 843
QY 123 ABRGIGIULUWHISGLIABRLEUPHERPHETYSERGIU-----ARGIUALAANARG 140
DB 844 GATGGGAAAGATTTGGGCAATCCCTTGGATATGAGATGATCATCCCTGAGGACAGACA 903
QY 141 SERARGABRLEUGIYALIAILEVALTYRCYVALGIVALLYABRPHIEANRGUININ 160
DB 904 GAG-----GGAATCATTTGCTACGTCATTTGGGGTGGAGATCCCTTCCGACAGTGA 954
QY 161 LEUALARG-----ILEALABRSETR-----LYABRPHISVALPHEPRO 173
DB 955 AATCCCGCAAGAGCTTAATACATGATCCAAAGCCGCTGTGATCAAGTGTTCAG 1014
```



```

Oy      174 ValaanaapgyPhgGlnAlaLeuengInglyIlelleHlaIseTleuLybysercys 193
Db      1015 GTGAATTAAC---TTTGAAGCTTTGAAGACATTTCAGAACCAAGCTTCGGAGAG- 1065
Oy      194 IleguileleuAlaAlaGluProSerThrIleCyAlaGlyIuSerPhgGlnValaI 213
Db      1066 -----ATCTTGGCATCGAGGGTACTCGACAGAGAGTAGAGCTCTTGAGCATGAG 1119
Oy      214 ValaTgGlyAenGlyPhaArgHlaIa 222
Db      1120 ATGTCTCAGAGAGGCTTCAGCGCTGCC 1146

RESULT 3
US-11-186-284-25
; Sequence 25, Application US/11186284
; Publication No. US20050266493a1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPW01-029P2RUM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11447
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(9192)
US-11-186-284-25

Alignment Scores:
Pred. No.: 0.000288 Length: 11447
Score: 131.00 Matches: 59
Percent Similarity: 48.98% Conservative: 38
Best Local Similarity: 29.80% Mismatches: 75
Query Match: 8.58% Indels: 26
DB: Gaps: 13

US-09-970-076-2_COPY_28_320 (1-793) x US-11-186-284-25 (1-11447)
Oy      17 AepLeuYrPhelIleuApyLySerGlySerVal---LeuHlaHlaItrpaGlnIle 35
Db      1318 GAAATGTGCTTTTGGATGAGTGGCTCTCATAGCATGGAGATTGCAGAACTTGTAAAGTT 1377
Oy      36 TyTyrPhaValaGluGlnLeuAlaHlaIbLybPhe---IleSerPro---GlnLeuArgMet 53
Db      1378 AGAGGCTTTTGGAAAGCTCTTGAAAAAGTTTGAATTTCACCAAAATAGAGGTCAAGTT 1437
Oy      54 SerPheIleValaPheSerThr-----ArgGlyThrThrIleuMetLybLeuThGlu 70
Db      1438 AGCTTTGCAATACAGCCGGGATCTCATATCTGAGTTCACCTTTGGAAAAATTGCACAAA 1497

```

```

OY 71 AsparagluGlnIleArgGlnGlyLeuclGluLeuGlnIlyValIleuPro-----Gly 88
Db 1498 GTTGAAGATATAATT-----GAGCAATAAACACCTTCCCTTACAGAGGA 15424
OY 89 GlyAspThrTyrmethIleGluGlyPheGluArgAlaSerGluGlnIleTyrrTyrluAsn 108
Db 1543 GGATCTACAAATATCGCGCAAGCAATGACTTATGTGCAGAGAGAAATATTGTGCTGAC 16024
OY 109 ArgGlnGlyTyrrArgThr-----AlaSerValIleIleAlaLeuThrAspGlyGluLeu 126
Db 1603 AAG--GGATCAAGAGCAAGCATGTGCCAAGGTCATGATCTTATACCGAGTGGGAAA-- 1656
OY 127 HisGluAspLeuPhePheTyrrSerGluArgIluAlaSerArgSerAspLeuGlyAla 146
Db 1657 TCATCAGATGCTTTC-----AGAGATCCTGGATATAACGTAGGAAATTCAGATGTT 17074
OY 147 IleValTyrrCyrrValGlyValIleAspPheAsnGluThrGlnLeuAlaArgIleAlaAsp 166
Db 1708 GAATCTTTGACGTTGGTGGTGAAGATGCCGTTGGCTCAGAAATTGGAAGCATTTGGCTCT 1764
OY 167 -----SerIlyAspPheIleValPheProValAsnAspGlyPheGlnAlaLeuGlnGlyIle 184
Db 1768 CCTCCGTCAGAGACCCATGTTGTTCAAGTGGAAAT--TTTGATGCTTTTCAAGAGATA 18244
OY 185 IleHisSerIleLeuIlyLysSerCyrrIleGluIle-----LeuAlaAla 199
Db 1825 TCTTTGAACTCACACAGCTTATCTGCTTGAATGAGCAAGAAATTGGCAGCT 1878

RESULT 4
US-10-750-185-39040/C
; Sequence 39040, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39040
; LENGTH: 2834
; TYPE: DNA
; ORGANISM: Bovine 19866880867914
US-10-750-185-39040

Alignment Scores:
Pred. No.: 0.000453 Length: 2834
Score: 122.00 Matches: 54
Percent Similarity: 50.00% Conservative: 39
Best Local Similarity: 29.03% Mismatches: 71
Query Match: 7.99% Indels: 24
                Gaps: 10

US-09-970-076-2_COPY_28_320 (1-293) x US-10-750-185-39040 (1-2834)

OY 17 AspleuTyrrPheIleLeuAspLysSerGlySerAlaLeuHisIleStrAsnGlu----- 34
Db 2115 GACATTTACTTCCTTATATGACGGGCTTGGCAGTACC-----CACCAAGACACTTTCTC 20624
OY 35 ---IleTyrrPheValGluGlnLeuAlaHisLysPhe---IleSerProGlnLeuArg 52
Db 2061 GCGATGAAGAGCTTTCATGATGAGTGAATGAATAAGATGTTCCACGTTGAGACCGGAC--AGA 20054
OY 53 MetSerPheIleVal-PheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspAr 72

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Db 2004 GTCGACATTGGAGTCCATTCAGTACTCGATGAGTCAAGTCCCGCATGTTTACCCCTCAGCCAG 1945
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 72 ggluglnlIeaarglnlYleuqlu-----gluIeuglnlyValIeuProgl 88
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1944 CACTCCAGTGTGGCAGGCGCTTGAGGTAGCCGTTGACAGCATCAGCAG-----AAGG 1891
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 88 yglIaerPhrTyMehNlsgluqlYpHeqluArAlaSerGluqlnIleTyTyrgluAs 108
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1890 AAGGGGACCAAGATGGGTGAGGCCGCG---GGCAGACATGATCCAGTCTTTTCCAGATC 1834
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 108 nArglnlYTyArgThraIaSerValIleIleAlaIeuThraPrglYglIeuhIseql 128
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1833 TGCTCCACAGCA-CGTGCCCTT-GGTATCTCATTTGTGTCACTGACGAGCCCAATCTATGA 1776
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 128 uAerPhrPheTySerGluArqluAlaAerSerArgAerPheqlYValIleVa 148
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1775 CCGCGTG-----GCTGATGCTGCAGAGCGCGTGAAGGCGCCATGAGATCACCAT 1728
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 148 lTyCyVaIglYValIyAerPheAerngluThrglnIeulAlaArgIleAlaAerSerly 168
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1727 TATGAGTGTGGATGAGATGCTATATGCTGAGCTTCAAGAGATTGCTGA-----1673
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 168 sAerPhIseAlPheProValAernglYpHeqlnAlaIeuglnlYleIleHIsSerIl 188
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1672 -GACAGAAATGTTTTTGTGTCATGAT---TTTGAAGTCTTGAAAGCATTCCACAGAGAGT 1617
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 188 eleuYerlySerCys 193
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1616 GGTAACAAGACATCTGT 1601
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

RESULT 5

```
US-10-750-185-56394
/ Sequence 56394, Application US/10750185
/ Publication No. US20050260603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMT GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENBERG, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ PRIOR FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: Patent version 3.1
/ SEO ID NO 56394
/ LENGTH: 1325
/ TYPE: DNA
/ ORGANISM: Bovine
US-10-750-185-56394
```

Alignment Scores:

```
pred. No.: 0.00163 Length: 1325
Score: 113.50 Matches: 58
Percent Similarity: 42.63% Conservative: 49
Best Local Similarity: 23.11% Mismatches: 93
Query Match: 7.44% Indels: 51
DB: 6 Gaps: 15
```

US-09-970-076-2_COPY_28_320 (1-293) x US-10-750-185-56394 (1-1325)

```
Qy 9 GlyProAlaCysTyrgly---GlyPheAerPheTyPheIleleuAerPheTySerGlySer 27
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 456 GCGAGCGCCTGTAGAACAGCGAGCGAGCTGTCTTTATCTATGACACTACCGCAGC 515
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 28 Val---LeuHIsHlStrPaengluIleTyTyPhe---ValgluIeulAlaHIsLys 45
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
Db 516 GTCAACACCCACAGTACGCAAGGTCAAGAGTTCATTGTGACATCTTGCAGTTCTTG 575
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 46 PheIleSerProglIeU---ArgMehSerPheIleValPheSerThraArgIlyThr 64
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 576 GACATTTGGCGCTGAGGTACCCGCTGGGTCTGCTCCAGTAT-----GGCAGCAG 626
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 65 Leu-----MetlyIeuthrgluAerPArggluIleArglnlYleu 79
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 627 GTCAAGAACAGATTTCTCCCTCAAGACCTTCAAGAGAGAGTCCAGGTGAGCGTCCGTC 686
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 80 glugluIeuglnlyValIeuProglYglIaerPhrTyMehNlsgluqlYpHeqluAr 99
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 687 AAGAGATGCGCATCTGTCACAGGACACATGACGAGGCTGCGCATCCAGTAC-----740
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 100 AlAserGluqlnIleTyTyrgluAernglnlYTyArg-----Thx 114
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 741 ---GCCCTGAACATGCGCTTTCGGAAGAGAGGCGCGCGCCCTGAGGAGAAATG 797
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 115 AlAserValIleIleAlaIeuThraPrglYglIeuhIseqlYpHeTySer 134
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 798 CCTCGGTCATATGATGCTGACTGATGAGGAGCGCCACAGACTCGGTG-----845
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 135 GluArqluAlaAernglYpHeTySerPheqlYAlaIleValTyCyVaIglYVal---153
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 846 GCCGAGGTGCGCGCAAAAGCCGAGACAGAGCATCTGATCTTGCCATCGGTGCGC 905
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 154 ---LyAerPhrAerngluThrglnIeulAlaArgIleAerSerlyAerPhIseValPhe 172
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 906 CAGGTGACATTCAACACGCTGAAGCCATTTGGAGAGAGCCCAAGAGACACAGCTTTC 965
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 173 ProValAernglYpHeqlnAlaIeuglnlYleIleHIsSerIleuYerlySer 192
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 966 CTGTGTGCGCAAC---TTCAGCCAGATTGAGAGCTGACCTCAGTGTCCAGAAAGTTG 1022
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 193 Cys-----IlegluIleuAlaIa-----Glu 200
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1023 TGCAAGTACTCTGCTCTGTGTGCTCTTCTCGGGGATCGTTGGAGATGAGTCAATTCA 1082
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 201 ProSerThrIle-----CysAlaGlyIuSerPheqln 211
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1083 CTTTCCCGGCTTCATTCTGTGCTACTGCTCCAGATGATGTGCTGCGAAGGGGTCTTAA 1142
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 212 ValIleValIaArgGlyAernglYpHeAerghIseAla 222
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1143 GCAAGGTGAG-----ATAAGACACAGT 1166
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

RESULT 6

```
US-10-821-234-182/c
/ Sequence 182, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andarmant, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methode for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ PRIOR FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pc_seq Version 1.0
/ SEO ID NO 182
/ LENGTH: 2501
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-821-234-182
```

US-10-821-234-182

```
Alignment Scores:
pred. No.: 0.00432 Length: 2501
Score: 113.50 Matches: 66
Percent Similarity: 38.28% Conservative: 63
```

Best Local Similarity: 19.58% Mismatches: 109
Query Match: 7.44% Indels: 99
DB: 6 Gaps: 17

US-09-970-076-2_COPY_28_320 (1-293) x US-10-821-234-182 (1-2501)

QY 1 GlnGlyGlyArgGlyLeuArgGly---GlyProAla----- 11
DB 1631 GAAGGAGTCGATCGTGAAGATCGGCACGCGCCAGGAGAACACAGAACGAGATCGTC 1572
QY 12 -----CytGlyGlyGlyPheAspLeuTyrrPheIleLeuAspLysSerGlySerVal--- 28
DB 1571 CTGACCTTCGAGCTGATGATCATCTGCTGCTGATGATGATGATGATGATGATGATGATG 1512
QY 29 -----LeuHisIleTyrPheAspLeuIleTyrrPheValGluGlnIleAlaHis 44
DB 1511 GCCAGCACTTCACAGAGCCAAAGTGTCTATCACTTAATGAGAGAGTGCAGAT 1452
QY 45 LysPheIleSerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThr 64
DB 1451 TATGCTGTAAGCCA-----AGATATGCTGATGATGATGATGATGATGATGATGATG 1398
QY 65 LeuMetLysLeuThrGlu-----AspArgGluGlnIleArgGlnGlyLeuGlu 80
DB 1397 TGGGTCAAGTGTCTGAAGCAGACAGACAGATGATGATGATGATGATGATGATGATGAT 1338
QY 81 GluLeu-----GlnLysValLeuProGlyGlyAspThrTyrrMetHisGluGly 96
DB 1337 GAATTCATATATGAGAACACACAGTGTGAGTCAAGGACCTAACACC----- 1293
QY 97 PheGlnArgAlaSerGlnGlnIleTyrrGluLeuArg----- 109
DB 1292 ---AAGAAAGCTTCACAGGAGTGTACAGCATGATGATGATGATGATGATGATGATGAT 1236
QY 110 GlnGlyTyrr---ArgThrAlaSerValIleIleAlaLeuThrAspGly----- 124
DB 1235 GAAGGCTGAAACCCGACCCGCTGATCATCTCTCACTGATGATGATGATGATGATGATG 1176
QY 125 -----GluLeuHisGluLeuAspLeuPhePheTyrrSerGlu 135
DB 1175 GCGCGGAGCCCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1116
QY 136 ArgGlnAlaAspArgSerArgAspLeuGlyAlaIleValTyrrCysValGly-----Val 153
DB 1115 CGCAAAACCCAGAGGAGATATCTGATGATGATGATGATGATGATGATGATGATGATG 1056
QY 154 LysAspPheAspGlnIleGlnIleAlaArgIleAlaAspSerLysAspHisValPhePro 173
DB 1055 AACCAAGTGAACATCAATGCTTGGCTTCCAGAAAGACATGACAAATGCTTCAAA 996
QY 174 ValAspAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 193
DB 995 GTCAAGAT---ATGAAACCTCGAAGATGTTTCTACAAAGATGATGATGATGATGATG 942
QY 194 IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyLysSerPheGlnValVal 213
DB 941 -----CACTCTCTGAGTCTCTGT----- 924
QY 214 ValArgGlyLysGlnGlyPheArgHisAlaArgHisValAspArgValLeuCysSerPheLys 233
DB 923 -----GCGCATGCTTGGAAACACAGAGAGGTACCGAT----- 891
QY 234 IleAspAspSerValThrLeuAspGlnLysPheProSerValGluAspThrTyrrLeuLeu 253
DB 890 -----TACCAC 855
QY 254 CysProAlaProIleLeuLysGluValGlyMetLysValAlaAlaLeuGlnValSerMetAsn 273
DB 854 -----ATTGCGCTTCACAAAGGAGACACAGAGAGCTGTATGGG----- 819
QY 274 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThrHisCys 290
DB 818 -----GCTGAGTGTCTGAGTACTTGTGCTGACAGACAGACATTTG 777

RESULT 7
US-10-131-826A-293
Sequence 293, Application US/10131826A
Publication No. US20050245730A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 293
LENGTH: 3449
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-826A-293

Alignment Scores:
Pred. No.: 0.00707 Length: 3449
Score: 113.50 Matches: 55
Percent Similarity: 43.90% Conservative: 53
Best Local Similarity: 22.36% Mismatches: 103
Query Match: 7.44% Indels: 35
DB: 6 Gaps: 13

US-09-970-076-2_COPY_28_320 (1-293) x US-10-131-826A-293 (1-3449)

QY 17 AspLeuTyrrPheIleLeuAspLysSerGlySerVal---LeuHisIleTyrPheAspGlnIle 35
DB 372 GACCTGCTTTTCATCTTACATGACCTTCGACGTGCAACACCATGATGATGCAAGATC 431
QY 36 TyrrTyrrPhe---ValGluGlnIleAlaHisLysPheIleSerProGlnLeu---ArgMet 53
DB 432 AAGAGTTCATCTGAGCATCTTTCGCAATTCCTTGACATTCGCTGATGATGATGATGATG 491

[illegible]

Score:	111.00	Matches:	49
Percent Similarity:	37.93%	Conservative:	28
Best Local Similarity:	24.14%	Mismatches:	88
Query Match:	7.27%	Indels:	38
DB:	6	Gaps:	9

US-09-970-076-2_COPY_28_320 (1-293) x US-10-601-368-20 (1-3564)

QY	12	CysfryglglypheapleuTYrPheIlleuaplySserGlySserValleuHieHis	31
DB	475	TGCCAGACTTACATGATGACATGCTGATCTTGAAGTGGCTCCAAACAGATC--TACCCC	531
QY	32	TrypanhluileTYrTYrPheValGluLeuIleuIleHisIlyPhe---IleSerPro---	49
DB	532	TGGGTGGAGGCTCCAAACCTTCTCATATATCTCTCAAAAAGTTCTACATTGGCCCCGGC	591
QY	50	GlnleuIrgMetSerPheIleValPheSerThrArgGlyThrThreuMetLysLeuThr	69
DB	592	CAGATCCAGGTCGGAATATGATCCAGTATGAGAAGATGCCGTCATGATTCACCTT---	648
QY	70	GluapbrArgGlnIleArgGlnGlyLeuGlnLeuGlnLysValleuProGlyGly	89
DB	649	AATACCTACAGGTCTGTAAAGATGTGTGGAGCCGCCAGCCACATTTGACAGAGAGA	708
QY	90	AspThrTYrMetHisGlnGlyPheGlu-----ArgIleSerGlnIleTYrTyr	106
DB	709	GGAGCAGAGACCCGACGCGCATTTGGCATTTGAATTTGCACGCTTGGAGGCTTTCCAGAG	768
QY	107	GluapbrArgGlnGlyTYrArgThrIleSerValleuIleuThrAspGlyGlnLeu	126
DB	769	GGTGGAGAAAGAGGGGCCAAG-----AAAGTATGATTTGTCATCAGCAGCGGGAATCC	822
QY	127	HisGluAsp-----	129
DB	823	CACGACAGCCACGACTGGAGAGGTGATCCGACAGACGAGAAAGCAACGTGACCA	882
QY	130	-----LeuPhePheTYrSerGlnArgGlnIleuIleuAsnArgSerArgAspLeu	144
DB	883	TACGCTGGCGCGCTTTTGGGCTTACTTACAAACGCGAGGGGATCAATCCAGACATTTTCTA	942
QY	145	GlyIleIleValTYrCysValGlyValIlyAsp-----PheAsnGluThrGln	160
DB	943	AATGAATCAATATCATGCGCAGGACCCGTGACAGACCACTTCTTCAAGCTCAGAGAT	1002
QY	161	LeuIleArgIleIleIleAspSerLysAspHisValPheProValIleuAspGlyPheGlnAla	180
DB	1003	GAGCGGCGCGCTG-----AAGACACTTGTGATGCCCTTGGGACAGGATCTTGAC	1053
QY	181	LeuGlnGly	183
DB	1054	TTGGAAAGGC	1062

RESULT 9
US-10-601-368-19
Sequence 19, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lora, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
CURRENT FILING DATE: 2003-06-23
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 4858
TYPE: DNA
ORGANISM: Mus musculus

```
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128) ... (3591)
US-10-601-368-19

Alignment Scores:
Pred. No.: 0.0245 Length: 4858
Score: 111.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Best Local Similarity: 24.14% Mismatches: 88
Query Match: 7.27% Indels: 38
DB: Gaps: 9

US-09-970-076-2_COPY_28_320 (1-293) x US-10-601-368-19 (1-4858)

OY 12 CysTyrGlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHis 31
DB 502 TGCCAGACTTACATGACATGCTCATTTGTCTTAGTGCTCCACAGCATC---TACCC 558
OY 32 TrpAsnGluIleTyrTyrPheValGluGlnLeuAlaHisLysPhe---IleSerPro--- 49
DB 559 TGGGTGAGGTCCACACTTCTCTCTCATATCTCTCAAAAGTTCTTACATTGGCCCGCC 618
OY 50 GluLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThr 69
DB 619 CAGATCCAGCTCGGAATGATGACATGAGAGATGCCGTCATGATTCACCTT--- 675
OY 70 GluAspArgGluGlnIleArgGlnGlyLeuGluGlnLysValLeuProGlyGly 89
DB 676 AATACATCAACAGCTGTAAAGATGTGTGAGAGCCGCCACCATTTGACAGAGAGA 735
OY 90 AspThrTyrMetHisGluGlyPheGlu-----ArgLAserGluGlnIleTyrTyr 106
DB 736 GGGACAGAGACCCGACGCGCATTTGGCATTAATTGCAAGCTTGGAGGCTTCCAGAG 795
OY 107 GluAsnArgGlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeu 126
DB 796 GGTGAGAGAAAGGGGCCAAG-----AAAGTATGATTTGTCATCACGAGGGGAATCC 849
OY 127 HisGluAsp----- 129
DB 850 CACGACAGCCGACCTGGAGAGAGTATCCGCGAGAGCGAAGACAAACGTACAGAGA 909
OY 130 -----LeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeu 144
DB 910 TACGCTGGCCGCTTTGGCTACTACACCGCAGGGGATCAATCCAGACATTTTCTA 969
OY 145 GlyAlaIleValTyrCysValGlyValLysAsp-----PheAsnGluThrGln 160
DB 970 AATGAATCAAAATCATCGCCAGGAGCCCTGACGACAAACACTTCTTCACTCAAGAT 1029
OY 161 LeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAla 180
DB 1030 GAGCGCGCCCTG-----AAGGACATTTGTATGCTTGGGGACAGATCTTGAC 1080
OY 181 LeuGlnGly 183
DB 1081 TTGGAAGGC 1089

RESULT 10
US-10-995-561-464
; Sequence 464, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: C0001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 464
; LENGTH: 3175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-464

Alignment Scores:
Pred. No.: 0.035 Length: 3175
Score: 107.50 Matches: 50
Percent Similarity: 40.28% Conservative: 37
Best Local Similarity: 23.15% Mismatches: 84
Query Match: 7.04% Indels: 45
DB: Gaps: 9

US-09-970-076-2_COPY_28_320 (1-293) x US-10-995-561-464 (1-3175)

OY 18 LeuTyrPheIleLeuAspLysSerGlySerVal----- 28
DB 243 GTGTACTTCGTCGACACCTCGAGAGCGTCACATGACAGTCCCGACGACATCCTG 302
OY 29 LeuHisHisTrpAsnGlu---IleTyrTyrPheValGluGlnLeuAlaHisLysPheIle 47
DB 303 CTCTTCCAGATGAAGCAGATTCTGTCGCGCAGTTTCATGACGCGAGAGAGACTTCTAC 362
OY 48 SerProGluLeuArgMetSerPhe-----IleValPheSerThrArgGlyThr 63
DB 363 CTGACACAGGTGGCGCTGAGCTGCGCTTATGCGCGCTGACATTTCTTACACAGTGGAG 422
OY 64 ThrLeuMetLysLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGluGln 83
DB 423 GTGTTACGCCACCGGCGAGGACCGGCGCTTCTTCAAGAACCTGACGAGGATCAGC 482
OY 84 LysValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgLAserGluGln 103
DB 483 TCCTTCCGCGCGCGC-----ACCTTCAACGACTGCGCGCTGCGCAATGACGAGACAG 536
OY 104 IleTyrTyrGluAsnArgGlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAsp 123
DB 537 ATCCGACAGACCGCAGCAGAGGCG-----ACGTCACATTCGCGCGTGCATACCGAC 590
OY 124 GlyLeuLeuHisGluAspLeuPheTyrSerGluArgGluAlaAsnArgSerArgAsp 143
DB 591 GGCACGCTCACCGGACGCGCTGCGGGGATCAAGTCAAGCGACGCGCGCGCGAG 650
OY 144 LeuGlyAlaIleValTyrCysVal-----GlyValLys 154
DB 651 GAGGCGATCCGCGCTTTCGCGCGGCGCCCAACGACCACTGAAGAGCAGGCGCTCGG 710
OY 155 AspPheAsnGluThr-----GlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 172
DB 711 GACATCGCCAGCAGCGCGCAGAGCTTACCGC-----AAGCACTACGCCAAC 758
OY 173 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu----- 189
DB 759 ATGCTGCCYATCTCCACGAGATGACACGAGACCACTCAACGCACTCAACAGTCAATG 818
OY 190 -----LysLysSerCysIleGluIle 196
DB 819 AAACACGAGACCTACGAGAGATGCTACAAAGTGAAGTGCCTCGGAATC 866

RESULT 11
US-10-995-561-465
; Sequence 465, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: C0001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
```

```
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 3464
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-465
```

Alignment Scores:

Pred. No.:	0.04	Length:	3464
Score:	107.50	Matches:	50
Percent Similarity:	40.28%	Conservative:	37
Best Local Similarity:	23.15%	Mismatches:	84
Query Match:	7.04%	Indels:	45
DB:	6	Gaps:	9

US-09-970-076-2_COPY_28_320 (1-293) x US-10-995-561-465 (1-3464)

```
QY 18 LeuTYrPheIleuAAspLySerGlySerVal-----28
DB 243 GTGTAATTCTGCTGGACACTCGAGAGCGTCACCATGCAATCCCCACGACATCTTG
QY 29 LeuHISHeTTPAsnGlu---IleTYrTYrPheValGluGluLeuAlaHisysPheIle 47
DB 303 CTCCTCCACATGAAGAGTTCTGCGCGAGTTCATCAGCCAGCTGCGAAGACGATCTTAC
QY 48 SerProGluLeuAArgMetSerPhe-----IleValPheSerThrArgGlyThr 63
DB 363 CTGACACAGGTGGCTGAGCTGAGCTGAGCGCGCTGACCTTCTTGACCAAGTGGAG 422
QY 64 ThrLeuMetLyLeuThrGluAAspArgGluGlnIleArgGlnIlyLeuGluLeuGln 83
DB 423 GTGTTACAGCCACCGGCGACGACCGGCGCTCTTCATCAAGAACTGCGAGGCGATCAGC 482
QY 84 LysValLeuProGlyGlyAAspThrTYrMetHISgluGlyPheGluArgAlaSerGluGln 103
DB 483 TCCTTCGCGCGCGGC-----ACCTTCACCGAGCTGCGCGCTGCGCAACATGAGCGAGCAG 536
QY 104 IleTYrTYrGluAAspArgGlnIlyTYrArgThrAlaSerValIleIleAlaLeuThrAsp 123
DB 537 ATCCGCGAGGACCGGCGACCAAGGCG-----ACCGTCACCTCCCGCGTGCATCACCAGC 590
QY 124 GlyGluLeuHISgluAAspLeuPhePheTYrSerGluAArgGluAlaAAspArgSerArgAsp 143
DB 591 GCGCAGCTCACCGGCGACCCCTGCGGGGCGATCAAGCTGCGAGCGCGCGAGCGCGCGAG 650
QY 144 LeuGlyAlaIleValTYrCysVal-----GlyValLys 154
DB 651 GAGGGCATCCGCGCTCTTCCGCGGCGCCCAACCAAGACTGAAGAGAGCGGCGCTGCGG 710
QY 155 AspPheAsnGluThr-----GlnLeuAlaArgIleAlaAspSerLyAspHisValPhe 172
DB 711 GACATGCCACGACGCGCGACGAGCTTACCGC-----AACGACTACGCCACC 758
QY 173 ProValAAspArgLyPheGlnAlaLeuGlnIlyIleIleHisSerIleLeu-----189
DB 759 ATGCTGCYGACTCCACCGAGATRACACGAGACACCATCAACGCGCATCATCAAGGTGATG 818
QY 190 -----LysLySerCysIleGluIle 196
DB 819 AAACACGAGCGCTACGAGAGAGTGTACAAAGGTGAGTGGCTGGAAATC 866

RESULT 12
US-10-995-561-466
; Sequence 466, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michelle et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
```

```
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 3468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-466
```

Alignment Scores:

Pred. No.:	0.0401	Length:	3468
Score:	107.50	Matches:	50
Percent Similarity:	40.28%	Conservative:	37
Best Local Similarity:	23.15%	Mismatches:	84
Query Match:	7.04%	Indels:	45
DB:	6	Gaps:	9

US-09-970-076-2_COPY_28_320 (1-293) x US-10-995-561-466 (1-3468)

```
QY 18 LeuTYrPheIleuAAspLySerGlySerVal-----28
DB 243 GTGTAATTCTGCTGGACACTCGAGAGCGTCACCATGCAATCCCCACGACATCTTG
QY 29 LeuHISHeTTPAsnGlu---IleTYrTYrPheValGluGluLeuAlaHisysPheIle 47
DB 303 CTCCTCCACATGAAGAGTTCTGCGCGAGTTCATCAGCCAGCTGCGAAGACGATCTTAC
QY 48 SerProGluLeuAArgMetSerPhe-----IleValPheSerThrArgGlyThr 63
DB 363 CTGACACAGGTGGCTGAGCTGAGCTGAGCGCGCTGACCTTCTTGACCAAGTGGAG 422
QY 64 ThrLeuMetLyLeuThrGluAAspArgGluGlnIleArgGlnIlyLeuGluLeuGln 83
DB 423 GTGTTACAGCCACCGGCGACGACCGGCGCTCTTCATCAAGAACTGCGAGGCGATCAGC 482
QY 84 LysValLeuProGlyGlyAAspThrTYrMetHISgluGlyPheGluArgAlaSerGluGln 103
DB 483 TCCTTCGCGCGCGGC-----ACCTTCACCGAGCTGCGCGCTGCGCAACATGAGCGAGCAG 536
QY 104 IleTYrTYrGluAAspArgGlnIlyTYrArgThrAlaSerValIleIleAlaLeuThrAsp 123
DB 537 ATCCGCGAGGACCGGCGACCAAGGCG-----ACCGTCACCTCCCGCGTGCATCACCAGC 590
QY 124 GlyGluLeuHISgluAAspLeuPhePheTYrSerGluAArgGluAlaAAspArgSerArgAsp 143
DB 591 GCGCAGCTCACCGGCGACCCCTGCGGGGCGATCAAGCTGCGAGCGCGCGAGCGCGCGAG 650
QY 144 LeuGlyAlaIleValTYrCysVal-----GlyValLys 154
DB 651 GAGGGCATCCGCGCTCTTCCGCGGCGCCCAACCAAGACTGAAGAGAGCGGCGCTGCGG 710
QY 155 AspPheAsnGluThr-----GlnLeuAlaArgIleAlaAspSerLyAspHisValPhe 172
DB 711 GACATGCCACGACGCGCGACGAGCTTACCGC-----AACGACTACGCCACC 758
QY 173 ProValAAspArgLyPheGlnAlaLeuGlnIlyIleIleHisSerIleLeu-----189
DB 759 ATGCTGCYGACTCCACCGAGATRACACGAGACACCATCAACGCGCATCATCAAGGTGATG 818
QY 190 -----LysLySerCysIleGluIle 196
DB 819 AAACACGAGCGCTACGAGAGAGTGTACAAAGGTGAGTGGCTGGAAATC 866

RESULT 13
US-10-601-368-2
; Sequence 2, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
```


DB 872 CACGACAGCCAGACCTGGAGAGGTGATCCAGCAAGGAAAGAGACAACGTTAACAGA 931
|||
|||
QY 130 -----LeuphetherYserGIuAgtGluAlaAsnArgserArgAspLeu 144
|||
|||
DB 932 TATGCGGTGCGCGCTCTGGGCTAATCAACCGAGGGGATCATCAAGAACTTTCTTA 991
|||
|||
QY 145 GYAAlaIleValTYrCYsValGIyValLYsAsp-----PheAsnGIuThrGIu 160
|||
|||
DB 992 AATGAATCAATACATCTGCCCATGTACCCTGATGACAGACATTCTTCAATGTCACTGAT 1051
|||
|||
QY 161 LeuAlaArgIleAlaAspserLYsAspHISValPheProValAsnAspGIyPheGIuAla 180
|||
|||
DB 1052 GAGGCGTCCCTTG-----AAGACATTTGTGATGCCCTGGGGGACAGAAATCTTCAGC 1102
|||
|||
QY 181 LeuGIuIngly 183
|||
|||
DB 1103 CTGGAAAGGC 1111

RESULT 15

US-11-000-463-102
/ Sequence 102, Application US/11000463
/ Publication No. US20050266423A1
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Qian, Xiaohong B.
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Zhang, Jie
/ APPLICANT: Zhou, Ping
/ APPLICANT: Cao, Yi-Cheng
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
/ FILE REFERENCE: 785CIP4CN
/ CURRENT APPLICATION NUMBER: US/11/000,463
/ PRIOR FILING DATE: 2004-11-29
/ PRIOR APPLICATION NUMBER: 10/291,265
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: PCT/US01/02623
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 09/922,279
/ PRIOR FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: 09/491,404
/ PRIOR FILING DATE: 2000-01-25
/ PRIOR APPLICATION NUMBER: 09/617,746
/ PRIOR FILING DATE: 2000-07-17
/ PRIOR APPLICATION NUMBER: 09/631,451
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: 09/633,870
/ PRIOR FILING DATE: 2000-09-15
/ NUMBER OF SEQ ID NOS: 944
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 102
/ LENGTH: 3969
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (52)..(3618)
US-11-000-463-102

Alignment Scores:

Pred. No.: 0.0569 Length: 3969
Score: 107.00 Matches: 49
Percent Similarity: 37.93% Conservative: 28
Beet Local Similarity: 24.14% Mismatches: 88
Query Match: 7.01% Indels: 38
DB: 7 Gaps: 9

US-09-970-076-2_COPY_28_320 (1-293) X US-11-000-463-102 (1-3969)

QY 12 CysTYrGIyGIyPheAspLeuTYrPheIleLeuAspLYsSerGIySerValLeuHISHis 31
|||
|||
DB 526 TCCAGACCTACATGAGATGTCATTTGCTCGATGGCTCCAGACGATC---TACCC 582
|||
|||
QY 32 TTPAsnGIuIleTYrTYrPheValGIuInLeuAlaHISlyPhe---IleSerPro--- 49
|||
|||
DB 583 TGGGTGAGGTTTCAGACACTTCTCTCATCAACATCCGMAAAAGTTTACATTGGCCAGG 642
|||
|||
QY 50 GlnLeuArgMetSerPheIleValPheSerThrArgGIyThrThreMetLYsLeuThr 69
|||
|||
DB 643 CAGATCCAGGTGGAGTTGCTGCAATGCGCAAGATGTGTCATGACATTCACCTC--- 699
|||
|||
QY 70 GIuAspArgGIuInGIleArgInglyLeuGIuInlyLeuValLeuProGIyGIy 89
|||
|||
DB 700 AACGACTACAGCTCTGTAAAGATGTGGTGAAGCTGCCAGCCACATTTGACAGAGAGA 759
|||
|||
QY 90 AspThrTYrMechIGluGIyPheGIu-----ArgAlaSerGIuInIleTYrTYr 106
|||
|||
DB 760 GGAAAGAGAGACCCGAGCGGCATTTGGCATTTGCAAGCTCAGAGGCTTTCCAGAA 819
|||
|||
QY 107 GIuAspArgGIuInGIyTYrArgThrAlaSerValIleIleAlaLeuThrAspGIyGIuLeu 126
|||
|||
DB 820 GGTGAGAGAGAGAGCCAG-----AAGGTGATGATTGTATCATCAATGGGAGTCC 873
|||
|||
QY 127 HISGIuAsp----- 129
|||
|||
DB 874 CACGACAGCCAGACCTGGAGAGGTGATCCAGCAAGGAAAGAGACAACGTTAACAGA 933
|||
|||
QY 130 -----LeuphetherYserGIuAgtGluAlaAsnArgserArgAspLeu 144
|||
|||
DB 934 TATGCGGTGCGCGCTCTGGGCTAATCAACCGAGGGGATCATCAAGAACTTTCTTA 993
|||
|||
QY 145 GYAAlaIleValTYrCYsValGIyValLYsAsp-----PheAsnGIuThrGIu 160
|||
|||
DB 994 AATGAATCAATACATCTGCCCATGTACCCTGATGACAGACATTCTTCAATGTCACTGAT 1053
|||
|||
QY 161 LeuAlaArgIleAlaAspserLYsAspHISValPheProValAsnAspGIyPheGIuAla 180
|||
|||
DB 1054 GAGGCGTCCCTTG-----AAGACATTTGTGATGCCCTGGGGGACAGAAATCTTCAGC 1104
|||
|||
QY 181 LeuGIuIngly 183
|||
|||
DB 1105 CTGGAAAGGC 1113

Search completed: December 19, 2005, 02:30:09
Job time : 258.436 secs


```

APPLICANT: Bajt, Mary L.
TITLE OF INVENTION: MAC-1 I-DOMAIN PROTEIN USEFUL IN
TITLE OF INVENTION: BLOCKING ADHESION AND MIGRATION OF NEUTROPHILS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Upjohn Company, Intellectual Property Law
STREET: 301 Henrietta
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Gateway 2000 P5-90
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04439
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Darnley, James D., Jr.
REGISTRATION NUMBER: 33,673
REFERENCE/DOCKET NUMBER: 4767.P CN1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/385-5210
TELEFAX: 616/385-6897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04439-1

Query Match      14.7%; Score 142.5; DB 4; Length 435;
Best Local Similarity 26.9%; Pred. No. 9,4e-08;
Matches 54; Conservative 41; Mismatches 67; Indels 39; Gaps 11

QY 1 GGFDLYFLDKSGSVL-HHMNELIYVEVQDLAHKFIISPOLRMSFIVSTRGTLMKLTD- 58
   |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 229 GGSDFIAFLDGGSSIIIPHDFRRMKKEVST-----VNEQLKKSKTLLS-----LMQISEEF 278
   ::::-----EEOIRQGDEBELOKVLPGGDTYMHGSEFERASEOIIYYENRGYRTA-SVII 106
   279 RIHTFFPKERQNPNPRSLVKPIITQLL--GRTHPATGIRKVRRLRELNTNGARKNAAFKILV 336
QY 107 ALTDGEHLMDLFPSYE--REANRSRLGAIIVCVGVKDFNETGLAR-----INDS--KDH 157
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
DB 337 VITDGKFKPDPLGYEDVIPEDARE--GVIRYVIGVDARFSKSRQELNLTIAKSPRDH 393
   158 VFVPNDGFQALOGIIHSILKK 178
QY ||||:-|-||::||::||::||::||::||::||::||::||::||::||::||::||
DB 394 VFQVNN-FEALKTTONQLREK 413

RESULT 3
US-08-286-889-37
Sequence 37, Application US/08286889
Patent No. 5470953
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vaeren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunitc
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States

```

```

1 ZIP: 60606-6402
2 COMPUTER READABLE FORM:
3 MEDIUM TYPE: Floppy disk
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: Patentin Release #1.0, Version #1.25
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/08/286, 889
8 FILING DATE:
9 CLASSIFICATION: 435
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: US 08/173,497
12 FILING DATE: 23-DEC-1993
13 ATTORNEY/AGENT INFORMATION:
14 NAME: Williams Jr., Joseph A.
15 REGISTRATION NUMBER: P38,659
16 REFERENCE/DOCKET NUMBER: 27866/32168
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: 312-474-6300
19 TELEFAX: 312-474-0448
20 TELEX: 25-3856
21 INFORMATION FOR SEQ ID NO: 37:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 1151 amino acids
24 TYPE: amino acid
25 TOPOLOGY: linear
26 MOLECULE TYPE: protein
27 US-08-286-889-37
28
29 Query Match 14.6%; Score 141.5; DB 1; Length 1151;
30 Best Local Similarity 27.7%; Pred. No. 5e-07;
31 Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;
32
33 QY 4 DLYPLDKSGGV-LHNNETIYFPBQLAHKRTISPOLRNSFYVFSRGTTLKLTG----- 57
34 DB 142 DIAFLDSSGSINORDFAQMDPFKALMGFEASTSTLFSLMQYSNLTHTFTFEFKNIL 201
35 QY 58 DREQROGLELELQKVLPGSDTYVMEHGEFRASEQIYENRGQRTA-SVIALTDGELHED 116
36 DB 202 DPOSIVDETVLQ-----GLTYTATGIRTMBELFHSKNGSRKAKKILLVTTDQKRD 256
37 QY 117 LFPESE--REANRSHDLGAIYCVGVKD-FNE-TQLARI-----ADSKDHVPVNDGFOA 167
38 DB 257 PLEYSDVIPADKA---GIRYALGVGDAPQEPALKEKLNTIGSA.PQDHVFKVGN-FAA 312
39 QY 168 LOGIHSILKK 178
40 DB 313 LRSIORLOEK 323
41
42 RESULT 4
43 US-08-485-618-37
44 ; Sequence 37, Application US/08485618
45 ; Patent No. 572853
46 ; GENERAL INFORMATION:
47 ; APPLICANT: Gallatin, W. Michael
48 ; APPLICANT: Van der Vieren, Monica
49 ; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
50 ; NUMBER OF SEQUENCES: 103
51 ; CORRESPONDENCE ADDRESS:
52 ; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
53 ; STREET: 233 South Wacker Drive, 6300 Sear Tower
54 ; CITY: Chicago
55 ; STATE: Illinois
56 ; COUNTRY: United States
57 ; ZIP: 60606-6402
58 ; COMPUTER READABLE FORM:
59 ; MEDIUM TYPE: Floppy disk
60 ; COMPUTER: IBM PC compatible
61 ; OPERATING SYSTEM: PC-DOS/MS-DOS
62 ; SOFTWARE: Patentin Release #1.0, Version #1.25
63 ; CURRENT APPLICATION DATA:
64 ; APPLICATION NUMBER: US/08/485,618
65 ;

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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-37

Query Match 14.6%; Score 141.5; DB 1; Length 1151;
Best Local Similarity 27.7%; Pred. No. 5e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

QY 4 DLYFLDKSGSV-LHNNELIYFVEQLAHKFIQPLKMSFIVSTGTLTKLTE----- 57
DB 142 DIAFLIDSGSSINQRFQKMDPVKALMGFASTSTLFSLMQSNILKHTFTPEFNIL 201
QY 58 DREQIRQGLBELKVLPGDVTYHMEGPERASEQIYYENRGYRTA-SVIALTDGELHED 116
DB 202 DPGSLVDPIYQLQ-----GLTYTATGIRTYMEELFHSKNGSRKSAKKILLVITDGGQYRD 256
QY 117 LFFYSE--REANRSRDGLAIVCVGYKD-FNE-TOLARI-----ADSKDHVPVNDGFOA 167
DB 257 PLEYSVDIYPAADKA---GIIRYALGVGDAPQEPALKEINTIGSAPPQDHVFKVGN-FAA 312
QY 168 LOGIHSILKK 178
DB 313 LRSTQROLQEK 323

RESULT 5
US-08-362-652-37
Sequence 37, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-37

Query Match 14.6%; Score 141.5; DB 1; Length 1151;
Best Local Similarity 27.7%; Pred. No. 5e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

QY 4 DLYFLDKSGSV-LHNNELIYFVEQLAHKFIQPLKMSFIVSTGTLTKLTE----- 57
DB 142 DIAFLIDSGSSINQRFQKMDPVKALMGFASTSTLFSLMQSNILKHTFTPEFNIL 201
QY 58 DREQIRQGLBELKVLPGDVTYHMEGPERASEQIYYENRGYRTA-SVIALTDGELHED 116
DB 202 DPGSLVDPIYQLQ-----GLTYTATGIRTYMEELFHSKNGSRKSAKKILLVITDGGQYRD 256
QY 117 LFFYSE--REANRSRDGLAIVCVGYKD-FNE-TOLARI-----ADSKDHVPVNDGFOA 167
DB 257 PLEYSVDIYPAADKA---GIIRYALGVGDAPQEPALKEINTIGSAPPQDHVFKVGN-FAA 312
QY 168 LOGIHSILKK 178
DB 313 LRSTQROLQEK 323

RESULT 6
US-08-605-672-37
Sequence 37, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889

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/
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1151 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-605-672-37

Query Match          14.6%; Score 141.5; DB 1; Length 1151;
Best Local Similarity 27.7%; Pred. No. Se-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

QY 4 DLYFLDKSGSV-LHHNMEIYFVEQLAHKFI SPQLRMSFIVSTRGTTLMKLT----- 57
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 142 DIAFLIDSGSINQRPFAQMDPVKALMGFEFASTLFLSMQYSLNLTHTFTTEPKNTL 201
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 58 DDEQIRQGLEELQKVLPGGDTYMHGFEFASQIYENRGYRTA-SVIALTDGELHED 116
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
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QY 117 LFFYSE--REANRSRLGAIYVCVKVD-FNE-TQLARI-----ADSKDHVPVNDGFOA 167
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 257 PLEYSVDVIPAADA--GIIRYALGVDAFQEPFLAKEINTIGSAPPODHVKVGN-FAA 312
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 168 LOGIHSILKK 178
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 313 LRSIORLOEK 323
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RESULT 7
/ US-08-482-293A-37
/ Sequence 37, Application US/08482293A
/ Patent No. 5831029
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/482,293A
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
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/
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1151 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-482-293A-37

Query Match          14.6%; Score 141.5; DB 1; Length 1151;
Best Local Similarity 27.7%; Pred. No. Se-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

QY 4 DLYFLDKSGSV-LHHNMEIYFVEQLAHKFI SPQLRMSFIVSTRGTTLMKLT----- 57
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 142 DIAFLIDSGSINQRPFAQMDPVKALMGFEFASTLFLSMQYSLNLTHTFTTEPKNTL 201
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 58 DDEQIRQGLEELQKVLPGGDTYMHGFEFASQIYENRGYRTA-SVIALTDGELHED 116
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 202 DQSLVDPIVQLQ-----GLTYATGIRTYMEELFHSKSKRSKAKILLVITDQKXND 256
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 117 LFFYSE--REANRSRLGAIYVCVKVD-FNE-TQLARI-----ADSKDHVPVNDGFOA 167
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 257 PLEYSVDVIPAADA--GIIRYALGVDAFQEPFLAKEINTIGSAPPODHVKVGN-FAA 312
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
QY 168 LOGIHSILKK 178
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
DB 313 LRSIORLOEK 323
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

RESULT 8
/ US-08-943-363-37
/ Sequence 37, Application US/08943363
/ Patent No. 5837478
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 114
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943,363
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
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Oy 4DIYFLEIKSGSGV-LHHNMEIYFVEOLAHKRSISQOLMSFVSTGTTLMKTE----- 57
 Db 142 DIAFILDSGSGVINGNDFAQMDPVKALMGEPASISITLSLMQYSNLIKTHFTFTEPKNIL 201
 Oy 58 DEBQIRQGLAEELQKVLPGSGDTYHHEGFRASQIYENNRQRTA-SVIALLDGSELHED 116
 Db 202 DPGSLVDPIVQLQ-----GLTYLATGRTVWEELFHSKNGSRSAKKILLVITDQGYKRD 256

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-55

Query Match 14.6%; Score 141.5; DB 1; Length 1161;
Best Local Similarity 27.7%; Pred. No. 5.1e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;
QY 4 DLYFILDKSGSV-LHNNELIYVVEQLAHKFIQSPQLMSFIVSTRTGTLMLKTE----- 57
DB 152 DIAFLIDGSSGINORDPAQKMDFFKALMGEPASTSTLFSLMQYSNLIKHTFTFEFNNIL 211
QY 58 DREGIRGLEBLQKVLPGSDTYMHEGFERASEQIYYENRQGYRTA-SVIALTDGELHED 116
DB 212 DPGSLVDPVQLQ-----GLTYATGIRTYWELFHSKNGSRKSAKKILLVITDGOQYRD 266
QY 117 LFFYSE--REANRSDIGAIYVCVVD-FNE-TQLARI-----ADSKDHFVPNDGFOA 167
DB 267 PLEYSVDVTPADKA--GIRYAIGVDAPQEPALKEMLTIGSAPPDHFVKGN-FAA 322
QY 168 LQGIHSILKK 178
DB 323 LRSIORQLQEK 333

RESULT 14
US-08-605-672-55
Sequence 55, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: Van der Vaeren, Monica
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-55

Query Match 14.6%; Score 141.5; DB 1; Length 1161;
Best Local Similarity 27.7%; Pred. No. 5.1e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;
QY 4 DLYFILDKSGSV-LHNNELIYVVEQLAHKFIQSPQLMSFIVSTRTGTLMLKTE----- 57
DB 152 DIAFLIDGSSGINORDPAQKMDFFKALMGEPASTSTLFSLMQYSNLIKHTFTFEFNNIL 211
QY 58 DREGIRGLEBLQKVLPGSDTYMHEGFERASEQIYYENRQGYRTA-SVIALTDGELHED 116
DB 212 DPGSLVDPVQLQ-----GLTYATGIRTYWELFHSKNGSRKSAKKILLVITDGOQYRD 266
QY 117 LFFYSE--REANRSDIGAIYVCVVD-FNE-TQLARI-----ADSKDHFVPNDGFOA 167
DB 267 PLEYSVDVTPADKA--GIRYAIGVDAPQEPALKEMLTIGSAPPDHFVKGN-FAA 322
QY 168 LQGIHSILKK 178
DB 323 LRSIORQLQEK 333

RESULT 15
US-08-482-293A-55
Sequence 55, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: Van der Vaeren, Monica
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO.: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-55

Query Match 14.6%; Score 141.5; DB 1; Length 1161;
Best Local Similarity 27.7%; Pred. No. 5.1e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

QY	4	DLYPIIDKSGSV-LHMHNEIYFPEQLAHKFIISPOLMSFIVSTRGTLMLKTE-----	57
DB	152	DIAPLIDSGSINQRPQMKDFVKALMGEPASTSTFLMQYSNIUKTHTFTFEKNIL	211
QY	58	DREQIRQGLEELQKVLPGDVTYMHGFERASEQIYYENROGYRTA-SVIALTDGELHED	116
DB	212	DPSLVDPYIQLQ-----GLTYATGIRTYMEELFHSKNGSRKSAKKILVITDQGYRD	266
QY	117	LFFYSE--REANRSRDIGAIYCVGVKD-FNE-TQLARI-----ADSKDHVPVNDGFOA	167
DB	267	PLEYSDVITPAADKA---GIIRYAIQVGDARFOEPTALKELNTIGSAPPQDHVFKVGN-FAA	322
QY	168	LOGIHSILKK	178
DB	323	LRSIQRLQEK	333

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GenCore version 5.1.6
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OM protein - protein search, using bw model

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(without alignments)
1386.897 Million cell updates/sec

Title: US-09-970-076-2_COPY_41_227

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Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	970	100.0	328	4 US-10-201-292-26	Sequence 26, Appl
3	970	100.0	333	3 US-09-796-753-12	Sequence 12, Appl
4	970	100.0	333	4 US-10-038-307-2	Sequence 2, Appl
5	970	100.0	333	4 US-10-201-292-2	Sequence 2, Appl
6	970	100.0	333	6 US-11-047-278-8	Sequence 8, Appl
7	970	100.0	342	4 US-10-038-307-22	Sequence 22, Appl
8	970	100.0	342	4 US-10-201-292-22	Sequence 22, Appl
9	970	100.0	345	4 US-10-038-307-24	Sequence 24, Appl
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11	970	100.0	368	6 US-11-047-278-2	Sequence 2, Appl
12	970	100.0	403	3 US-09-833-245-621	Sequence 621, Appl
13	970	100.0	460	4 US-10-201-292-28	Sequence 28, Appl
14	970	100.0	479	4 US-10-201-292-32	Sequence 32, Appl
15	970	100.0	504	4 US-10-201-292-34	Sequence 34, Appl
16	970	100.0	529	4 US-10-201-292-36	Sequence 36, Appl
17	970	100.0	551	4 US-10-038-307-18	Sequence 18, Appl
18	970	100.0	551	4 US-10-201-292-18	Sequence 18, Appl
19	970	100.0	564	3 US-09-918-715-187	Sequence 187, Appl
20	970	100.0	564	3 US-09-918-715-232	Sequence 232, Appl
21	970	100.0	564	4 US-10-038-307-20	Sequence 20, Appl
22	970	100.0	564	4 US-10-201-292-20	Sequence 20, Appl
23	970	100.0	564	4 US-10-301-822-199	Sequence 199, Appl
24	970	100.0	564	4 US-10-408-765A-1823	Sequence 1823, Appl
25	970	100.0	564	4 US-10-474-794-187	Sequence 187, Appl
26	970	100.0	564	4 US-10-474-794-232	Sequence 232, Appl
27	970	100.0	564	5 US-10-979-159-187	Sequence 187, Appl

28	970	100.0	564	5 US-10-979-159-232	Sequence 232, Appl
29	970	100.0	564	6 US-11-047-278-6	Sequence 6, Appl
30	965	99.5	403	3 US-09-833-245-620	Sequence 620, Appl
31	961	99.1	562	3 US-09-918-715-194	Sequence 194, Appl
32	961	99.1	562	3 US-09-918-715-301	Sequence 301, Appl
33	961	99.1	562	4 US-10-474-794-194	Sequence 194, Appl
34	961	99.1	562	4 US-10-474-794-301	Sequence 301, Appl
35	961	99.1	562	5 US-10-979-159-194	Sequence 194, Appl
36	961	99.1	562	5 US-10-979-159-301	Sequence 301, Appl
37	960	99.0	460	4 US-10-201-292-30	Sequence 30, Appl
38	949	97.8	534	4 US-10-038-307-12	Sequence 12, Appl
39	949	97.8	534	4 US-10-201-292-12	Sequence 12, Appl
40	949	97.8	543	4 US-10-038-307-10	Sequence 10, Appl
41	949	97.8	543	4 US-10-038-307-14	Sequence 14, Appl
42	949	97.8	543	4 US-10-038-307-16	Sequence 16, Appl
43	949	97.8	543	4 US-10-201-292-10	Sequence 10, Appl
44	949	97.8	543	4 US-10-201-292-14	Sequence 14, Appl
45	949	97.8	543	4 US-10-201-292-16	Sequence 16, Appl

ALIGNMENTS

```
RESULT 1
US-10-038-307-26
; Sequence 26, Application US/10038307
; Publication No. US20030134766A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; TITLE OR INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-26

Query Match      100.0%; Score 970; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 6,6e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGFDLVFLDKSGSVLHHNMEIYYFVEQLAKHFIPTSLRMSFIYFSTRTTLMKLTEDRE 60
Db      41 GGFDLVFLDKSGSVLHHNMEIYYFVEQLAKHFIPTSLRMSFIYFSTRTTLMKLTEDRE 100
QY      61 QIRQGELELOKVLPGSDTYVHBSFERASEQIYYENRGYRTASVIALTDGEIHEDLFFY 120
Db      101 QIRQGELELOKVLPGSDTYVHBSFERASEQIYYENRGYRTASVIALTDGEIHEDLFFY 160
QY      121 SEREARSRLGAIYVCVGYKDPNEQTOLARIASKHVFPVNDGFQALQGIHSLKSC 180
Db      161 SEREARSRLGAIYVCVGYKDPNEQTOLARIASKHVFPVNDGFQALQGIHSLKSC 220
QY      181 IETILAAE 187
Db      221 IETILAAE 227

RESULT 2
US-10-201-292-26
; Sequence 26, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
```

```
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 26
/ LENGTH: 328
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-201-292-26

Query Match      100.0%; Score 970; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 6, 6e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGFDFYFLDKSGSVLHNNIYYPVEQLAHKFIISPOLMSFVFSRGTTLTKLTEDRE 60
DB      41 GGFDFYFLDKSGSVLHNNIYYPVEQLAHKFIISPOLMSFVFSRGTTLTKLTEDRE 100
QY      61 QIRQGLEELQKVLPGSDTYMHGFEFASBQIYYENRQGYRTASVIALTDGELHEDLFFY 120
DB      101 QIRQGLEELQKVLPGSDTYMHGFEFASBQIYYENRQGYRTASVIALTDGELHEDLFFY 160
QY      121 SEREANSRDLGAIYVCVGVKDFNETQLARIADSKDHPVNDGFQALOGIHSILKSGC 180
DB      161 SEREANSRDLGAIYVCVGVKDFNETQLARIADSKDHPVNDGFQALOGIHSILKSGC 220
QY      181 IETLAAE 187
DB      221 IETLAAE 227

RESULT 3
US-09-796-753-12
/ Sequence 12, Application US/09796753
/ Publication No. US20030027998A1
/ GENERAL INFORMATION:
/ APPLICANT: McCarthy, Sean A.
/ TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
/ FILE REFERENCE: 7853-227-999
/ CURRENT APPLICATION NUMBER: US/09/796,753
/ CURRENT FILING DATE: 2001-03-01
/ PRIOR APPLICATION NUMBER: 09/183,175
/ PRIOR FILING DATE: 1998-10-30
/ PRIOR APPLICATION NUMBER: 09/223,094
/ PRIOR FILING DATE: 1998-12-30
/ PRIOR APPLICATION NUMBER: 09/223,546
/ PRIOR FILING DATE: 1998-12-30
/ PRIOR APPLICATION NUMBER: 09/224,246
/ PRIOR FILING DATE: 1998-12-30
/ PRIOR APPLICATION NUMBER: 09/259,388
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/122,458
/ PRIOR FILING DATE: 1999-03-01
/ PRIOR APPLICATION NUMBER: 09/312,359
/ PRIOR FILING DATE: 1999-05-14
/ PRIOR APPLICATION NUMBER: 09/336,536
/ PRIOR FILING DATE: 1999-06-18
/ PRIOR APPLICATION NUMBER: 09/342,687
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: 09/345,464
/ PRIOR FILING DATE: 1999-06-30
/ PRIOR APPLICATION NUMBER: 09/365,164
/ PRIOR FILING DATE: 1999-07-30
/ PRIOR APPLICATION NUMBER: 09/399,723
/ PRIOR FILING DATE: 1999-09-20
/ PRIOR APPLICATION NUMBER: 09/409,634
/ PRIOR FILING DATE: 1999-09-30
/ PRIOR APPLICATION NUMBER: 09/471,179
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: 09/474,071
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/ PRIOR FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: 09/474,072
/ PRIOR FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: 09/514,010
/ PRIOR FILING DATE: 2000-02-25
/ PRIOR APPLICATION NUMBER: 09/516,745
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: 09/572,002
/ PRIOR FILING DATE: 2000-05-14
/ PRIOR APPLICATION NUMBER: 09/597,993
/ PRIOR FILING DATE: 2000-06-19
/ PRIOR APPLICATION NUMBER: 09/599,596
/ PRIOR FILING DATE: 2000-06-22
/ PRIOR APPLICATION NUMBER: 09/630,334
/ PRIOR FILING DATE: 2000-07-31
/ PRIOR APPLICATION NUMBER: 09/606,565
/ PRIOR FILING DATE: 2000-06-29
/ PRIOR APPLICATION NUMBER: 09/606,317
/ PRIOR FILING DATE: 2000-06-29
/ PRIOR APPLICATION NUMBER: 09/665,666
/ PRIOR FILING DATE: 2000-09-20
/ PRIOR APPLICATION NUMBER: 09/677,751
/ PRIOR FILING DATE: 2000-09-30
/ NUMBER OF SEQ ID NOS: 162
/ SEQ ID NO 12
/ LENGTH: 333
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-796-753-12

Query Match      100.0%; Score 970; DB 3; Length 333;
Best Local Similarity 100.0%; Pred. No. 6, 7e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGFDFYFLDKSGSVLHNNIYYPVEQLAHKFIISPOLMSFVFSRGTTLTKLTEDRE 60
DB      41 GGFDFYFLDKSGSVLHNNIYYPVEQLAHKFIISPOLMSFVFSRGTTLTKLTEDRE 100
QY      61 QIRQGLEELQKVLPGSDTYMHGFEFASBQIYYENRQGYRTASVIALTDGELHEDLFFY 120
DB      101 QIRQGLEELQKVLPGSDTYMHGFEFASBQIYYENRQGYRTASVIALTDGELHEDLFFY 160
QY      121 SEREANSRDLGAIYVCVGVKDFNETQLARIADSKDHPVNDGFQALOGIHSILKSGC 180
DB      161 SEREANSRDLGAIYVCVGVKDFNETQLARIADSKDHPVNDGFQALOGIHSILKSGC 220
QY      181 IETLAAE 187
DB      221 IETLAAE 227

RESULT 4
US-10-038-307-2
/ Sequence 2, Application US/10038307
/ Publication No. US20030134786A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/038,307
/ CURRENT FILING DATE: 2002-06-28
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 333
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-038-307-2

Query Match      100.0%; Score 970; DB 4; Length 333;
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Best Local Similarity 100.0%; Pred. No. 6.7e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GGFPLVFLDKSGSVLHHMNEIYFVEQLAHKFTSPQLRMSFIYFSTRGTTMLKLTEDRE 60
    |||
DB 41 GGFPLVFLDKSGSVLHHMNEIYFVEQLAHKFTSPQLRMSFIYFSTRGTTMLKLTEDRE 100
OY 61 QIRGLEELQKVLPGGDTYMHGFEFRASEQIYYENRQGYRTASVIALTDGELHEDLFFY 120
    |||
DB 101 QIRGLEELQKVLPGGDTYMHGFEFRASEQIYYENRQGYRTASVIALTDGELHEDLFFY 160
OY 121 SEREANSRDLGAIYVCVGDVFNFTOLARIADSKDHVPVNDGFQALOGIHSILKKSC 180
    |||
DB 161 SEREANSRDLGAIYVCVGDVFNFTOLARIADSKDHVPVNDGFQALOGIHSILKKSC 220
OY 181 IEILAAE 187
    |||
DB 221 IEILAAE 227

RESULT 5
US-10-201-292-2
; Sequence 2, Application US/10201292
; Publication No. US20030144193a1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Englin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT FILING DATE: US/10/201,292
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-2
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Query Match 100.0%; Score 970; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 6.7e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GGFPLVFLDKSGSVLHHMNEIYFVEQLAHKFTSPQLRMSFIYFSTRGTTMLKLTEDRE 60
    |||
DB 41 GGFPLVFLDKSGSVLHHMNEIYFVEQLAHKFTSPQLRMSFIYFSTRGTTMLKLTEDRE 100
OY 61 QIRGLEELQKVLPGGDTYMHGFEFRASEQIYYENRQGYRTASVIALTDGELHEDLFFY 120
    |||
DB 101 QIRGLEELQKVLPGGDTYMHGFEFRASEQIYYENRQGYRTASVIALTDGELHEDLFFY 160
OY 121 SEREANSRDLGAIYVCVGDVFNFTOLARIADSKDHVPVNDGFQALOGIHSILKKSC 180
    |||
DB 161 SEREANSRDLGAIYVCVGDVFNFTOLARIADSKDHVPVNDGFQALOGIHSILKKSC 220
OY 181 IEILAAE 187
    |||
DB 221 IEILAAE 227

RESULT 6
US-11-047-278-8
; Sequence 8, Application US/11047278
; Publication No. US20050196407a1
; GENERAL INFORMATION:
; APPLICANT: Young, John A. T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
```

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; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-047-278-8
```

Query Match 100.0%; Score 970; DB 6; Length 333;
Best Local Similarity 100.0%; Pred. No. 6.7e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GGFPLVFLDKSGSVLHHMNEIYFVEQLAHKFTSPQLRMSFIYFSTRGTTMLKLTEDRE 60
    |||
DB 41 GGFPLVFLDKSGSVLHHMNEIYFVEQLAHKFTSPQLRMSFIYFSTRGTTMLKLTEDRE 100
OY 61 QIRGLEELQKVLPGGDTYMHGFEFRASEQIYYENRQGYRTASVIALTDGELHEDLFFY 120
    |||
DB 101 QIRGLEELQKVLPGGDTYMHGFEFRASEQIYYENRQGYRTASVIALTDGELHEDLFFY 160
OY 121 SEREANSRDLGAIYVCVGDVFNFTOLARIADSKDHVPVNDGFQALOGIHSILKKSC 180
    |||
DB 161 SEREANSRDLGAIYVCVGDVFNFTOLARIADSKDHVPVNDGFQALOGIHSILKKSC 220
OY 181 IEILAAE 187
    |||
DB 221 IEILAAE 227
```

```
RESULT 7
US-10-038-307-22
; Sequence 22, Application US/10038307
; Publication No. US20030134786a1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Englin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-22
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Query Match 100.0%; Score 970; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 6.9e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 GGFPLVFLDKSGSVLHHMNEIYFVEQLAHKFTSPQLRMSFIYFSTRGTTMLKLTEDRE 60
    |||
DB 50 GGFPLVFLDKSGSVLHHMNEIYFVEQLAHKFTSPQLRMSFIYFSTRGTTMLKLTEDRE 109
OY 61 QIRGLEELQKVLPGGDTYMHGFEFRASEQIYYENRQGYRTASVIALTDGELHEDLFFY 120
    |||
DB 110 QIRGLEELQKVLPGGDTYMHGFEFRASEQIYYENRQGYRTASVIALTDGELHEDLFFY 169
OY 121 SEREANSRDLGAIYVCVGDVFNFTOLARIADSKDHVPVNDGFQALOGIHSILKKSC 180
    |||
DB 170 SEREANSRDLGAIYVCVGDVFNFTOLARIADSKDHVPVNDGFQALOGIHSILKKSC 229
OY 181 IEILAAE 187
```

Db 230 IEIILAE 236

RESULT 8

US-10-201-292-22
; Sequence 22, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-22

Query Match 100.0%; Score 970; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 6, 9e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIYFSTRGTTLMKLTEDRE 60
DB 50 GGFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIYFSTRGTTLMKLTEDRE 109
QY 61 QIROGLEELQKVLPGGDTYMHGFERASEQIYYENRGYRTASVIALTDGELHEDLFFY 120
DB 110 QIROGLEELQKVLPGGDTYMHGFERASEQIYYENRGYRTASVIALTDGELHEDLFFY 169
QY 121 SEREANSRDLGAIYVCVGDYKDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKSC 180
DB 170 SEREANSRDLGAIYVCVGDYKDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKSC 229
QY 181 IEIILAE 187
DB 230 IEIILAE 236

RESULT 9

US-10-038-307-24
; Sequence 24, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-24

Query Match 100.0%; Score 970; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 7e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIYFSTRGTTLMKLTEDRE 60

Db 41 GGFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIYFSTRGTTLMKLTEDRE 100

QY 61 QIROGLEELQKVLPGGDTYMHGFERASEQIYYENRGYRTASVIALTDGELHEDLFFY 120
DB 101 QIROGLEELQKVLPGGDTYMHGFERASEQIYYENRGYRTASVIALTDGELHEDLFFY 160

QY 121 SEREANSRDLGAIYVCVGDYKDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKSC 180
DB 161 SEREANSRDLGAIYVCVGDYKDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKSC 220

QY 181 IEIILAE 187
DB 221 IEIILAE 227

RESULT 10

US-10-201-292-24
; Sequence 24, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-24

Query Match 100.0%; Score 970; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 7e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIYFSTRGTTLMKLTEDRE 60
DB 41 GGFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIYFSTRGTTLMKLTEDRE 100
QY 61 QIROGLEELQKVLPGGDTYMHGFERASEQIYYENRGYRTASVIALTDGELHEDLFFY 120
DB 101 QIROGLEELQKVLPGGDTYMHGFERASEQIYYENRGYRTASVIALTDGELHEDLFFY 160
QY 121 SEREANSRDLGAIYVCVGDYKDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKSC 180
DB 161 SEREANSRDLGAIYVCVGDYKDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKSC 220
QY 181 IEIILAE 187
DB 221 IEIILAE 227

RESULT 11

US-11-047-278-2
; Sequence 2, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481

PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 368
TYPE: PRT
ORGANISM: Homo sapiens
US-11-047-278-2

Query Match 100.0%; Score 970; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 7.7e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFDFLYIILDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRE 60
DB 41 GGFDFLYIILDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRE 100
QY 61 QIRQGLEELQKVLPGGDTYMHGEPERASEQIYYENRGYRTASVIALTDGELHEDLFFY 120
DB 101 QIRQGLEELQKVLPGGDTYMHGEPERASEQIYYENRGYRTASVIALTDGELHEDLFFY 160
QY 121 SEREANSRDLGAIYVCVGYKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSC 180
DB 161 SEREANSRDLGAIYVCVGYKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSC 220
QY 181 IETILAAE 187
DB 221 IETILAAE 227

RESULT 12

US-09-833-245-621
Sequence 621, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PPS46PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 621
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
US-09-833-245-621

Query Match 100.0%; Score 970; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 8.7e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFDFLYIILDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRE 60
DB 41 GGFDFLYIILDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRE 100
QY 61 QIRQGLEELQKVLPGGDTYMHGEPERASEQIYYENRGYRTASVIALTDGELHEDLFFY 120
DB 101 QIRQGLEELQKVLPGGDTYMHGEPERASEQIYYENRGYRTASVIALTDGELHEDLFFY 160
QY 121 SEREANSRDLGAIYVCVGYKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSC 180
DB 161 SEREANSRDLGAIYVCVGYKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSC 220
QY 181 IETILAAE 187
DB 221 IETILAAE 227

RESULT 13

US-10-201-292-28
Sequence 28, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 460
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-28

Query Match 100.0%; Score 970; DB 4; Length 460;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFDFLYIILDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRE 60
DB 41 GGFDFLYIILDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRE 100
QY 61 QIRQGLEELQKVLPGGDTYMHGEPERASEQIYYENRGYRTASVIALTDGELHEDLFFY 120
DB 101 QIRQGLEELQKVLPGGDTYMHGEPERASEQIYYENRGYRTASVIALTDGELHEDLFFY 160
QY 121 SEREANSRDLGAIYVCVGYKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSC 180
DB 161 SEREANSRDLGAIYVCVGYKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSC 220
QY 181 IETILAAE 187
DB 221 IETILAAE 227

RESULT 14

US-10-201-292-32
Sequence 32, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-32

Query Match 100.0%; Score 970; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.1e-92;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFDFLYIILDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRE 60
DB 41 GGFDFLYIILDKSGSVLHHMNEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRE 100

```

QY 61 QIRGGLLELOKVLPGGDTYMHGFEFASQIYYENRQGYRTASVIALTDGELHEDLFFY 120
DB 101 QIRGGLLELOKVLPGGDTYMHGFEFASQIYYENRQGYRTASVIALTDGELHEDLFFY 160
QY 121 SEREANSRDLGAIYVCVGVKDFNETQIARIADSKDHFVPVNDGFQALQGIHSHILKSC 180
DB 161 SEREANSRDLGAIYVCVGVKDFNETQIARIADSKDHFVPVNDGFQALQGIHSHILKSC 220
QY 181 IEILAAE 187
DB 221 IEILAAE 227

```

RESULT 15
US-10-201-292-34

```

; Sequence 34, Application US/10201292
; Publication No. US2003014193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYRAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PaetSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 504
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-201-292-34

```

Query Match 100.0%; Score 970; DB 4; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GGFDLYFIIDKSGSVLHNMNEIYYFVQQLAHKFIISPOLRMSFTVFSRGTTLMKLTEDRE 60
DB 41 GGFDLYFIIDKSGSVLHNMNEIYYFVQQLAHKFIISPOLRMSFTVFSRGTTLMKLTEDRE 100
QY 61 QIRGGLLELOKVLPGGDTYMHGFEFASQIYYENRQGYRTASVIALTDGELHEDLFFY 120
DB 101 QIRGGLLELOKVLPGGDTYMHGFEFASQIYYENRQGYRTASVIALTDGELHEDLFFY 160
QY 121 SEREANSRDLGAIYVCVGVKDFNETQIARIADSKDHFVPVNDGFQALQGIHSHILKSC 180
DB 161 SEREANSRDLGAIYVCVGVKDFNETQIARIADSKDHFVPVNDGFQALQGIHSHILKSC 220
QY 181 IEILAAE 187
DB 221 IEILAAE 227

```

Search completed: December 14, 2005, 11:59:00
Job time : 56.504 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 11:18:48 ; Search time 2.74816 Seconds
(without alignments)
458.218 Million cell updates/sec

Title: US-09-970-076-2_COPY_41_227

Perfect score: 970
Sequence: 1 GGFDFYFLDKSGSVLHMNN.....LOGIHSILKKSCTEILAAE 187

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51441 seqs, 6734002 residues

Total number of hits satisfying chosen parameters: 51441

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database :

Published Applications AA New:
1: /cgn2_6/prodata/1/pubppa/US09_NEW_PUB.pap:*
2: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pap:*
3: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pap:*
4: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB.pap:*
5: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB.pap:*
6: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB.pap:*
7: /cgn2_6/prodata/1/pubppa/US11_NEW_PUB.pap:*
8: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	970	100.0	564	7	US-11-186-284-199 Sequence 199, App
2	132.5	13.7	1152	7	US-11-080-026-4 Sequence 4, App1
3	131	13.5	3053	7	US-11-186-284-26 Sequence 26, App1
4	111.5	11.5	739	7	US-11-057-047-2 Sequence 2, App1
5	111.5	11.5	764	7	US-11-057-047-1 Sequence 1, App1
6	111.5	11.5	798	6	US-10-821-234-1034 Sequence 1034, Ap
7	109	11.2	955	6	US-10-131-825A-294 Sequence 294, App
8	109	11.2	985	7	US-11-113-424-39 Sequence 39, App1
9	108	11.1	1141	6	US-10-601-368-24 Sequence 24, App1
10	108	11.1	1166	6	US-10-601-368-22 Sequence 22, App1
11	108	11.1	1188	6	US-10-601-368-21 Sequence 21, App1
12	104.5	10.8	828	6	US-10-995-561-983 Sequence 983, App
13	104.5	10.8	918	6	US-10-995-561-981 Sequence 981, App
14	104.5	10.8	1019	6	US-10-995-561-982 Sequence 982, App
15	104	10.7	1141	6	US-10-601-368-6 Sequence 6, App1
16	104	10.7	1166	6	US-10-601-368-4 Sequence 4, App1
17	104	10.7	1188	6	US-10-601-368-3 Sequence 3, App1
18	104	10.7	1188	7	US-11-000-463-338 Sequence 338, App
19	104	10.7	1188	7	US-11-000-463-810 Sequence 810, App
20	103.5	10.7	182	6	US-10-601-368-25 Sequence 25, App1
21	103.5	10.7	761	7	US-11-057-047-6 Sequence 6, App1
22	99.5	10.3	182	6	US-10-601-368-7 Sequence 7, App1
23	95.5	9.8	1179	7	US-11-097-125-1 Sequence 1, App1
24	95.5	9.8	1196	6	US-10-995-561-921 Sequence 921, App
25	94	9.7	678	7	US-11-102-240-34 Sequence 34, App1

26	91.5	9.4	1167	7	US-11-097-125-2 Sequence 2, App1
27	90	9.3	1167	6	US-10-601-368-18 Sequence 18, App1
28	89.5	9.2	353	7	US-11-137-465-44 Sequence 44, App1
29	89.5	9.2	448	7	US-11-137-465-45 Sequence 45, App1
30	74	7.6	384	6	US-10-510-386-158 Sequence 158, App
31	73.5	7.6	509	6	US-10-793-626-2880 Sequence 2880, App
32	73.5	7.6	1804	6	US-10-513-786-2 Sequence 2, App1
33	73.5	7.6	3704	6	US-10-513-786-1 Sequence 1, App1
34	73	7.5	264	6	US-10-793-626-388 Sequence 388, App
35	73	7.5	292	6	US-10-793-626-2636 Sequence 2636, App
36	72	7.4	786	6	US-10-467-962B-103 Sequence 103, App
37	71	7.3	629	6	US-10-467-962B-250 Sequence 250, App
38	71	7.3	629	6	US-10-467-657-3084 Sequence 3084, App
39	70	7.2	468	6	US-10-467-657-5696 Sequence 5696, App
40	69.5	7.2	489	6	US-10-467-657-7846 Sequence 7846, App
41	69	7.1	242	6	US-10-467-657-7306 Sequence 7306, App
42	69	7.1	1170	7	US-11-080-026-2 Sequence 2, App1
43	68.5	7.1	1734	7	US-11-192-967-6 Sequence 6, App1
44	68.5	7.1	1734	7	US-11-193-715-6 Sequence 6, App1
45	68	7.0	348	6	US-10-674-767-4 Sequence 4, App1

ALIGNMENTS

```
RESULT 1
US-11-186-284-199
; Sequence 199, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamekake, Shuhangai
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John B.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MP001-0292PRM
; CURRENT APPLICATION NUMBER: US/11/186,284
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-199

Query Match      100.0%  Score 970;  DB 7;  Length 564;
Best Local Similarity 100.0%;  Pred No. 8.4e-87;
Matches 187;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

1 GGFDFYFLDKSGSVLHMNNIYFVEQLAHKRFISPOLMSFIVSTRTITLKLTEDE 60
41 GGFDFYFLDKSGSVLHMNNIYFVEQLAHKRFISPOLMSFIVSTRTITLKLTEDE 100
61 QIRGIEELQKLPQGDITMHEGFERASQIYENRQGYRTASVIALTDGSLHELFY 120
101 QIRGIEELQKLPQGDITMHEGFERASQIYENRQGYRTASVIALTDGSLHELFY 160
121 SEREARRSDLAIVYCVGVDFNERQGLARIADSKDHVPFVNDGFOALGGIHSILKSC 180

```
Db      161 SREANRSDLAIVYCVGVKDFNQTOLARIDSDHVPVNDGQALQGIHSLKXSC 220
      181 IETLAEE 187
      221 IETLAEE 227

RESULT 2
US-11-080-026-4
; Sequence 4, Application US/11080026
; Publication No. US20050260192A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Lu, Chafan
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; FILE REFERENCE: CFEF-P02-021
; CURRENT APPLICATION NUMBER: US/11/080,026
; CURRENT FILING DATE: 2005-03-15
; PRIOR APPLICATION NUMBER: 09/945,265
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,700
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-026-4

Query Match      13.7%; Score 132.5; DB 7; Length 1152;
Best Local Similarity 26.3%; Pred. No. 3.6e-05;
Matches 52; Conservative 41; Mismatches 66; Indels 39; Gaps 11;

QY      4 DLYFLIDKSGSV-LHHMNEIYFVEQLAKHFI-SPQIRMSFIVSTGTTLMKLTED----- 58
      150 DIAFLIDSGSIIIPHFRRKKEFVST-----VNEQLKSKSTLPS-----LMQYSEFRH 199
      59 -----REQIRQGLELOKVLPGSDTYMHGEFPERASEQIYENRGYRTA-SVITIALT 109
      200 FTFRKQNNPNRPSLYKPIQQL--GRTHPATIRKRVHLEPITNGARKNAKLIIVIT 257
      110 DGLHEDLFFYSE--REANRSDLAIVYCVGVKDFNQTOLAR-----IADG--KHVP 160
      258 DGEKFGDPLGYRDPVPEADRE---GVIRYVIGVDGDAFRSEKRSQELNTIASKEPRDHVFO 314
      161 VNDGQALQGIHSLKX 178
      315 VNN-PEALKTIQNLREK 331
      DB

RESULT 3
US-11-186-284-26
; Sequence 26, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Tribodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MEM01-029P2RMM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
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      ; PRIOR APPLICATION NUMBER: US/10/301,822
      ; PRIOR FILING DATE: 2002-11-21
      ; PRIOR APPLICATION NUMBER: US 60/339,971
      ; PRIOR FILING DATE: 2001-12-10
      ; PRIOR APPLICATION NUMBER: US 60/361,978
      ; PRIOR FILING DATE: 2002-03-05
      ; PRIOR APPLICATION NUMBER: US 60/381,988
      ; PRIOR FILING DATE: 2002-05-20
      ; NUMBER OF SEQ ID NOS: 228
      ; SOFTWARE: FastSeq for Windows Version 4.0
      ; SEQ ID NO 26
      ; LENGTH: 3063
      ; TYPE: PRT
      ; ORGANISM: Homo Sapiens
      US-11-186-284-26

Query Match      13.5%; Score 131; DB 7; Length 3063;
Best Local Similarity 29.8%; Pred. No. 0.00018;
Matches 59; Conservative 38; Mismatches 75; Indels 26; Gaps 13;

QY      4 DLYFLIDKSGSV-LHHMNEIYFVEQLAKHFI-SP-QIRMSFIVST---RGTTLMKLT 57
      440 DIVFLVDSSYSIGIANFVKRAFLVAVKSEISPNRQISLVQXSRDPHTEFTLKRTK 499
      58 DREQIRQGLELOKVLPGSDTYMHGEFPERASEQIYENRGYRTA-SVITIALTDEL 113
      500 VEDIL-----EAINTFPRGSGTNTGKAMTYVREKIFVPSK-GSRSNVPMKMIITDGR- 552
      114 HEDLFFYSEREANRSDLAIVYCVGVKDFNQTOLARID--SKHVPVNDGQALQGI 171
      553 SSDAF---RDPALIKLRNSDVEIFAIVGVDAVRASELEAIASPAETHVTFVED-PDAFQRI 608
      172 IHSILKSGCIEI---LAA 186
      DB
      609 SPETQSGICLRLEQLAA 626
      QY
      DB

RESULT 4
US-11-057-047-2
; Sequence 2, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilkeson, Gary
; TITLE OF INVENTION: Identification of Factor B, The Alternative Complement Pathway and
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057,047
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; PRIOR FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 2
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
      US-11-057-047-2

Query Match      11.5%; Score 111.5; DB 7; Length 739;
Best Local Similarity 22.8%; Pred. No. 0.0022;
Matches 49; Conservative 44; Mismatches 77; Indels 45; Gaps 10;

QY      1 GGFDLYFLIDKSGSV-----LHHMNEIYFVEQLAKHFI-SPQIRMSFIVSTGTTLMK 55
      242 GSNRIVLVLDGSDSIGASNFTGAKKCLVNLIERVAVGVKP--RYGLVYATYATPKIWKV 299
      DB
```



```

OY 56 E-----DRQIQOGJEEL-----QKVLPGSGTYVHGEPRASQEIYYENR-----QGY- 99
Db 300 SEADSSNMAWVKQLQELNEIYEDHKLSGNT-----KKLQGVYSSMSGPPDDPPEGMN 353
OY 100 RTASYIATLDG-----ELHEDLPFYSSREANRSADLAIYCVG--VYDFN 144
Db 354 RTRHYIILMTDGLAHNMGDPITYIDEIRDLLYGKGRKQKPREDYLDVYVGAPLVNQVN 413
OY 145 ETQLARIADSKDHFVFNDFQALQGIHLSILTKS 179
Db 414 INALASKDNEQHVFVKVD-MENLEBVFYQMIDES 447

```

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RESULT 5
US-11-057-047-1
; Sequence 1, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Edwin
; APPLICANT: Gilkeson, Gary
; TITLE OF INVENTION: Inhibition of Factor B. The Alternative Complement Pathway and
; TITLE OF INVENTION: Methods Related Thereto
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057.047
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; PRIOR FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 764
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-057-047-1

```

```

Query Match Similarity      11.5%; Score 11.5; DB 7; Length 764;
Best Local Similarity      22.8%; Pred. No. 0.0023;
Matches    49; Conservative   44; Mismatches    77; Indels   45; Gaps   10.

Oy      1 GGFPLYLILDKGSV-----LHMHNEIYFVEQLAHKFIISPOLRNSFIVSTRTGTLMLK 55
          : :: | | | | : : : : | | : : : : | :
Db     267 GSMNIYLVLDSDSDSIGASNFTGAKKKLVNLEIKVASYGKP--RGVLTYATYPRKIWKV 324
          : : : : | : : : | : : : | : : : : | :

Oy      56 TE---DREQIRQGLEEL---OKVLPGGDITYMHEGFRASEQIYYENR-----OGY- 99
          : : : : : : : : : : : : : : : : : : : :
Db     325 SEADSNADWWTJKOLNEINVEDHKLKSGTNT-----KKALQAVYSMMSPDPDPEEGWN 378
          : : : : : : : : : : : : : : : : : : : :

Oy      100 RTASVIILITDG-----ELHMEDLFYSEREANSRDGLAIVYCIG--VKDFN 144
          : | | | | | : : : : : : : : : : : : : :
Db     379 RTRHHVILMTGGLHNMGDDPIYTVIDEIRDLLYTGDRKNRPREDYLDVVYFGVPLNVGN 438
          : : : : | : : : | : : : | : : : | : : : |

Oy      145 ETOLARIADSKOHFPVNDGFOALGGIHSILKKS 179
          : : | | | | : : : : : : : : : : : : : :
Db     439 INALLASKKDNEOHVFVKXD-MENLEDVIFYQMIDES 472
          : : : : | | : : : : : : : : : : : : : :

RESULT 6
US-10-821-234-1034
; Sequence 1034, Application US/10821234
; Publication No. US20050255114al
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgitc
; APPLICANT: Andermani, Susan
; APPLICANT: Tang, Y. Tom
```

```

; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 82JA
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_gene Version 1.0
; SEQ ID NO 1034
; LENGTH: 798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1034

Query Match      11.5%; Score 111.5; DB 6; Length 798;
Best Local Similarity 22.8%; Pred. No. 0.0024;
Matches 49; Conservative 44; Mismatches 77; Indels 45; Gaps 10;

Cy    1 GGPDLPYLIDKSGV-----LHMNNEYFYVEQALAHFISPOLRMSTIVSTRGTTMLKL 55
       ::::|::|:|::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    301 GSMNIYIVLDGSDSIDGASNPFGAKCKLVNLIEKVASGVXPR--RYGLVIATYPEKIWIWV 358
       :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Cy    56 TE-----DREOIRQLGEEL-----OKVLPGGPDTVMHGEFPERASEOIYYENR-----OGY- 99
       :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    359 SEADSSNADNWTKOLNEINTEHDRLKSGTNT-----KKALQAVYSMMMSNPDDVPREGMN 412
       :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Cy    100 RTASVIIALTDC-----ELMHEDLFFYSEERANRSRDLCAIYVCV--VKDFN 144
        |::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    413 RTRVAIIILMTDGLHNMGDPITVIDEIRDLLIYGKRKNPREDELYDVVFVGVLNVQN 472
        ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Cy    145 ETOLARIADSNDHYFPYNDDGFOLQGIIHSILIKS 179
        ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    473 INALASKKDNEQHAFVKVD--MENLEEDVFYQIDES 506
        ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

```

```

1      RESULT 7
2      US-10-131-826A-294
3      Sequence 294, Application US/10131826A
4      Publication No. US20050245730A1
5      GENERAL INFORMATION:
6      APPLICANT: Baker, Kevin P.
7      APPLICANT: Beresini, Maureen
8      APPLICANT: DeForge, Laura
9      APPLICANT: Deenoyers, Luc
10     APPLICANT: Filvaroff, Ellen
11     APPLICANT: Gao, Wei-Qiang
12     APPLICANT: Gerritsen, Mary E.
13     APPLICANT: Goddard, Audrey
14     APPLICANT: Godowski, Paul J.
15     APPLICANT: Gurney, Austin L.
16     APPLICANT: Sherwood, Steven
17     APPLICANT: Smith, Victoria
18     APPLICANT: Stewart, Timothy A.
19     APPLICANT: Tumas, Daniel
20     APPLICANT: Watanabe, Colin K
21     APPLICANT: Wood, William
22     APPLICANT: Zhang, Zemin
23     TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
24     ACIDS ENCODING THE SAME
25     FILE REFERENCE: P330R1C128
26     CURRENT APPLICATION NUMBER: US/10/131,826A
27     PRIOR FILING DATE: 2002-04-24
28     PRIOR APPLICATION NUMBER: 60/049911
29     PRIOR FILING DATE: 1997-06-18
30     PRIOR APPLICATION NUMBER: 60/056974
31     PRIOR FILING DATE: 1997-08-26
32     PRIOR APPLICATION NUMBER: 60/059113
33     PRIOR FILING DATE: 1997-09-17
34     PRIOR APPLICATION NUMBER: 60/059115
35     PRIOR FILING DATE: 1997-09-17
36     PRIOR APPLICATION NUMBER: 60/059117
37     PRIOR FILING DATE: 1997-09-17
38     PRIOR APPLICATION NUMBER: 60/059122

```

```

: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/05184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See File Wrapper or PALM
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 294
: LENGTH: 915
: TYPE: PRT
: ORGANISM: Homo Sapien
: OS-10-131-826A-294

```

Query Match	11.2%	Score 109;	DB 6;	Length 915;
Best Local Similarity	24.0%	Pred. No. 0.0051;		
Matches 46;	Conservative 43;	Mismatches 77;	Indels 26;	Gaps 10

```

Qy      4 DVEFIIDKSSV--LHHNNIYYE--VEQLAHKFIISPOL--RMSPIVSTAGTIL-----MKL 55
Db      57 DLVFIIDSSNSVTHDYAKKEFIYVILQFLDIGDPVTRVGLIQY---GSTVYKNEFSIKT 1133
Qy      56 TEDREQIRQGLLEBLOKLPFGDITVMEHGEGERASEQIYYENRQGYR-----TASYIALTD 110
Db      114 FKRSSEVERAVKMRHLSITGTMTGLAIQY---ALNAPSEAGCAPLRENPVRYIMLYTD 170
Qy      111 GELHEDIIFYSEREBANSRDGLAIYCVGV--KDENEIQLARIADSKCHFVPVNDGFOAL 166
Db      171 GRPQDSV----AEVAAKARPTGILLIPALIGQVDFTLLKSIGSEPHEDHVEFLVAN--FSQI 225
Qy      169 QGRIHSILKKSC 180
Db      226 ETLTIVSEFOKKLC 237

```

```

RESULT 8
US-11-113-424-39
; Sequence 39, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 956
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-39

```

Query Match	11.2%	Score 109;	DB 7;	Length 956;
Best Local Similarity	24.0%	Pred. No. 0.0054;		
Matches 46;	Conservative 43;	Mismatches 77;	Indels 26;	Gaps 10;

QY 4 DLVFLIDKSGSV-LHHNNIYYF-VEGLAKHFISPOL-RMSEFIYSRGTTL-----MKL 55
Db 57 DLVFLIDSSRSVNTHDYAKVEFIYDILQPLDIDGPDYTRVGLLOY---GSTVKNIEFSLKT 113
QY 56 TEDREQIRGLEBELQVLPFGSDTYMHGEFERSAQIYYENRQYR-----TASVIALTD 110
Db 114 FKRSSEVAIVKRMHRLSTGTWTTGAIQY---ALINAFSEAGARPURENVPRVIMYTD 170
QY 111 GEIHEDLFFYSEREARNSHDLGAIYYCQV--KQFNEIQLARINDSDNHVPPVNDGQAL 168
Db 171 GRPQSDV---AEVAKARDTGILIFALGVQVDFTNLKISGSEPHEDHFLVAN-PSQI 225
QY 169 QGIHSHILKKSC 180
Db 226 ETLTSVFQKKLC 237

```

RESULT 9
US-10-601-368-24
; Sequence 24, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Lorea, Jose M.
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275801
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/332,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 1141
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-601-368-24

```

Query Match	11.1%;	Score 108;	DB 6;	Length 1141;
Best Local Similarity	24.2%;	Pred. No. 0.0085;		
Matches	48;	Conservative	28;	Mismatches 84;
			Indels	38;
			Gaps	9

```

QY 1 DYAFELIDSGSVLAHHNNEIYYFVEOLAHKF--ISP--QLMMSFVFESTRTGLTMKLTREQ 61
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 164 DVIYVLDGSSNI--YPMVEVQHFLINILKKFYIGPQIQIGVQVGEDAVHEFHL--NDYRS 222
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 62 IROGLEELQKVLPGGDTYMHGEF--RASBOIYYENRQYRTASVIALTDGELHED-- 116
    ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 222 VKQVVELASHIIERGGETERTRTAFGIEFASSEAFQKGGKAKK--KVMIVLDGSHSDPD 278
    ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 117 -----LFFYSREANRSRDIGAIYYCVGVKD-----ENFQOLARIA 157
    ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 280 LEKVIROSEKONTRYAAVAVLGYNNRGINPETFLNEIKYIASDPDDKHFPNVTDDEAL-- 338
    ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 153 DSKDHVEPPVNDGFQALQG 170
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 339 --KDIVDALGDRIFSLSEG 354
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

```

RESULT 10
US-10-601-368-22
; Sequence 22, Application US/10601368
; Publication NO. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.

Best Local Similarity 23.1%; Pred. No. 0.014;
Matches 50; Conservative 37; Mismatches 84; Indels 45; Gaps 9

[illegible]

RESULT 14

```

US-10-995-561-982
; Sequence 982, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 982
; LENGTH: 1019
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-982

```

Query Match	10.8%	Score 104.5;	DB 6;	Length 1019;	.
Best Local Similarity	23.1%;	Pred. No. 0.016;			
Matches	50;	Conservative	37;	Mismatches	84;
				Indels	45;
				Gaps	9

```

Oy 5 IYFEIIDKSSV-----LHNMN-IYFVGCILAHKFTSPOLKMSF-----IVFSRGRT 50
Db 47 YFVELDTSSVMQSFPTDILLFPMKQFVHOFSQLONEFLDVALISMRYGJLHFSQVE 106
Oy 51 TLMKLTDEBQIRQGLEELQKVLPGGDVTWNEHGFERASEQIYVENRGQYVTASVIALTD 110
Db 107 VSPRPGSDASPTIKVLQGISPPRG--TPTDCLAMNTDEIRDRSGK--TVNPAVITD 162
Oy 111 GELHEDLFFYSSREANRSPDLGAIYVCV-----GVKDFNET--QLARIADSKDHF 159
Db 163 GHVTSPPCGGIKLOARAREEGIRFLPAVANPQNLKEGGLDIASTPEHYLR---NDYAT 218
Oy 160 PVNDGQALOGIITHSL-----KKSGIEI 183
Db 219 MLPDSTEIDQDTINRIILKVMKNEAYECYKVSCLIEI 254

```

RESULT 15

```

US-10-601-368-6
; Sequence 6, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A

```

```

; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1141
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(122)
US-10-601-368-6

```

Query Match	Score	DB	Length
10.7%	104	6	1141

Best Local Similarity 24.2%; Pred. No. 0.021;
Matches 48; Conservative 28; Mismatches 84; Indels 38; Gaps 9

```

QY 4 LLYLFILDSGSLVHMMNIYFVEEDLAKF--ISP-QLRNSFVFSNRTGLMKLTEDREQ 61
Db DIVIVLDSNSI-YFVWVQHFLINILKKFYIGPQOIQGVVQIGEDVNHFFL-NDYKS 221
QY 62 IROGLEBEOKLPGSDIYMHGFE---RASEQIYENRQGYRTASYIALTDGELHED-- 116
Db 222 VKDVVEASHLEQRGSTETRTAFGLEPFRSEAFQKGRKGAR--KMMIYITLOSΗΣDSD 279
QY 117 -----LFFYSEREARNSRDICAIYVCVKVD---FNETOIARIA 152
Db 280 LEKVIOQSERDNTVRYAVAVLGYNRRGINPETFLINEIKYIASDPDDKHFPVUTDEAAL-- 338
QY 153 DSKDHVPVNDGFPALOG 170
Db 339 --KOIVDALGRIFSLLEG 354

```

Search completed: December 14, 2005, 11:59:29
Job time : 3.74816 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:35:12 ; Search time 599.1 Seconds

(without alignments)
2581.163 Million cell updates/sec

Title: US-09-970-076-2_COPY_41_227

Perfect score: 970
Sequence: 1 GGFDDYFILDKSGSVLHMN.....LOGIHSILKSCIEIILAAE 187

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Litering filter 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh
-O/cgn2_1/USPTO_bpool/US09970076/runat_14122005_11852_21035/app_query.fasta_1_2410
-DB=Published Applications NA Main -QPMF=fastcap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOCPU=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blonum62
-TRANS=human4.ctd -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076 @CGN_1_1_2715 @runat_14122005_11852_21035
-NCPU=6 -ICPU=3 -NO MAP -LAARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA Main:

1: /cgn2_6/ptoddata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptoddata/1/pubpna/US09_PUBCOMB.seq:*
3: /cgn2_6/ptoddata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptoddata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptoddata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptoddata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptoddata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptoddata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptoddata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptoddata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	970	100.0	1008	6	US-10-038-307-25
2	970	100.0	1008	6	US-10-201-292-25
3	970	100.0	1047	6	US-10-038-307-21
4	970	100.0	1047	6	US-10-201-292-21
5	970	100.0	1056	6	US-10-038-307-23
6	970	100.0	1056	6	US-10-201-292-23
7	970	100.0	1401	6	US-10-201-292-27
8	970	100.0	1401	6	US-10-201-292-29

9	970	100.0	1414	10	US-11-047-278-1	Sequence 1, Appl1
10	970	100.0	1436	10	US-11-047-278-9	Sequence 9, Appl1
11	970	100.0	1454	6	US-10-133-937-58	Sequence 58, Appl1
12	970	100.0	1454	6	US-10-159-563-58	Sequence 58, Appl1
13	970	100.0	1464	6	US-10-201-292-31	Sequence 31, Appl1
14	970	100.0	1534	6	US-10-201-292-33	Sequence 33, Appl1
15	970	100.0	1608	6	US-10-037-292-35	Sequence 35, Appl1
16	970	100.0	1609	5	US-10-037-270-8	Sequence 8, Appl1
17	970	100.0	1609	6	US-10-117-722-8	Sequence 8, Appl1
18	970	100.0	1609	9	US-10-122-851-8	Sequence 8, Appl1
19	970	100.0	1623	6	US-10-038-307-11	Sequence 11, Appl1
20	970	100.0	1623	6	US-10-201-292-11	Sequence 11, Appl1
21	970	100.0	1650	6	US-10-038-307-9	Sequence 9, Appl1
22	970	100.0	1650	6	US-10-038-307-13	Sequence 13, Appl1
23	970	100.0	1650	6	US-10-038-307-15	Sequence 15, Appl1
24	970	100.0	1650	6	US-10-201-292-9	Sequence 9, Appl1
25	970	100.0	1650	6	US-10-201-292-13	Sequence 13, Appl1
26	970	100.0	1650	6	US-10-201-292-15	Sequence 15, Appl1
27	970	100.0	1674	6	US-10-038-307-17	Sequence 17, Appl1
28	970	100.0	1674	6	US-10-201-292-17	Sequence 17, Appl1
29	970	100.0	1713	6	US-10-038-307-19	Sequence 19, Appl1
30	970	100.0	1713	6	US-10-201-292-19	Sequence 19, Appl1
31	970	100.0	1718	8	US-10-357-930-30300	Sequence 30300, A
32	970	100.0	2112	10	US-11-047-278-7	Sequence 7, Appl1
33	970	100.0	2272	3	US-09-796-753-11	Sequence 11, Appl1
34	970	100.0	2272	6	US-10-038-307-1	Sequence 1, Appl1
35	970	100.0	2272	6	US-10-201-292-1	Sequence 1, Appl1
36	970	100.0	2353	5	US-10-198-846-9957	Sequence 9957, Ap
37	970	100.0	5540	3	US-09-918-715-176	Sequence 176, App
38	970	100.0	5540	3	US-09-918-715-231	Sequence 231, App
39	970	100.0	5540	6	US-10-301-822-198	Sequence 198, App
40	970	100.0	5540	8	US-10-474-794-176	Sequence 176, App
41	970	100.0	5540	8	US-10-474-794-231	Sequence 231, App
42	970	100.0	5540	9	US-10-979-159-176	Sequence 176, App
43	970	100.0	5540	9	US-10-979-159-231	Sequence 231, App
44	970	100.0	5540	10	US-11-047-278-5	Sequence 5, Appl1
45	961	99.1	5220	3	US-09-918-715-186	Sequence 186, App

ALIGNMENTS

RESULT 1
US-10-038-307-25
; Sequence 25, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatsSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-25

Alignment Scores:

Pred. No.: 7.35e-120 Length: 1008
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_41_227 (1-187) * US-10-038-307-25 (1-1008)

QY 1 G[YG]YpneapneutryrphelleleuApplysSecdlyseerValleuHstHstRPaSn 20

```
DB 133 GGGGGATTGACCTGACTTTCATTTTGGACCAATTCAGAAAGTGTGTCGACCACTGGAAAT 192
QY 21 G|U|I|E|T|Y|T|P|H|E|V|A|G|U|G|I|N|U|E|U|A|A|H|I|S|Y|P|H|E|I|S|E|P|P|R|O|G|I|N|U|E|U|A|A|G|T|G|G|A|A|A|G 40
DB 193 GAAATCTATTAATCTTTGTGGAAACAGTTGGCTCACAATTCATTCAGCCACAGTTGGAAGAAG 252
QY 41 SerPheI|E|V|A|P|H|E|S|E|T|H|R|A|G|I|Y|T|H|R|L|E|U|E|T|H|S|E|P|H|E|U|T|H|R|G|U|A|S|P|A|R|G|U| 60
DB 253 TCCCTTAATGTTTCTTCCACCCGAGAACCACTTAAATGAACTGACAGAAAGACAGAA 312
QY 61 G|U|I|E|A|R|G|I|N|U|E|U|G|I|U|E|U|G|I|N|U|E|V|A|L|L|E|U|P|R|O|G|I|Y|G|I|Y|A|S|P|H|T|R|Y|T|E|T 80
DB 313 CAATCCGTCAGAGCCCTAGAAAGAACTCCAGAAAGTTCTGCGACAGAGACACTTACAGT 372
QY 81 H|S|G|U|G|Y|P|H|E|U|A|R|G|I|A|S|E|R|G|U|G|I|N|I|E|T|Y|T|R|G|U|A|S|P|A|R|G|I|N|U|Y|T|R|A|G 100
DB 373 CATGAAGGATTTGAAAGGGCCAGTGAAGCAGATTATTAAGAAACAGACAGAGGATACAG 432
QY 101 ThrA|S|e|V|a|I|I|e|I|e|A|l|e|U|T|H|R|A|S|P|G|I|Y|G|I|U|E|U|H|I|S|G|I|U|A|S|P|L|E|U|P|H|E|P|H|E|Y|R 120
DB 433 ACAGCCAGGCTCATCTATGCTTTGACTGATGAGAACTCATGAAGATCTTTTCTAT 492
QY 121 SerG|U|A|R|G|I|U|A|A|S|P|A|R|S|E|R|A|R|G|A|S|P|L|E|U|G|I|Y|A|I|I|E|V|A|I|Y|R|C|Y|S|V|A|I|G|I|Y|V|A|I 140
DB 493 TCAGAGAGGAGGCTAATAGCTCTCGAGATCTTGTCGCAATGTTTACTGTGTGTGTG 552
QY 141 LysA|S|P|H|E|A|S|P|H|E|U|T|H|R|G|I|N|U|E|U|A|I|A|R|G|I|E|A|I|A|S|P|S|E|R|Y|A|S|P|H|I|S|V|A|I|P|H|E|P|R|O 160
DB 553 AAAGATTTCAATAGACACACAGCTGGCCGGATGGCGACAGTAAAGATCATGTGTTTCCC 612
QY 161 ValA|S|P|A|S|P|G|I|Y|P|H|E|G|I|N|A|L|E|U|G|I|Y|I|E|I|H|I|S|E|R|I|L|E|U|Y|S|L|Y|S|E|R|C|Y|S 180
DB 613 GTGAATGACGGCTTTCAGGCTCTGCAAGGACATCATCAATTTTGAAGAAGTCTGCG 672
QY 181 I|E|G|I|U|I|L|E|U|A|I|A|A|G|I|U 187
DB 673 ATCGAAATTTCTAGCAGCTGAA 693
```

RESULT 2

```
US-10-201-292-25
/ Sequence 25, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 25
/ LENGTH: 1008
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-201-292-25
```

Alignment Scores:

```
Pred. No.: 7,35e-120 Length: 1008
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
```

US-09-970-076-2_COPY_41_227 (1-187) x US-10-201-292-25 (1-1008)

```
QY 1 G|Y|G|Y|P|H|A|S|P|E|U|T|Y|P|H|E|I|L|E|U|A|S|P|Y|S|E|R|G|I|S|E|R|V|A|I|L|E|U|H|I|S|I|S|T|R|P|A|S|N 20
DB 133 GGGGATTTGACCTGACTTTCATTTTGGACCAATTCAGAAAGTGTGTCGACCACTGGAAAT 192
```

```
QY 21 G|U|I|E|T|Y|T|P|H|E|V|A|G|U|G|I|N|U|E|U|A|A|H|I|S|Y|P|H|E|I|S|E|P|P|R|O|G|I|N|U|E|U|A|A|G|T|G|G|A|A|A|G 40
DB 193 GAAATCTATTAATCTTTGTGGAAACAGTTGGCTCACAATTCATTCAGCCACAGTTGGAAGAAG 252
QY 41 SerPheI|E|V|A|P|H|E|S|E|T|H|R|A|G|I|Y|T|H|R|L|E|U|E|T|H|S|E|P|H|E|U|T|H|R|G|U|A|S|P|A|R|G|U| 60
DB 253 TCCCTTAATGTTTCTTCCACCCGAGAACCACTTAAATGAACTGACAGAAAGACAGAA 312
QY 61 G|U|I|E|A|R|G|I|N|U|E|U|G|I|U|E|U|G|I|N|U|E|V|A|L|L|E|U|P|R|O|G|I|Y|G|I|Y|A|S|P|H|T|R|Y|T|E|T 80
DB 313 CAATCCGTCAGAGCCCTAGAAAGAACTCCAGAAAGTTCTGCGACAGAGACACTTACAGT 372
QY 81 H|S|G|U|G|Y|P|H|E|U|A|R|G|I|A|S|E|R|G|U|G|I|N|I|E|T|Y|T|R|G|U|A|S|P|A|R|G|I|N|U|Y|T|R|A|G 100
DB 373 CATGAAGGATTTGAAAGGGCCAGTGAAGCAGATTATTAAGAAACAGACAGAGGATACAG 432
QY 101 ThrA|S|e|V|a|I|I|e|I|e|A|l|e|U|T|H|R|A|S|P|G|I|Y|G|I|U|E|U|H|I|S|G|I|U|A|S|P|L|E|U|P|H|E|P|H|E|Y|R 120
DB 433 ACAGCCAGGCTCATCTATGCTTTGACTGATGAGAACTCCATGAAGATCTTTTCTAT 492
QY 121 SerG|U|A|R|G|I|U|A|A|S|P|A|R|S|E|R|A|R|G|A|S|P|L|E|U|G|I|Y|A|I|I|E|V|A|I|Y|R|C|Y|S|V|A|I|G|I|Y|V|A|I 140
DB 493 TCAGAGAGGAGGCTAATAGCTCTCGAGATCTTGTCGCAATGTTTACTGTGTGTGTG 552
QY 141 LysA|S|P|H|E|A|S|P|H|E|U|T|H|R|G|I|N|U|E|U|A|I|A|R|G|I|E|A|I|A|S|P|S|E|R|Y|A|S|P|H|I|S|V|A|I|P|H|E|P|R|O 160
DB 553 AAAGATTTCAATAGACACACAGCTGGCCGGATGGCGACAGTAAAGATCATGTGTTTCCC 612
QY 161 ValA|S|P|A|S|P|G|I|Y|P|H|E|G|I|N|A|L|E|U|G|I|Y|I|E|I|H|I|S|E|R|I|L|E|U|Y|S|L|Y|S|E|R|C|Y|S 180
DB 613 GTGAATGACGGCTTTCAGGCTCTGCAAGGACATCATCAATTTTGAAGAAGTCTGCG 672
QY 181 I|E|G|I|U|I|L|E|U|A|I|A|A|G|I|U 187
DB 673 ATCGAAATTTCTAGCAGCTGAA 693
```

RESULT 3

```
US-10-038-307-21
/ Sequence 21, Application US/10038307
/ Publication No. US20030134786A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/038,307
/ CURRENT FILING DATE: 2002-06-28
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 21
/ LENGTH: 1047
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-038-307-21
```

Alignment Scores:

```
Pred. No.: 7,79e-120 Length: 1047
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
```

US-09-970-076-2_COPY_41_227 (1-187) x US-10-038-307-21 (1-1047)

```
QY 1 G|Y|G|Y|P|H|A|S|P|E|U|T|Y|P|H|E|I|L|E|U|A|S|P|Y|S|E|R|G|I|S|E|R|V|A|I|L|E|U|H|I|S|I|S|T|R|P|A|S|N 20
DB 160 GGGGATTTGACCTGACTTTCATTTTGGACCAATTCAGAAAGTGTGTCGACCACTGGAAAT 219
QY 21 G|U|I|E|T|Y|T|P|H|E|V|A|G|U|G|I|N|U|E|U|A|A|H|I|S|Y|P|H|E|I|S|E|P|P|R|O|G|I|N|U|E|U|A|A|G|T|G|G|A|A|A|G 40
```

```
Db 220 GAATCTATTACTTGTGGAAACAGTGGCTCACAAATTCATCAGCCACAGTTGAGATG 279
Qy 41 SerPheIleValPheSerThrArgGlyThrThreumetLysLeuThrGluAspArgGlu 60
Db 280 TCCCTTATTGTTTCTTCACCCGAGAACACTTAATGAACTGACAGAAACAGGAA 339
Qy 61 GlnIleArgGlnIleuGlnIleuGlnIleValLeuProGlyIleAspThrTyMet 80
Db 340 CAATCCGTCAAGGCTTGAAGAACTCCAGAACTCTCCAGAGAGAGACATTACATG 399
Qy 81 HisGlnIlePheGlnIleuArgIleSerGlnIleTyThrGluAsnArgGlnIleTyArg 100
Db 400 CAGGAAGATTGAAAGGCGCAGTGAACAGATTATGAAACAGACAGGTTACAGG 459
Qy 101 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTy 120
Db 460 ACGCCAGCGTCATCATCTTGTGACTGATGAGAACTCCATGAAAGATCTTTTCTAT 519
Qy 121 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrcysValGlyVal 140
Db 520 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTCATTTGTTACTGTGTGTG 579
Qy 141 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
Db 580 AAGATTTCATATGACACACAGCTGCCCGGATTCGGACAGTAAAGATCATGTGTTCCC 639
Qy 161 ValAsnAspGlyPheGlnIleuGlnIleIleHisSerIleuLysLysSerCys 180
Db 640 GTGAATGACGGCTTTCAGGCTTCGCAAGGATCATCATCAATTTTGAAGAGTCTGCG 659
Qy 181 IleGluIleLeuAlaIleGlu 187
Db 700 ATCGAAATTCACGACCTGAA 720
```

RESULT 4

```
US-10-201-292-21
; Sequence 21, Application US/10201292
; Publication No. US2003014193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-21
```

```
Alignment Scores:
Pred. No.: 7,79e-120 Length: 1047
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
```

US-09-970-076-2_COPY_41_227 (1-187) x US-10-201-292-21 (1-1047)

```
Qy 1 GlyGlyPheAspLeuTyrrPheIleLeuAspLysSerGlySerValLeuHisHisTrpAsn 20
Db 160 GGGGAGATTGACCTGTAATCTTTCATTTTGGACAAATCAGGAAGTGTGTCACCACTGGAA 219
Qy 21 GlnIleTyrrTyrrPheValGlnIleuAlaHisLysPheIleSerProGlnLeuArgMet 40
Db 220 GAATCTATTACTTGTGGAAACAGTGGCTCACAAATTCATCAGCCACAGTTGAGATG 279
```

```
Qy 41 SerPheIleValPheSerThrArgGlyThrThreumetLysLeuThrGluAspArgGlu 60
Db 280 TCCCTTATTGTTTCTTCACCCGAGAACACTTAATGAACTGACAGAAACAGGAA 339
Qy 61 GlnIleArgGlnIleuGlnIleuGlnIleValLeuProGlyIleAspThrTyMet 80
Db 340 CAATCCGTCAAGGCTTGAAGAACTCCAGAACTCTCCAGAGAGAGACATTACATG 399
Qy 81 HisGlnIlePheGlnIleuArgIleSerGlnIleTyThrGluAsnArgGlnIleTyArg 100
Db 400 CAGGAAGATTGAAAGGCGCAGTGAACAGATTATGAAACAGACAGGTTACAGG 459
Qy 101 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTy 120
Db 460 ACGCCAGCGTCATCATCTTGTGACTGATGAGAACTCCATGAAAGATCTTTTCTAT 519
Qy 121 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrcysValGlyVal 140
Db 520 TCAGAGAGGAGGCTTAATAGTCTCGAGATCTTGTCATTTGTTACTGTGTGTG 579
Qy 141 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
Db 580 AAGATTTCATATGACACACAGCTGCCCGGATTCGGACAGTAAAGATCATGTGTTCCC 639
Qy 161 ValAsnAspGlyPheGlnIleuGlnIleIleHisSerIleuLysLysSerCys 180
Db 640 GTGAATGACGGCTTTCAGGCTTCGCAAGGATCATCATCAATTTTGAAGAGTCTGCG 659
Qy 181 IleGluIleLeuAlaIleGlu 187
Db 700 ATCGAAATTCACGACCTGAA 720
```

RESULT 5

```
US-10-038-307-23
; Sequence 23, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-23
```

```
Alignment Scores:
Pred. No.: 7,89e-120 Length: 1056
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
```

US-09-970-076-2_COPY_41_227 (1-187) x US-10-038-307-23 (1-1056)

```
Qy 1 GlyGlyPheAspLeuTyrrPheIleLeuAspLysSerGlySerValLeuHisHisTrpAsn 20
Db 133 GGGGAGATTGACCTGTAATCTTTCATTTTGGACAAATCAGGAAGTGTGTCACCACTGGAA 192
Qy 21 GlnIleTyrrTyrrPheValGlnIleuAlaHisLysPheIleSerProGlnLeuArgMet 40
Db 193 GAATCTATTACTTGTGGAAACAGTGGCTCACAAATTCATCAGCCACAGTTGAGAAAG 252
Qy 41 SerPheIleValPheSerThrArgGlyThrThreumetLysLeuThrGluAspArgGlu 60
```

```
Db 253 TCCCTTATTGTTTCTCCACCGAGGAAACAACCTTATGAAACTGACAGAGACAGAGAA 312
Qy 61 GlnIleArgGlnGlyLeuGlnGluLeuGlnIleValLeuProGlyGlyAspThrTyrMet 80
Db 313 CAATCCGTCACAGCGCTTAGAAGAACTCCAGAAAGTCTCGACAGAGAGACACTTACATG 372
Qy 81 HisGlnGlyPheGlnIleValLeuGlnIleTyrTyrGlnIleValLeuGlnIleValTyrArg 100
Db 373 CATGAAGGATTTGAAAGGGCCGATGACAGATTTATTTGAAACAGACAGAGGTCACAG 432
Qy 101 ThrIleSerValIleIleAlaLeuThrAspGlyGluLeuHisGlnIleValLeuPhePheTyr 120
Db 433 ACAGCCAGCGTCATCATGCTTTGACTGATGAGAACTCATGAAGATCTCTTTTCTAT 492
Qy 121 SerGluArgGlnIleValLeuGlnIleValLeuGlnIleValTyrCysValGlyVal 140
Db 493 TCAGAGAGGAGGCTTATAGTCTCGAGATCTTGCGCAATGTTACTGTGTGTGTG 552
Qy 141 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
Db 553 AAAGATTTCAATGACACACAGCTGCGCCGATTCGAGACAGTACATCATGCTTTCCC 612
Qy 161 ValAsnAspGlyPheGlnIleValLeuGlnIleIleHisSerIleLeuIleValLysSerCys 180
Db 613 GTGAATGACGCGCTTTCAGGCTCTGCAAGGATCATCATCAATTTTGAAGAGTCTGCG 672
Qy 181 IleGlnIleLeuAlaIleGln 187
Db 673 ATCGAAATTCCTAGCAGCTGAA 693
```

RESULT 6

```
US-10-201-292-23
/ Sequence 23, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Englin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ. ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 23
/ LENGTH: 1056
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-201-292-23
```

Alignment Scores:

```
Pred. No.: 7,896-120 Length: 1056
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
```

US-09-970-076-2_copy_41_227 (1-187) x US-10-201-292-23 (1-1056)

```
Qy 1 GtlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValIleuHisIleTyrPaaN 20
Db 133 GGGGAGATTGACCTGTACTTCAATTTTGACAAATCAGAAAGTGTGCGCACTGGAAAT 192
Qy 21 GlnIleTyrTyrPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 40
Db 193 GAAATCTATTACTTTGTGGAAACAGTTGGCTACAAATTCATCACCCACAGTTGAGAAATG 252
Qy 41 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGlnAspArgGln 60
Db 253 TCCCTTATTGTTTCTCCACCGAGGAAACAACCTTATGAAACTGACAGAAAGACAGAGAA 312
```

```
Qy 61 GlnIleArgGlnGlyLeuGlnGluLeuGlnIleValLeuProGlyGlyAspThrTyrMet 80
Db 313 CAATCCGTCACAGCGCTTAGAAGAACTCCAGAAAGTCTCGACAGAGAGACACTTACATG 372
Qy 81 HisGlnGlyPheGlnIleValLeuGlnIleTyrTyrGlnIleValLeuGlnIleValTyrArg 100
Db 373 CATGAAGGATTTGAAAGGGCCGATGACAGATTTATTTGAAACAGACAGAGGTCACAG 432
Qy 101 ThrIleSerValIleIleAlaLeuThrAspGlyGluLeuHisGlnIleValLeuPhePheTyr 120
Db 433 ACAGCCAGCGTCATCATGCTTTGACTGATGAGAACTCATGAAGATCTCTTTTCTAT 492
Qy 121 SerGluArgGlnIleValLeuGlnIleValLeuGlnIleValTyrCysValGlyVal 140
Db 493 TCAGAGAGGAGGCTTATAGTCTCGAGATCTTGCGCAATGTTACTGTGTGTGTG 552
Qy 141 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
Db 553 AAAGATTTCAATGACACACAGCTGCGCCGATTCGAGACAGTACATCATGCTTTCCC 612
Qy 161 ValAsnAspGlyPheGlnIleValLeuGlnIleIleHisSerIleLeuIleValLysSerCys 180
Db 613 GTGAATGACGCGCTTTCAGGCTCTGCAAGGATCATCATCAATTTTGAAGAGTCTGCG 672
Qy 181 IleGlnIleLeuAlaIleGln 187
Db 673 ATCGAAATTCCTAGCAGCTGAA 693
```

RESULT 7

```
US-10-201-292-27
/ Sequence 27, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Englin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ. ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 27
/ LENGTH: 1401
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-201-292-27
```

Alignment Scores:

```
Pred. No.: 1,226-119 Length: 1401
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
```

US-09-970-076-2_copy_41_227 (1-187) x US-10-201-292-27 (1-1401)

```
Qy 1 GtlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValIleuHisIleTyrPaaN 20
Db 133 GGGGAGATTGACCTGTACTTCAATTTTGACAAATCAGAAAGTGTGCGCACTGGAAAT 192
Qy 21 GlnIleTyrTyrPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 40
Db 193 GAAATCTATTACTTTGTGGAAACAGTTGGCTACAAATTCATCACCCACAGTTGAGAAATG 252
Qy 41 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGlnAspArgGln 60
Db 253 TCCCTTATTGTTTCTCCACCGAGGAAACAACCTTATGAAACTGACAGAAAGACAGAGAA 312
Qy 61 GlnIleArgGlnGlyLeuGlnGluLeuGlnIleValLeuProGlyGlyAspThrTyrMet 80
```



```
DB 313 CAATCCGTCAGCGCTAGAAAGAACTCCAGAAATCTTCGACAGAGAGACACTTACATG 372
QY 81 HIGLUGLYPHEGLUARGALASERGLUGNILETYRTYRGLUENARGINGLYTYRARG 100
DB 373 CATGAGAGATTGTGAAAGGGCCAGTGCAGCATTTATATGAAACACAGAGGGTACAGG 432
QY 101 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTy 120
DB 433 ACAGCCAGCGCTCATCTTCTTACCTGATGAGAACTCCATGAAAGATCTCTTTCTAT 492
QY 121 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTYRQysValGlyVal 140
DB 493 TCAGAGAGGAGGCTTAATAGCTTCGAGATCTTGTCCAATTGTTTACTGTGTGTG 552
QY 141 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
DB 553 AAGATTTCATATGACACACAGCTGGCCCGATTCCGACAGTACATCATGTGTCTCC 612
QY 161 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 180
DB 613 GTGATATGACGGCTTTCAGGCTTCGACAGGATCATCTCATATTGTAAGAGTCTCTGC 672
QY 181 ILeGluIleLeuAlaAlaGlu 187
DB 673 ATCGAAATTCAGACGCTGAA 693
```

RESULT 8

```
US-10-201-292-29
; Sequence 29, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYMAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201.292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-201-292-29
```

Alignment Scores:

Pred. No.:	1,22e-119	Length:	1401
Score:	970.00	Matches:	187
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-970-076-2_COPY_41_227 (1-187) x US-10-201-292-29 (1-1401)

```
QY 1 GLyGlyPheAspLeuTYrPheIleLeuAspLysSerGlySerValLeuHisSTRPAsn 20
DB 133 GCGGAGATTGACCTGTACTTTCATTTTGACAAATCAGAAAGTGTGTCGACCACTGGAAT 192
QY 21 GlnIleTYrTYrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 40
DB 193 GAATCTATTAATTGTGGAAAGCTTGCTCACAAATTCATCAGCCACAGTTGAGATG 252
QY 41 SerPheIleValPheSerThrArgGlyThrThreuMetLysLeuThrGluAspArgGlu 60
DB 253 TCTTTATTTGTTTCTCACCCAGAGAACACTTAAATGAACTGACAGAGACAGAGAA 312
QY 61 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyLysAspThrTYrMet 80
DB 313 CAATCCGTCAGCGCTAGAAAGAACTCCAGAAATCTTCGACAGAGAGACACTTACATG 372
```

```
QY 81 HIGLUGLYPHEGLUARGALASERGLUGNILETYRTYRGLUENARGINGLYTYRARG 100
DB 373 CATGAGAGATTGTGAAAGGGCCAGTGCAGCATTTATATGAAACACAGAGGGTACAGG 432
QY 101 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTy 120
DB 433 ACAGCCAGCGCTCATCTTCTTACCTGATGAGAACTCCATGAAAGATCTCTTTCTAT 492
QY 121 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTYRQysValGlyVal 140
DB 493 TCAGAGAGGAGGCTTAATAGCTTCGAGATCTTGTCCAATTGTTTACTGTGTGTG 552
QY 141 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
DB 553 AAGATTTCATATGACACACAGCTGGCCCGATTCCGACAGTACATCATGTGTCTCC 612
QY 161 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 180
DB 613 GTGATATGACGGCTTTCAGGCTTCGACAGGATCATCTCATATTGTAAGAGTCTCTGC 672
QY 181 ILeGluIleLeuAlaAlaGlu 187
DB 673 ATCGAAATTCAGACGCTGAA 693
```

RESULT 9

US-11-047-278-1

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; Sequence 1, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047.278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970.076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251.481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)..(1207)
; US-11-047-278-1
```

Alignment Scores:

Pred. No.:	1,24e-119	Length:	1414
Score:	970.00	Matches:	187
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-970-076-2_COPY_41_227 (1-187) x US-11-047-278-1 (1-1414)

```
QY 1 GLyGlyPheAspLeuTYrPheIleLeuAspLysSerGlySerValLeuHisSTRPAsn 20
DB 224 GCGGAGATTGACCTGTACTTTCATTTTGACAAATCAGAAAGTGTGTCGACCACTGGAAT 283
QY 21 GlnIleTYrTYrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 40
DB 284 GAATCTATTAATTGTGGAAAGCTTGCTCACAAATTCATCAGCCACAGTTGAGATG 343
QY 41 SerPheIleValPheSerThrArgGlyThrThreuMetLysLeuThrGluAspArgGlu 60
```

DB 344 TCGTTATTGTTTTCACCCGAGGAGAACCTTATGAAACTGACAGAGACAGAGA 403
QY 61 GlnlleArgGlnGlyLeuGlnGluValLeuProGlyGlyAspThrTyrmec 80
DB 404 CAATTCGTCAGAGGCTTGAAGAACTCCAGAAAGTTCTGCAGAGAGACACTTACATG 463
QY 81 HisGlnGlyPheGlnuArgAlaSerGlnGlnIleTyrcTyrcGlnuAsnArgGlnGlyTyraG 100
DB 464 CATGAAGATTTCAGAAAGGCGCATGACGATTATTATGAAACAGACAGAGGTACAG 523
QY 101 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGlnuAspLeuPhePheTy 120
DB 524 ACAGCAGCGGTCACTCATTTGCTTGCATGAGAACTCCATGAAATCATCTTTTCTAT 583
QY 121 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrcysValGlyVal 140
DB 584 TCAGAGAGGAGGCTTATAGTCTCGAGATCTTGCGCAATTTTAACTGTGTGTGTG 643
QY 141 LysAspPheAsnGlnuThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
DB 644 AAAGATTTCATAGACACACAGCTGCGCCGATTCGAGACATGATCATGTGTTCCC 703
QY 161 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 180
DB 704 GTGAATGACGGCTTTCAGGCTTCGCAAGGCATCATCATTTTGAAGAAGTCTGCG 763
QY 181 IleGlnIleLeuAlaIleGln 187
DB 764 ATCGAAATTTCTAGCAGCTGAA 784

RESULT 10

US-11-047-278-9
; Sequence 9, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296, 97745
; CURRENT APPLICATION NUMBER: US/11/047, 278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970, 076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251, 481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (380)..(1033)
US-11-047-278-9

Alignment Scores:
Pred. No.: 1,27e-119 Length: 1436
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-970-076-2_COPY_41_227 (1-187) x US-11-047-278-9 (1-1436)

QY 1 GlnGlyPheAspLeuTyrcPheIleLeuAspLysSerGlySerValLeuHisThrPAsn 20
DB 263 GGGGAGTTTGAACCTGTACTTCTTATTTGGACAAATCAGAAAGTGTGTCACCACTGGAA 322
QY 21 GlnIleTyrcTyrcPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 40

DB 323 GAAATCTTACTTGTGGAAACAGTTGGCTCCAAATTCATCAGCCACAGTTGAGAA 382
QY 41 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGlnuAspArgGlu 60
DB 383 TCGTTATTGTTTTCACCCGAGAGAACACTTATAGAACTGACAGAGACAGAGAA 442
QY 61 GlnlleArgGlnGlyLeuGlnGluValLeuProGlyGlyAspThrTyrmec 80
DB 443 CAATTCGTCAGAGGCTTGAAGAACTCCAGAAAGTTCTGCAGAGAGACACTTACATG 502
QY 81 HisGlnGlyPheGlnuArgAlaSerGlnGlnIleTyrcTyrcGlnuAsnArgGlnGlyTyraG 100
DB 503 CATGAAGATTTCAGAAAGGCGCATGACGAGATTATTATGAAACAGACAGAGGTACAG 562
QY 101 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGlnuAspLeuPhePheTy 120
DB 563 ACAGCTAGCGGTCACTCATTTGCTTGCATGAGAACTCCATGAAATCATCTTTTCTAT 622
QY 121 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrcysValGlyVal 140
DB 623 TCAGAGAGGAGGCTTATAGTCTCGAGATCTTGCGCAATTTTAACTGTGTGTGTG 682
QY 141 LysAspPheAsnGlnuThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
DB 683 AAAGATTTCATAGACACACAGCTGCGCCGATTCGAGACATGATCATGTGTTCCC 742
QY 161 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 180
DB 743 GTGAATGACGGCTTTCAGGCTTCGCAAGGCATCATCATTTTGAAGAAGTCTGCG 802
QY 181 IleGlnIleLeuAlaIleGln 187
DB 803 ATCGAAATTTCTAGCAGCTGAA 823

RESULT 11

US-10-133-937-58
; Sequence 58, Application US/10133937
; Publication No. US20030207278A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Melzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; FILE REFERENCE: 11613, 56US01
; CURRENT APPLICATION NUMBER: US/10/133, 937
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-937-58

Alignment Scores:
Pred. No.: 1,29e-119 Length: 1454
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_41_227 (1-187) x US-10-133-937-58 (1-1454)

QY 1 GlnGlyPheAspLeuTyrcPheIleLeuAspLysSerGlySerValLeuHisThrPAsn 20
DB 264 GGGGAGTTTGAACCTGTACTTCTTATTTGGACAAATCAGAAAGTGTGTCACCACTGGAA 323
QY 21 GlnIleTyrcTyrcPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 40

DB 324 GAATCTATTACTTGTGGAAAGAGTTGGCTCACAAATTCATCAGCCACAGTTGAGAAATG 383
QY SerPheIleValPheSerThrArgGlyThrThreumelysLeuThrGluAspArgGlu 60
DB 384 TCCCTTAATGTTTCTTCACCCGAGAACAACTTAATGAACTGACAGAGAACAGAGAA 443
QY GluIleArgGlnGlyLeuGlnGlyLeuGlnValLeuProGlyGlyAspThrTyrMet 80
DB 444 CAATCCGTCAGAGCCCTAGAGAACTCCAGAAATTTCCGACGAGAGACACTTACATG 503
QY HisGlnGlyPheGlnArgAlaSerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 100
DB 504 CATGAAGATTGTAAGAGGCGCAGTACAGATTTATATGAAAACAGACAGAGGTACAG 563
QY ThrAlaSerValIleIleAlaLeuThrAspGlyGlyLeuHisGlyAspLeuPhePheTyr 120
DB 564 ACAGCCAGCGTCATCATCTTGTGACTGATGAGAACTCCATGAAATCTCTTTTCTAT 623
QY SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 140
DB 624 TCAGAGAGGAGGCTTAATAGTCTTCGAGATCTTGTCAAATGTTTACTGTGTGTG 683
QY LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
DB 684 AAGATTTCATAGACACACAGCTGCGCCGAGTTCCGACAGTAAAGATCATGTGTTCCC 743
QY ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuYsLysSerCys 180
DB 744 GTCAATGACGGCTTTCAGGCTCTGCAAGGATCATCATCAATTTGAAGAAGTCTGCG 803
QY 181 IlegluIleLeuAlaIleGlu 187
DB 804 ATCGAAATTTCTAGCAGCTGAA 824

RESULT 12

US-10-159-563-58

Sequence 58, Application US/10159563

Publication No. US20040009154A1

GENERAL INFORMATION:

APPLICANT: Khan, Javed

APPLICANT: Ringner, Markus

APPLICANT: Peterson, Carsten

APPLICANT: Melzer, Paul

TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR

FILE REFERENCE: 11613.56US11

CURRENT APPLICATION NUMBER: US/10/159,563

CURRENT FILING DATE: 2002-12-09

PRIOR APPLICATION NUMBER: US 10/133,937

PRIOR FILING DATE: 2002-04-25

NUMBER OF SEQ ID NOS: 444

SOFTWARE: PatentIn version 3.1

SEQ ID NO 58

LENGTH: 1454

TYPE: DNA

ORGANISM: Homo sapiens

US-10-159-563-58

Alignment Scores:

Pred. No.: 1,298-119

Score: 970.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 6

Gaps: 0

US-09-970-076-2_COPY_41_227 (1-187) x US-10-159-563-58 (1-1454)

QY 1 GlyGlyPheAspLeuTyrPheIleLeuAlaAspLysSerGlySerValLeuHisIleSTPaaN 20
DB 264 GCGGATTTGACCTGTACTTCATTTGACAAATTCAGAAAGTGTGTCACACATCGAAAT 323

QY 21 GluIleTyrPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 40
DB 324 GAATCTATTACTTGTGGAAAGAGTTGGCTCACAAATTCATCAGCCACAGTTGAGAAATG 383
QY SerPheIleValPheSerThrArgGlyThrThreumelysLeuThrGluAspArgGlu 60
DB 384 TCCCTTAATGTTTCTTCACCCGAGAACAACTTAATGAACTGACAGAGAACAGAGAA 443
QY GluIleArgGlnGlyLeuGlnGlyLeuGlnValLeuProGlyGlyAspThrTyrMet 80
DB 444 CAATCCGTCAGAGCCCTAGAGAACTCCAGAAATTTCCGACGAGAGACACTTACATG 503
QY HisGlnGlyPheGlnArgAlaSerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 100
DB 504 CATGAAGATTGTAAGAGGCGCAGTACAGATTTATATGAAAACAGACAGAGGTACAG 563
QY ThrAlaSerValIleIleAlaLeuThrAspGlyGlyLeuHisGlyAspLeuPhePheTyr 120
DB 564 ACAGCCAGCGTCATCATCTTGTGACTGATGAGAACTCCATGAAATCTCTTTTCTAT 623
QY SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 140
DB 624 TCAGAGAGGAGGCTTAATAGTCTTCGAGATCTTGTCAAATGTTTACTGTGTGTG 683
QY LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
DB 684 AAGATTTCATAGACACACAGCTGCGCCGAGTTCCGACAGTAAAGATCATGTGTTCCC 743
QY ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuYsLysSerCys 180
DB 744 GTCAATGACGGCTTTCAGGCTCTGCAAGGATCATCATCAATTTGAAGAAGTCTGCG 803
QY 181 IlegluIleLeuAlaIleGlu 187
DB 804 ATCGAAATTTCTAGCAGCTGAA 824

RESULT 13

US-10-201-292-31

Sequence 31, Application US/10201292

Publication No. US2003014193A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/201,292

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatcSeq for Windows Version 4.0

SEQ ID NO 31

LENGTH: 1464

TYPE: DNA

ORGANISM: Homo sapiens

US-10-201-292-31

Alignment Scores:

Pred. No.: 1,318-119

Score: 970.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 6

Gaps: 0

US-09-970-076-2_COPY_41_227 (1-187) x US-10-201-292-31 (1-1464)

QY 1 GlyGlyPheAspLeuTyrPheIleLeuAlaAspLysSerGlySerValLeuHisIleSTPaaN 20
DB 133 GCGGATTTGACCTGTACTTCATTTGACAAATTCAGAAAGTGTGTCACACATCGAAAT 192
QY 21 GluIleTyrPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 40

```
Db 193 GAATCTATTACTTTGTGGACAGTTGGCTCAAAATTGATCGACCCACAGTTAGAAATG 252
Qy 41 SerpHeilValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 60
Db 253 TCCTTTATTGTTTCTCCACCCGAGGAAACAACCTTAATGAAACTGACAGAAACAGAGAA 312
Qy 61 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrmec 80
Db 313 CAAATCCGTCAGAGGCTTAGAAGAACTCCAGAAAGTTCTCCAGAGAGACACTTACATG 372
Qy 81 HisGluGlyPheGluArgAlaSerGluGlnIleTyThrGluAspArgGlnGlyTyArg 100
Db 373 CATGAAGATTGAAAGGCCAGTGACAGATTTATTAAGAAACAGACAGAGGTACAGG 432
Qy 101 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTy 120
Db 433 ACAGCCAGCGTCATCATCTTGTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTAT 492
Qy 121 SerGluArgGluAlaAspArgSerArgAspLeuGlyAlaIleValTyrcyValGlyVal 140
Db 493 TCAGAGAGGAGGCTTAATAGGCTTCAGAGATCTTGAGCAATTGTTACTGTGTGTGTG 552
Qy 141 LysAspPheAspGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
Db 553 AAGATTTCATATGACACACAGCTGGCCCGATTGGCGACAGTAAAGATCATGTGTTCCC 612
Qy 161 ValAspAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 180
Db 613 GTGAATGACGGCTTTCAGGCTTCGCAAGGATCATCATCAATTTTGAAGAAGTCTTCC 672
Qy 181 IleGluIleLeuAlaIleGlu 187
Db 673 ATCGAAATTTCTAGCAGCTGAA 693
```

RESULT 14
US-10-201-292-33

```
/ Sequence 33, Application US/10201292
/ Publication No. US2003014193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 33
/ LENGTH: 1534
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-201-292-33
```

Alignment Scores:
Pred. No.: 1,4e-119 Length: 1534
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_41_227 (1-187) x US-10-201-292-33 (1-1534)

```
Qy 1 G|G|G|yPheAspLeuTyrrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 20
Db 133 GGGGATTGACCTGTACTTATTTGGACAAATCGAAGATGTGCTGCACCACTGGAAT 192
Qy 21 G|u|l|e|T|y|r|P|h|e|V|a|l|G|u|G|l|n|L|e|u|A|l|a|I|e|I|e|S|e|r|P|r|o|G|l|n|L|e|u|A|r|G|e|c 40
Db 193 GAAATCTATTACTTTGTGGACAGTTGGCTCAAAATTGATCGACCCACAGTTAGAAATG 252
```

```
Qy 41 SerpHeilValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 60
Db 253 TCCTTTATTGTTTCTCCACCCGAGGAAACAACCTTAATGAAACTGACAGAAACAGAGAA 312
Qy 61 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrmec 80
Db 313 CAAATCCGTCAGAGGCTTAGAAGAACTCCAGAAAGTTCTCCAGAGAGACACTTACATG 372
Qy 81 HisGluGlyPheGluArgAlaSerGluGlnIleTyThrGluAspArgGlnGlyTyArg 100
Db 373 CATGAAGATTGAAAGGCCAGTGACAGATTTATTAAGAAACAGACAGAGGTACAGG 432
Qy 101 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTy 120
Db 433 ACAGCCAGCGTCATCATCTTGTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTAT 492
Qy 121 SerGluArgGluAlaAspArgSerArgAspLeuGlyAlaIleValTyrcyValGlyVal 140
Db 493 TCAGAGAGGAGGCTTAATAGGCTTCAGAGATCTTGATGCAATTGTTACTGTGTGTGTG 552
Qy 141 LysAspPheAspGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
Db 553 AAGATTTCATATGACACACAGCTGGCCCGATTGGCGACAGTAAAGATCATGTGTTCCC 612
Qy 161 ValAspAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 180
Db 613 GTGAATGACGGCTTTCAGGCTTCGCAAGGATCATCATCAATTTTGAAGAAGTCTTCC 672
Qy 181 IleGluIleLeuAlaIleGlu 187
Db 673 ATCGAAATTTCTAGCAGCTGAA 693
```

RESULT 15
US-10-201-292-35

```
/ Sequence 35, Application US/10201292
/ Publication No. US2003014193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 35
/ LENGTH: 1608
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-201-292-35
```

Alignment Scores:
Pred. No.: 1,51e-119 Length: 1608
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_41_227 (1-187) x US-10-201-292-35 (1-1608)

```
Qy 1 G|G|G|yPheAspLeuTyrrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 20
Db 133 GGGGATTGACCTGTACTTATTTGGACAAATCGAAGATGTGCTGCACCACTGGAAT 192
Qy 21 G|u|l|e|T|y|r|P|h|e|V|a|l|G|u|G|l|n|L|e|u|A|l|a|I|e|I|e|S|e|r|P|r|o|G|l|n|L|e|u|A|r|G|e|c 40
Db 193 GAAATCTATTACTTTGTGGACAGTTGGCTCAAAATTGATCGACCCACAGTTAGAAATG 252
Qy 41 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 60
```

```
Db      253 TCCTTTATTGTTTCTCCACCCGAGAACACTTAATGAACAGACAGAGAA 312
Qy      61  GlnIleArgInglYleuGlnIleuValIleuProGlyAspThrTyrMet 80
Db      313 CAATCCGTCAGGCTTAGAAGAACTCAGAAAGTTCTGCCAGGAGAGACATTACATG 372
Qy      81  HisGlnGlyPheGlnArgAlaSerGlnGlnIleTyrTyrGlnAsnArgGlnGlyTyrArg 100
Db      373 CATGAAGGATTTGAAAGGCCAGTAGACAGATTATATGAAAACAGACAAAGGTACAGG 432
Qy      101 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGlnAspLeuPhePheTyr 120
Db      433 ACAGCCAGCGTCATCATTTGCTTGTGATGAGAGAACTCCATGAAAGATCTTTTCTAT 492
Qy      121 SerGlnArgGlnIleAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 140
Db      493 TCAGAGAGGAGGCTAATAGGTCTCGAGATCTTGGTCAATGTGTACTGTGTGTGTG 552
Qy      141 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 160
Db      553 AAAGATTTCATATGAGACACAGCTGGCCCGATTGCCGACAGTAAAGATCATGTGTTCCC 612
Qy      161 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 180
Db      613 GTGAATGACGGCTTTCAGGCTCTGCAAGGATCATCCACTCAATTGGAAGAAGTCTCTGC 672
Qy      181 IleGlnIleLeuAlaIleGln 187
Db      673 ATCGAATCTAGCAGCTGAA 693
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Job time : 606.1 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:41:36 ; Search time 150.899 Seconds
(without alignments)
607.449 Million cell updates/sec

Title: US-09-970-076-2_COPY_41_227

Perfect score: 970
Sequence: 1 GCGDLYFILDKSGSVLHMN.....LOGIHSILKSCIBILAIE 187

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 416131 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+g2n.model -DEV=x1h
-Q/cg21_1/USPTO.epool/US09970076/runat_14122005_11853_21065/app_query.fasta_1_2410
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.csl -LIST=45 -DOCALL=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076_@CGN_1_1_675_@runat_14122005_11853_21065
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA New:

1: /cg21_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
2: /cg21_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
3: /cg21_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
4: /cg21_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
5: /cg21_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
6: /cg21_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
7: /cg21_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
8: /cg21_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
9: /cg21_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
10: /cg21_6/ptodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	970	100.0	5540	7 US-11-186-284-198	Sequence 198, App
2	132.5	13.7	4740	7 US-11-080-026-3	Sequence 3, Appl
3	131	13.6	11447	7 US-11-186-284-25	Sequence 25, Appl
4	122	12.6	2834	6 US-10-750-185-39040	Sequence 39040, A
5	111.5	11.5	2501	6 US-10-821-234-182	Sequence 182, App
6	109	11.2	3449	6 US-10-131-826A-293	Sequence 293, App
7	108	11.1	3564	6 US-10-601-368-20	Sequence 20, Appl
8	108	11.1	4858	6 US-10-601-368-19	Sequence 19, Appl

9	107.5	11.1	3175	6 US-10-995-561-464	Sequence 464, App
10	107.5	11.1	3464	6 US-10-995-561-465	Sequence 465, App
11	107.5	11.1	3468	6 US-10-995-561-466	Sequence 466, App
12	107	11.0	1325	6 US-10-750-185-56394	Sequence 56394, A
13	104	10.7	3564	6 US-10-601-368-2	Sequence 2, Appl
14	104	10.7	3967	7 US-11-000-463-574	Sequence 574, App
15	104	10.7	3969	7 US-11-000-463-102	Sequence 102, App
16	104	10.7	5042	6 US-10-601-368-1	Sequence 1, Appl
17	101.5	10.5	47572	6 US-10-995-561-13356	Sequence 13356, A
18	98.5	9.8	3868	6 US-10-995-561-404	Sequence 404, App
19	95	9.8	3884	6 US-10-601-368-17	Sequence 17, Appl
20	94	9.7	2773	7 US-11-102-240-33	Sequence 33, Appl
21	89.5	9.2	1062	7 US-11-137-465-11	Sequence 11, Appl
22	89.5	9.2	1347	7 US-11-137-465-12	Sequence 12, Appl
23	79.5	8.2	3366	6 US-10-467-657-6111	Sequence 6111, App
24	75	7.7	3435	6 US-10-793-626-3648	Sequence 3648, App
25	74	7.6	1688	6 US-10-510-386-157	Sequence 157, App
26	73.5	7.6	1530	6 US-10-793-626-2879	Sequence 2879, App
27	73.5	7.6	2996	6 US-10-793-626-3563	Sequence 3563, App
28	73.5	7.6	3092	6 US-10-793-626-3559	Sequence 3559, App
29	73.5	7.6	3900	6 US-10-793-626-4177	Sequence 4177, App
30	73.5	7.6	1115	6 US-10-513-786-6	Sequence 6, Appl
31	73.5	7.6	1115	6 US-10-513-786-8	Sequence 8, Appl
32	73	7.5	795	6 US-10-793-626-387	Sequence 387, App
33	73	7.5	876	6 US-10-793-626-2635	Sequence 2635, App
34	73	7.5	2657	6 US-10-793-626-3472	Sequence 3472, App
35	73	7.5	3281	6 US-10-793-626-4324	Sequence 4324, App
36	73	7.5	3290	6 US-10-793-626-4360	Sequence 4360, App
37	73	7.5	3633	6 US-10-793-626-4307	Sequence 4307, App
38	73	7.5	4828	6 US-10-750-185-56813	Sequence 56813, A
39	72	7.4	2361	6 US-10-467-657-249	Sequence 249, App
40	71	7.3	1887	6 US-10-467-657-3083	Sequence 3083, App
41	71	7.3	1887	6 US-10-467-657-3083	Sequence 3083, App
42	70	7.2	1305	6 US-10-467-657-5693	Sequence 5693, App
43	70	7.2	1404	6 US-10-467-657-5695	Sequence 5695, App
44	70	7.2	96988	7 US-11-117-187-196	Sequence 196, App
45	69.5	7.2	730	6 US-10-750-185-61019	Sequence 61019, A

ALIGNMENTS

RESULT 1
US-11-186-284-198
; Sequence 198, Application US/111866284
; Publication No. US2005026493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John B.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCES: MP01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 5540
; TYPE: DNA

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; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144) .. (1838)
US-11-186-284-198

Alignment Scores:
Pred. No.: 4,946-117 Length: 5540
Score: 970.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-970-076-2_COPY_41_227 (1-187) x US-11-186-284-198 (1-5540)

QY 1 G1G1G1PheAspLeuTyrrPhe11eLeuAspLySerG1SerVal1euh1sh1trPaen 20
DB 264 GGGGATTTCAGCTTGAATCTTCAATTTGGACAAATCGAAGTGTGCTGCACCTGGAAT 323
QY 21 G1u1eTyrrTyrrPheVal1GluGlnLeu1ah1sYrPhe11eSerProGlnLeu1gMc 40
DB 324 GAATCTAATTAATCTTGCGAAGAGTGGCTCACAAATTCATCGCCACAGTTGAGAAATG 383
QY 41 SerPhe11eValPheSerThrArgG1YThrThrLeuMetLySerThrg1uAparG1u 60
DB 384 TCTTTAATGTTTCTTCACCCAGAACAACTTAACTGACAGAGACAGAA 443
QY 61 Gln1eArgGln1yLeuGlnGlnLeuGlnLyVal1euproG1yG1yAspThryrMet 80
DB 444 CAATCCGTCAAGCCGTGAGAAAGAACTCCAGAAAGTTCTGCAGAGAGAGACCTTACATG 503
QY 81 H1eG1uG1yPheG1uArg1aSerGlnGln11eTyrrTyrrGlnAsnArgGlnG1yTyrrArg 100
DB 504 CATGAAGAGATTGAAAGGCGCAGTGAAGACATTTATTAATAACAGACAAAGGTTACAGG 563
QY 101 Thr1aSerVal11e11e1aLeuThrAspG1yGlnLeuH1eG1uAspLeuPhePheTyrr 120
DB 564 ACAGCCAGCTCATCTTGGCTTGGATCGATGAGAACTCCATGAAGATCTCTTTTCTAT 623
QY 121 SerG1uArgG1u1aAsnArgSerArgAspLeuG1yAla11eVal1TyrrCyVal1G1yVal 140
DB 624 TCAGAGAGGAGGCTAATAGTGTCTCGAGATCTTGTCATATGTTTACTGTGTGGTGTG 683
QY 141 LysAspPheAsnG1uThrg1nLeu1aArg11eAlaAspSerLyAspRph1sValPhePro 160
DB 684 AAAGATTTCATGACAGACAGCTGGCCCGATTCGCGACAGTAAAGATCATGTGTTCC 743
QY 161 ValAsnAspG1yPheGln1aLeuGlnG1y11e11e1sSer11eLeuLySerserCys 180
DB 744 GTGAATGACGCTTTCAGGCTGTGCAAGGCAATCATCACTCATATTGTAAGAAAGTCTGC 803
QY 181 11eG1u1eLeu1a1aG1u 187
DB 804 ATCGAATTTCTAGCAGCTGAA 824

RESULT 2
US-11-080-026-3
; Sequence 3, Application US/11080026
; Publication No. US20050260192A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Lu, Chafen
; APPLICANT: Shimaoka, Motomu
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; FILE REFERENCE: CBRF-P02-021
; CURRENT APPLICATION NUMBER: US/11/080,026
; PRIOR FILING DATE: 2005-03-15
; PRIOR APPLICATION NUMBER: 09/945,265
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,700
; PRIOR FILING DATE: 2000-09-01
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; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-080-026-3

Alignment Scores:
Pred. No.: 3,496-06 Length: 4740
Score: 132.50 Matches: 52
Percent Similarity: 46.97% Conservative: 41
Best Local Similarity: 26.26% Mismatches: 66
Query Match: 13.66% Indels: 39
DB: 7 Gaps: 11

US-09-970-076-2_COPY_41_227 (1-187) x US-11-080-026-3 (1-4740)

QY 4 AspLeuTyrrPhe11eLeuAspLySerG1SerVal1euh1sh1trPaenG1u1e 22
DB 520 GACATTGCTCTTGTATGATGATGCTGTGATGATCATCCATGATGATGCTGCGCGATG 579
QY 23 TyrrTyrrPheVal1GluGlnLeu1ah1sYrPhe11eSerProGlnLeu1gMcSerPhe 42
DB 580 MAGAGTTTGCTCACT-----GTGATGAGCAATTAATAAGTTCCAA 624
QY 43 11eValPheSerThrArgG1YThrThrLeuMetLySerThrg1uApar----- 58
DB 625 ACCCTGTTCTT-----TTGATGCAAGTACTGGAAGAAATCCGGAATTC 669
QY 59 -----ArgGlnGln1eArgGlnG1yLeuGlnGlnLeuGln 70
DB 670 TTACCTTCAAGAGTTCAGAAACCAACCTTAACCAAGATCATGCTGTAAGCCAAATTAAG 729
QY 71 LysVal1euproG1yG1yAspThryrMetH1eG1uG1yPheG1uArg1aSerGlnGln 90
DB 730 CAGCTGCTT-----GGGGGACACACACAGCCAGCGGCGATCCGCAAGTGTGACAGAG 783
QY 91 11eTyrrTyrrGlnAsnArgGlnG1yTyrrArgThra1a-----SerVal11e1aLeuThr 109
DB 784 CTGTTAATCATCAACCAAGGAGCCGAAAGAAATGCTTTAAATCTTAATGTTGATCATCAG 843
QY 110 AspG1yGlnLeuH1eG1uAspLeuPhePheTyrrSerGln-----ArgG1u1aAsnArg 127
DB 844 GATGAGAAAGAGTTGGCGATCCCTGGATGATGAGAGATGATCCCTGAGCAGACAGA 903
QY 128 SerArgAspLeuG1yAla11eVal1TyrrCyVal1G1yVal1yAspPheAsnG1uThrg1n 147
DB 904 GAG-----GAGTCAATGCTCACTGATGGGTGGAGATGCTTCCGCACTGAG 954
QY 148 Leu1aArg-----11eAlaAspSer-----LysAspRph1sValPhePro 160
DB 955 AAATCCCGCAAGAGCTTAATACATGATGATCCCAAGCCGCTGTATCATCGTTTCCAG 1014
QY 161 ValAsnAspG1yPheGln1aLeuGlnG1y11e11e1sSer11eLeuLySers 178
DB 1015 GTGAATTAAC---TTTGAGGCTGTGAAGACCATTCAGAACAGCTTGGAGAGAG 1065

RESULT 3
US-11-186-284-25
; Sequence 25, Application US/11186284
; Publication No. US2005026493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamackar, Shubhang1
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
```


TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MEMO1-0292RMM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: ParseSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 11447
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(9192)
US-11-186-284-25

Alignment Scores:
Pred. No.: 2,02e-05 Length: 11447
Score: 131.00 Matches: 59
Percent Similarity: 48.99% Conservative: 38
Best Local Similarity: 29.80% Mismatches: 75
Query Match: 13.51% Indels: 26
Gaps: 13

US-09-970-076-2_COPY_41_227 (1-187) x US-11-186-284-25 (1-11447)

QY 4 AspleutyRheileuaplySerGlySerVal--leuHsiStrPaenglu 22
DB 1318 GATATTCGTCTTTGGTGTGATGCTCTATGAGATTCGCAACTTTGTTAAAGTT 1377
QY 23 TyTyRheValGluGluLeuAlaHisLysPhe---IleSerPro---GlnLeuArgMet 40
DB 1378 AGAGCCTTTTGGAAAGTCTGTGTAAGAAATTCACCAATTAAGGCTCCAGATT 1437
QY 41 SerPheIleValPheSerThr-----ArgGlyThrLeuMetLysLeuThrGlu 57
DB 1438 AGCTTGTGCAATACACCCGAGATCTCATAGTCACTTGGAAATAATTCACCAAA 1497
QY 58 AsparGluGluGlnIleArgGlnGlyLeuGluGluLeuValLeuPro-----Gly 75
DB 1498 GTTGAAGATATTAATT-----GAGACATTAACACCTTCCCTTACAGAGA 1542
QY 76 GlyAspThrTyRheHisGluGlyPheGluArgAlaSerGluGlnIleTyTyRgluAsn 95
DB 1543 GGAATCTCAAAATACCTGGCAAGCAATGATTATGTCAGAGAAATTTGTGCTTAC 1602
QY 96 ArgGlnGlyTyRArgThr-----AlaSerValIleIleAlaLeuThrAspGlyGluLeu 113
DB 1603 AAG---GGATCAGACAGCAATGTCGCAAGAGTCTATGTTCTTATCAGCGATGGAAA--- 1556
QY 114 HisGluAspLeuPhePheTyRSerGluArgGluAlaAsnArgSerArgAspLeuGlyAla 133
DB 1657 TCATCAGATGCTTTC-----AGAGATCTGCGATTAACAGAGAAATTCAGATGTT 1707
QY 134 IleValTyRcyValAlaGlyValLysAspPheAsnGluThrGlnLeuAlaGlyIleAlaAsp 153
DB 1708 GAAATCTTTCAGTGTGTGTAAGAGATGCGTTCGTCAGAAATTCGAAAGCTATTGCTCT 1767
QY 154 -----SerLysAspHisValAlaPheProValAsnAspGlyPheGlnAlaLeuGlnGlyIle 171
DB 1768 CTCCTCCAGACAGACCACTGTCTTTCACAGTGAAGAT---TTTATGCTTTTTCACAGAGATA 1824
QY 172 IleHisSerIleLeuLysLysSerCysIleGluIle-----IleuAlaAla 186
DB 1825 TCTTTGAACCTCACACAGTCTATCTGCTTGAATGAGCAAGAAATTCGAGCT 1878

RESULT 4

US-10-750-185-39040/c
Sequence 39040, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFIELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 39040
LENGTH: 2834
TYPE: DNA
ORGANISM: Bovine
US-10-750-185-39040

Alignment Scores:
Pred. No.: 4.03e-05 Length: 2834
Score: 122.00 Matches: 54
Percent Similarity: 50.00% Conservative: 39
Best Local Similarity: 29.03% Mismatches: 71
Query Match: 12.58% Indels: 24
Gaps: 10

US-09-970-076-2_COPY_41_227 (1-187) x US-10-750-185-39040 (1-2834)

QY 4 AspleutyRheileuaplySerGlySerValleuHsiStrPaenglu----- 21
DB 2115 GACATTTACTTCTTTATGACGCGGTCTGCGAGTACC-----CACCAAGCAGCTTCTC 2062
QY 22 ---IleTyTyRheValGluGluLeuAlaHisLysPhe---IleSerProGlnLeuArg 39
DB 2061 GCGATGAAGGTGTCATGAAATGAGTGATTAAGATGTTCCAGTGGACCGAGC---AGA 2005
QY 40 MetSerPheIleVal-PheSerThrArgGlyThrLeuMetLysLeuThrGluAsp 59
DB 2004 GTCCAGTTTGAGAGTCTGCTCAGTCTCGAGTAAGATCCAGATTACCTCAGCCAG 1945
QY 59 GlnGluGlnIleArgGlnGlyLeuGlu-----GlnLeuGlnLysValLeuProGlu 75
DB 1944 CACTCAGTGTGGCAGGCGCTTGAGGCTTGACAGCATCAGAG---AAGGG 1891
QY 75 YGlyAspThrTyRheHisGluGlyPheGluArgAlaSerGluGlnIleTyTyRgluAs 95
DB 1890 AGGGGAGCAGCAATAGGTGAGGCGCTG---GGCAGATGATCCAGGTCTTTCAGAGCTC 1834
QY 95 nArgGlnGlyTyRArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGlu 115
DB 1833 TGCTCCAGAGCA--CGTCCCTT--GCTATCTCATTTGTTGTACACGAGCGCAATCTATGGA 1776
QY 115 uAspLeuPhePheTyRSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleVal 135
DB 1775 CCGCGGTG-----GCTGATGCTGACAGGCGCTGAGGCGCATGAGTCAACCAT 1728
QY 135 TyTyRcyValAlaGlyValLysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLys 155
DB 1727 TTATGAGTGTGAGTCAAGATGCTATATATGCTGAGCTTCAAGAGATTGCTGAA----- 1673
QY 155 sAspHisValAlaPheProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIle 175
DB 1672 -GACAGAAATGTTTGTGTCATGAT---TTTGAGTCTCTTGAAAGCAATCCAAACAGAAAGT 1617
QY 175 eLeuLysLysSerCys 180

```
Db      1616 GGTACAGACATCTGT 1601
      :
      :
      :
RESULT 5
US-10-821-234-182/C
/ Sequence 182, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andarmant, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for diagnosis and treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ PRIOR FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pt_seq_genes Version 1.0
/ SEQ ID NO 182
/ LENGTH: 2501
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-821-234-182

Alignment Scores:
Pred. No.:      0.00824      Length:      2501
Score:          11.50        Matches:      49
Percent Similarity: 43.26%   Conservative: 44
Best Local Similarity: 22.79% Mismatches: 77
Query Match:    11.49%      Indels:      45
DB:             6           Gaps:       10

US-09-970-076-2_COPY_41_227 (1-187) x US-10-821-234-182 (1-2501)

QY      1 GlyGlyPheAapLeuTyRPhelIleuAapLySerGlySerVal----- 15
      :
      :
      :
Db      1559 GGTTCATGAACATCTACCTCGGTGCTAGATGATGACAGACGACTTGGGGCCAGCAATTC 1500
      :
      :
      :
QY      16 LeuH1h1s1TpaNgLu1eTyTyRPhEva1GlU1nLeu1Ahi1slyPhe1Ise1 35
      :
      :
      :
Db      1499 ACAGAGCCAAAAAGTCTTACATCAATTAAATGAGAGGTGCAGATTAAGTGTGAAG 1440
      :
      :
      :
QY      36 ProG1nLeuAryMetSerPhe1IleValPheSerThArGlyThrThrLeuMetLySeu 55
      :
      :
      :
Db      1439 CCA-----AGATATGCTGTAGTACATATGCCACATACCCCAAAATTTGGGTCAAGTG 1386
      :
      :
      :
QY      56 ThrGlu-----AapArGglUg1n1leArGg1nGlyLeuGluGluLeu----- 69
      :
      :
      :
Db      1385 TCTGAAAGCAGACAGACGATATGACAGACTGGGTACGAGAGCTCAATGAATCAATTAT 1326
      :
      :
      :
QY      70 -----GlnLyValLeuPfoGlyGlyAapThTyRweCh1seGluGlyPheGluAArgAla 87
      :
      :
      :
Db      1325 GAAGACCACCAAGTTGAAGTCAGGAGACTAACACCC-----AAGAAAGGCC 1284
      :
      :
      :
QY      88 SerGluGln1eTyTyRg1uAanArg-----GlnGlyTyR----- 99
      :
      :
      :
Db      1283 CTCGAGCGAGTGTACAGCATGATGAGCTGGCCAGATGACCTCCTCTGAGGCTGGAC 1224
      :
      :
      :
QY      100 ArgThrAlaSerVal1le1lealAleuThrAapGly----- 111
      :
      :
      :
Db      1223 CGGACCCGCGCATCTCATCTCATATGATGATGACAAACATGGCGGGGAGCCCA 1164
      :
      :
      :
QY      112 -----GluLeuH1sGluAapLeuPhePheTyRserGluAArgGlu1AaSn 126
      :
      :
      :
Db      1163 ATTACTGTCAATTGATGATCCGGGAGCTGTCTATACATTGGCAAGATCCCAAAACCCA 1104
      :
      :
      :
QY      127 ArgSerArgAapLeuGlyAla1leValTyRcyEValGly-----ValLyAapPheAaSn 144
      :
      :
      :
Db      1103 AGGAGGATTAATCTCGATGTCTATGTGTGGGGTCTTGGGCTTGGTGAACCAAGTGAAC 1044
      :
      :
      :
QY      145 GluThrGlnLeuAlaArg1leAlaAapSerLyAapH1eValPheProValAaSnAapGly 164
```

```
Db      1043 ATCAATGCTTGTGCTCCAGAAAGACATGACGAACATGTGTTCAAAAGTCAAGAT--- 987
      :
      :
      :
QY      165 PheGlnAlaLeuGlnGly1le1le1sSer1leLeuLy1sLySeR 179
      :
      :
      :
Db      986 ATGGAAGAACCTGGAAAGATGTTTCTACCAAAATGATGATGAAGC 942
      :
      :
      :
RESULT 6
US-10-131-826A-293
/ Sequence 293, Application US/10131826A
/ Publication No. US20050245730A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: DeForge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3330R1C128
/ CURRENT APPLICATION NUMBER: US/10/131,826A
/ PRIOR FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: 60/049911
/ PRIOR FILING DATE: 1997-06-18
/ PRIOR APPLICATION NUMBER: 60/056974
/ PRIOR FILING DATE: 1997-08-26
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059115
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059117
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059122
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059184
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059352
/ PRIOR FILING DATE: 1997-09-19
/ PRIOR APPLICATION NUMBER: 60/059588
/ PRIOR FILING DATE: 1997-09-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 293
/ LENGTH: 3449
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-131-826A-293

Alignment Scores:
Pred. No.:      0.00284      Length:      3449
Score:          109.00        Matches:      46
Percent Similarity: 46.35%   Conservative: 43
Best Local Similarity: 23.96% Mismatches: 77
Query Match:    11.24%      Indels:      26
DB:             6           Gaps:       10

US-09-970-076-2_COPY_41_227 (1-187) x US-10-131-826A-293 (1-3449)

QY      4 AapLeuTyRPhelIleuAapLySerGlySerVal--LeuH1h1s1TpaNgLu1le 22
```

```

Db      372  GACCTGGTTTCATCATGACAGCTTCGACAGTCTCAACACCATGACTATGCAAGAGTC 431
Qy      23  TyrTyrPhe---ValGluGlnLeuAlaHisLeuPheHisSerProGlnLeu---ArgMet 40
Db      432  AAGAGATTCTATCTGTCACATCTTGCAATCTTGAGCATCTGTCCTGTATGTCACCCGAGTG 491
Qy      41  SerPheIleValPheSerThrArgGlyThrThrLeu-----MetLeuLeu 55
Db      492  GGGCTGCTCCAAAT-----GGCAGCATCTCAAGATGATTCCTCCTCMAAGC 542
Qy      56  ThrGluAspArgGluGlnIleArgGlnGlyLeuGlnGluLeuGlnValLeuProGly 75
Db      543  TTCAGAGAGAAAGTCCGAGTGAAGCTGCTGTCAAGAGATGGGGCATCTGTCCAGGGC 602
Qy      76  GlyAspThrTyrMetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsn 95
Db      603  ACCATGACTGGGTGGGTCATCCAGTAT-----GCCCTGAACATCGCATTCACAGA 653
Qy      96  ArgGlnGlyTyrArg-----ThrAlaSerValIleIleAlaLeuThrAsp 110
Db      654  GCAGAGGGGGCCGGCCCTGAGGAGAGATGCCACGGGTCAATATGATCGTACAGAT 713
Qy      111  GlyGluLeuHisGluAspLeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAsp 130
Db      714  GGGAGACCTCAGACACTCGTG-----GCCAGGTGGCTGTCTAAGGACGGGAC 761
Qy      131  LeuGlyAlaIleValTyrCysValGlyVal-----LysAspPheAsnGlnThrGlnLeu 148
Db      762  ACCGGGACTCTTAATCTTGGCATTTGGTGGGCGCAGAGTACATTCACACCTTGAGATCC 821
Qy      149  AlaArgIleAlaAspSerLysAspHisLeuAlaPheProValAsnAspGlyPheGlnAlaLeu 168
Db      822  ATTGGAGATGAGCCCATGAGACCATGTCTCTTGAGCCCAAT--TTCAGCCAGATT 878
Qy      169  GlnGlyIleIleHisSerIleLeuLysSerCys 180
Db      879  GAGACGCTGACCTCCGCTTCCAGAGAGATGTGTC 914

RESULT 7
US-10-601-368-20
; Sequence 20, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 3564
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3564)
US-10-601-368-20

Alignment Scores:
Pred. No.: 0.00404      Length: 3564
Score: 108.00      Matches: 48
Percent Similarity: 38.38%      Conservative: 28
Best Local Similarity: 24.24%      Mismatches: 84
Query Match: 11.13%      Indels: 38
DB: 6      Gaps: 9

```

```

US-09-970-076-2_COPY_41_227 (1-187) x US-10-601-368-20 (1-3564)
Qy      4  AspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleThrPheAsnGlnIleTyr 23
Db      490  GACATGCTCATTTGCTTGAATGGCTCCACAGCATC--TACCCTGGAGTGAAGTCA 546
Qy      24  TyrPheValGluGlnLeuAlaHisLeuPhe---IleSerPro---GlnLeuArgMetSer 41
Db      547  CACTTCTCATCAATATCCCAAAAAGTTTACATTTGGCCCGGCGGACATCCAGTCCGA 606
Qy      42  PheIleValPheSerThrArgGlyThrThrLeuMetLeuValLeuThrGluArgGluGln 61
Db      607  ATAGTCAGATGAGAGAGATGCCGTCCATGAGTTCCACTT--AATGCTCAGAGTCT 663
Qy      62  IleArgGlnGlyLeuGlnGluLeuGlnValLeuProGlyLysAspThrTyrMetHis 81
Db      664  GTAAAAGATGTGGTGAAGCCGCCACCCATTTGACGACAGAGAGAGAGAGAGAGAG 723
Qy      82  GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGly 98
Db      724  ACCGCAATTTGGCATTTGAATTTGACCGCTCGAGGCTTCCAGAGGTTGGAAGAAAAG 763
Qy      99  TyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp----- 116
Db      784  GCCAAG-----AAGTATGATTTGATCATCAGGAGGGGAATCCACAGACCCAGAC 837
Qy      116  ----- 116
Db      838  CTGAGAGAGGTGATCCGGCAGACCGAGAGAGACAGTGCACAGATACCTGTGGCCGTT 897
Qy      117  LeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyr 136
Db      898  TTGGCTACTCAACACCGCAGGGGATCAATCCAGACACTTTTAAATGAATCAAAATAC 957
Qy      137  CysValGlyValLysAsp-----PheAsnGlnThrGlnLeuAlaArgIleAla 152
Db      958  ATGCCAGACACCTCGACGACAGACACTTCTTCAAGTCCACAGATGAGCGCGCCCTG 1014
Qy      153  AspSerLysAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGly 170
Db      1015  -----AAGGACATTGTGATGCTTGGGAGACAGATTTCACTTGAGAGGC 1062

RESULT 8
US-10-601-368-19
; Sequence 19, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 4858
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (28)...(3591)
US-10-601-368-19

Alignment Scores:
Pred. No.: 0.00638      Length: 4858
Score: 108.00      Matches: 48
Percent Similarity: 38.38%      Conservative: 28
Best Local Similarity: 24.24%      Mismatches: 84

```

[illegible]

US-09-970-076_2_COPY_41_227 (1-187) x US-10-995-561-464 (1-3175)	
QY 5 LeuYrPhelIleuAspIysSerGlySerVal-----	15
Db 243 GTGAACTTCGAGCTGACACCTCGGAGAGCGCTACCATGACAGTCCCGACGAGCATCTCG	302
QY 16 LeuHshIstrPamgLu---IleTyrTrpPheValGluGlnIleuAlaHisIysPheIle	34
Db 303 CTTTCCACATGAAGCAAGTTCGTGCGGACGATTCATCAGCCAGCTGACAGAACAGATTCTAC	362
QY 35 SerProGlnLeuAArgMetSerPhe-----IleValPheSerThrArgIlyThr	50
Db 363 CTGACACCAAGGTGGCGGTACGCTGGCGGCTAAGCGCGGCTGCACTTCTTGCACAGGTGAG	422
QY 51 ThrLeuMetIysLeuThrGluAspArgGluGlnIleArgGlnIlyLeuGluGluGln	70
Db 423 GTGTTACAGCCACCGGAGCGAGCGAGCGGCGCTCTTCATCAAGAACTGCAGCGGATCACG	482
QY 71 LysValIleuProGlyIlyAspThrTrpMetHisGluGlyPheGluAlaArgIAserGluGln	90
Db 483 TCCTTCCGCGCGGCG-----ACCTTCACCGCATGCGGCGTGGCCAACTAGACGAGCGAG	536
QY 91 IleTyrTrpGluAsnArgGlnGlyTrpArgThrAlaSerValIleIleAlaLeuThrAsp	110
Db 537 ATCCGGCAGACCGGACGAGCAAGGCG-----ACCGTCCACTTGGCGGTGTATCAACGAC	590
QY 111 GlyIleuLeuHisGluAspLeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAsp	130
Db 591 GCGCACGTCACCGCGGACGCGCCCTCGGAGGAGCATCAAGCTGCAGCGGAGCGGCGCGAG	650
QY 131 LeuGlyAlaIleValIlyTrpCysVal-----GlyValLys	141
Db 651 GAGGCGATCTCCGCGCTCTTCGCGGTGCGCCCGCCCAACAGAACTGAAGAGCAGGCGCTGCGG	710
QY 142 AspPheAsnGluThr-----GlnIleuAlaArgIleAlaAspSerIysAspHisValPhe	159
Db 711 GACATCGCCAGACACCGCGCAGCATCTTACCGC-----AACGACTACGCGACC	758
QY 160 ProValAsnAspArgIlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu-----	176
Db 759 ATGCTGCGCGATCTCCACCGAGATCRAACAGACACCATCAACGCGATCATCAAGTCATG	818
QY 177 -----LysIysSerCysIleGluIle	183
Db 819 AAACACGAAGCCTACGAGAGTGTCTAACAGGTGAGCTGCTGGAATC	866
RESULT 10	
US-10-995-561-465	
/ Sequence 465, Application US/10995561	
/ Publication No. US20050272054A1	
/ GENERAL INFORMATION:	
APPLICANT: CARGILL, Michele et al.	
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH	
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF	
TITLE OF INVENTION: DETECTION AND USES THEREOF	
FILE REFERENCE: CL001559	
CURRENT APPLICATION NUMBER: US/10/995,561	
CURRENT FILING DATE: 2004-11-24	
NUMBER OF SEQ ID NOS: 85702	
/ SOFTWARE: FastSeq for Windows Version 4.0	
/ SEQ ID NO 465	
/ LENGTH: 3464	
/ TYPE: DNA	
/ ORGANISM: Homo sapiens	
US-10-995-561-465	
Alignment Scores:	
Pred. No.:	0.00451
Score:	107.50
Percent Similarity:	40.28%
Best Local Similarity:	23.15%
Query Match:	11.08%
DB:	6
	9
Length:	3464
Matches:	50
Conservative:	37
Mismatches:	84
Indels:	45
Gaps:	9

US-09-970-076-2_COPY_41_227 (1-187) x US-10-995-561-465 (1-3464)

QY 5 LeuTYRPhel1eLeuArylserylserval----- 15
DB 243 GTGTAATCTGCTGACACCTCGAGAGGTCCATGACATGCCCGGACATCTCG 302
QY 16 LeuN1h1e1tRpaNg1u---11eTYrTYrPhelA1g1u1nLeuA1h1e1s1yPhe11e 34
DB 303 CTCTTCACATGAAGCAAGTTCGCGCCAGTTCAAGCAGCTGCAGAAAGATTCTAC 362
QY 35 SerProG1nLeuArymEserPhe-----11eValPheSerThrArg1yThr 50
DB 363 CTGACACAGGTGGCGCTGACCTGCGCTAYAGCGCGCTGCACTTCTGTGACAGGTGAG 422
QY 51 Th1eUmet1y1eUthrg1uAryA1rg1u1n11eA1rg1n1y1eUg1n1y1eUg1n 70
DB 423 GTGTCAGCCCGGACCGGACCGGCGCTCTTCATCAAGAACTGCAGGGCATAGC 482
QY 71 LyVal1LeuProG1yG1AryThrTYrMetH1eG1uG1yPheG1uA1rg1A1sery1uG1n 90
DB 483 TCCTTCGCGCGCGG-----ACCTTCACCGACTGCGCGCTGCACATGACGAGAG 536
QY 91 11eTYrTYrG1uAryA1rg1n1yTYrArgThrA1seryA11e11eA1eUth1AsP 110
DB 537 ATCCGCGAGGACCGGACGAGGCG-----ACGTCACATTCGCGCGGTGCATCACCGAC 590
QY 111 G1yG1u1eUth1eG1uAryPhePheTYrSeryG1uA1rg1u1A1a1nA1rgSeryA1rgA1P 130
DB 591 GGCACACTCACCGGACCGGCGCGGAGCATCAAGCTGCAGCGCGGCGCGGAG 650
QY 131 LeuG1yA1A1eVal1yTYrGyVal-----G1yVal1yA 141
DB 651 GAGGCGATCCGCGCTTCGCGCGTGGCCCGACACGAGAACTGAAGAGCAGGCGCTGCGG 710
QY 142 AspPheA1nG1uThr-----G1nLeuA1A1rg11eA1A1sery1yA1rH1sValPhe 159
DB 711 GACATGCCGACGACCGCGGACGAGCTTACCG-----AACGACTACGCCACC 758
QY 160 ProValA1nA1rP1yPheG1nA1A1eUg1n1y11e1h1e1sery1eU----- 176
DB 759 ATCTGCGYGACTCCACCGAGATCRAACAGACACCATCAACCGCATCATCAAGTTCATG 818
QY 177 -----Ly1ySerCyA11eG1u11e 183
DB 819 AAACAGAGAGCTTACGAGAGTGTCTACAGGTGAGCTGCTGGAATC 866

RESULT 11

US-10-995-561-466
Sequence 466, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CU001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 466
LENGTH: 3468
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-466

Alignment Scores:

Pred. No.: 0.00452 Length: 3468
Score: 107.50 Matches: 50
Percent Similarity: 40.28% Conservative: 37
Best Local Similarity: 23.15% Mismatches: 84
Query Match: 11.08% Indels: 45

DB: 6 Gaps: 9

US-09-970-076-2_COPY_41_227 (1-187) x US-10-995-561-466 (1-3468)

QY 5 LeuTYRPhel1eLeuArylserylserval----- 15
DB 243 GTGTAATCTGCTGACACCTCGAGAGGTCCATGACATGCCCGGACATCTCG 302
QY 16 LeuN1h1e1tRpaNg1u---11eTYrTYrPhelA1g1u1nLeuA1h1e1s1yPhe11e 34
DB 303 CTCTTCACATGAAGCAAGTTCGCGCCAGTTCAAGCAGCTGCAGAAAGATTCTAC 362
QY 35 SerProG1nLeuArymEserPhe-----11eValPheSerThrArg1yThr 50
DB 363 CTGACACAGGTGGCGCTGACCTGCGCTAYAGCGCGCTGCACTTCTGTGACAGGTGAG 422
QY 51 Th1eUmet1y1eUthrg1uAryA1rg1u1n11eA1rg1n1y1eUg1n1y1eUg1n 70
DB 423 GTGTCAGCCCGGACCGGACCGGCGCTCTTCATCAAGAACTGCAGGGCATAGC 482
QY 71 LyVal1LeuProG1yG1AryThrTYrMetH1eG1uG1yPheG1uA1rg1A1sery1uG1n 90
DB 483 TCCTTCGCGCGCGG-----ACCTTCACCGACTGCGCGCTGCACATGACGAGAG 536
QY 91 11eTYrTYrG1uAryA1rg1n1yTYrArgThrA1seryA11e11eA1eUth1AsP 110
DB 537 ATCCGCGAGGACCGGACGAGGCG-----ACGTCACATTCGCGCGGTGCATCACCGAC 590
QY 111 G1yG1u1eUth1eG1uAryPhePheTYrSeryG1uA1rg1u1A1a1nA1rgSeryA1rgA1P 130
DB 591 GGCACACTCACCGGACCGGCGCGGAGCATCAAGCTGCAGCGCGGCGCGGAG 650
QY 131 LeuG1yA1A1eVal1yTYrGyVal-----G1yVal1yA 141
DB 651 GAGGCGATCCGCGCTTCGCGCGTGGCCCGACACGAGAACTGAAGAGCAGGCGCTGCGG 710
QY 142 AspPheA1nG1uThr-----G1nLeuA1A1rg11eA1A1sery1yA1rH1sValPhe 159
DB 711 GACATGCCGACGACCGCGGACGAGCTTACCG-----AACGACTACGCCACC 758
QY 160 ProValA1nA1rP1yPheG1nA1A1eUg1n1y11e1h1e1sery1eU----- 176
DB 759 ATCTGCGYGACTCCACCGAGATCRAACAGACACCATCAACCGCATCATCAAGTTCATG 818
QY 177 -----Ly1ySerCyA11eG1u11e 183
DB 819 AAACAGAGAGCTTACGAGAGTGTCTACAGGTGAGCTGCTGGAATC 866

RESULT 12

US-10-750-185-56394
Sequence 56394, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFIELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 56394
LENGTH: 1325
TYPE: DNA
ORGANISM: Bovine
US-10-750-185-56394


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Db      775 ACGGCAATTGGCATTTGCAACGCTCAGAGGCTTTCAGAAAGGTGGAAGGA 834
Qy      99 TyrArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluasp----- 116
Db      835 GCCAAG-----AAGGTGATGATTGTCTATCAGATGGGAGTCCACGACAGCCAGAC 888
Qy      116 ----- 116
Db      889 CTGGAGAAAGTGATCCAGCAAGCAAGAGACACGTAAACAATATGCGGTGGCCGTC 948
Qy      117 LeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyr 136
Db      949 CTGGGCTACTACAAACCGCAGGGGATCAATCCAGAAACTTTTCTAAATGAAATCAATAC 1008
Qy      137 CysValGlyValLysasp-----PheAsnGluThrGlnLeuAlaArgIleAla 152
Db      1009 ATCGCCAGTGACCCCTGATGACAAAGCACTTCTCAATGTCTCATGATGAGGCTGCTTG--- 1065
Qy      153 AspSerLysAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGly 170
Db      1066 -----AAGGACATTTGTTCGATGCCCTGGGGGACAGAACTTTCAGCCTGGAGGC 1113
```

Search completed: December 19, 2005, 02:30:25
Job time : 166.899 secs

STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-889-37

Query Match 15.0%; Score 141.5; DB 1; Length 1151;
Best Local Similarity 27.7%; Pred. No. 4.7e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;
QY 3 DLYFLDKSGSV-LHHMNEIYFVEQLAHKFI SPOLRMSPFIYSTGTTLMLKLT----- 56
DB 142 DIAFLDGGSSINQDFAPMKDVFVAKLMGEFASTSTLSLMQSNILKTHFTTEPKNLL 201
QY 57 DREQIRQGLEELQKVLPGSDTYMHGFEFASSEQIYENRQGYRTA-SVIALTDGELHED 115
DB 202 DPQSLVDPIVQD-----GLTYTATGIRTYMBELFHSKXSRKSAKKILLVITDGGKYND 256
QY 116 LEFYSE--REANRSRLGAIYVCVGYKD-FNE-TOLARI-----ADSKDHVPVNDGFOA 166
DB 257 PLEYSDVTPADKA---GIIRYAIQVGDAFOEPTALKEINTIGSAPPODHVFKVGN-FAA 312
QY 167 LGGIHSILKK 177
DB 313 LRSIQROLOEK 323

RESULT 3
US-08-485-618-37
Sequence 37, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-37

Query Match 15.0%; Score 141.5; DB 1; Length 1151;
Best Local Similarity 27.7%; Pred. No. 4.7e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;
QY 3 DLYFLDKSGSV-LHHMNEIYFVEQLAHKFI SPOLRMSPFIYSTGTTLMLKLT----- 56
DB 142 DIAFLDGGSSINQDFAPMKDVFVAKLMGEFASTSTLSLMQSNILKTHFTTEPKNLL 201
QY 57 DREQIRQGLEELQKVLPGSDTYMHGFEFASSEQIYENRQGYRTA-SVIALTDGELHED 115
DB 202 DPQSLVDPIVQD-----GLTYTATGIRTYMBELFHSKXSRKSAKKILLVITDGGKYND 256
QY 116 LEFYSE--REANRSRLGAIYVCVGYKD-FNE-TOLARI-----ADSKDHVPVNDGFOA 166
DB 257 PLEYSDVTPADKA---GIIRYAIQVGDAFOEPTALKEINTIGSAPPODHVFKVGN-FAA 312
QY 167 LGGIHSILKK 177
DB 313 LRSIQROLOEK 323

RESULT 4
US-08-362-652-37
Sequence 37, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Seear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-37

Query Match 15.0%; Score 141.5; DB 1; Length 1151;
Best Local Similarity 27.7%; Pred. No. 4,7e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

QY 3 DLYFIIDKSGSV-LHMHNEIYFVEQLAHKFIISPOLMSPFIVSTGTTLMKLT-----56
DB 142 DIAFLIDSGSINQRPQAKDFKALMGFASTSTLFSIMQYSNILKHTFTPEFNIL 201
QY 57 DRQIQGLELELQKVLPGDPTMHGEPERASQIYYENRGYRTA-SVITALDGELEHD 115
DB 202 DPQSLVDPIVQLD-----GLTYATGIRTYMELFHSKNGSRKSAKKILIVITDGOQYRD 256
QY 116 LFFYSE--REANRSRDGAIVYCVGYD-FNE-TOLARI-----ADSKDHVPVNDGFOA 166
DB 257 PLEYSDIVPADKA---GIIRYALGVDAFQEPFLKELNTIGSAPPQDHVFKGN-FAA 312
QY 167 LQGIHSLKK 177
DB 313 LRSTQRLQLEK 323

RESULT 5
US-08-605-672-37
Sequence 37, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-37

Query Match 15.0%; Score 141.5; DB 1; Length 1151;
Best Local Similarity 27.7%; Pred. No. 4,7e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

QY 3 DLYFIIDKSGSV-LHMHNEIYFVEQLAHKFIISPOLMSPFIVSTGTTLMKLT-----56
DB 142 DIAFLIDSGSINQRPQAKDFKALMGFASTSTLFSIMQYSNILKHTFTPEFNIL 201
QY 57 DRQIQGLELELQKVLPGDPTMHGEPERASQIYYENRGYRTA-SVITALDGELEHD 115
DB 202 DPQSLVDPIVQLD-----GLTYATGIRTYMELFHSKNGSRKSAKKILIVITDGOQYRD 256
QY 116 LFFYSE--REANRSRDGAIVYCVGYD-FNE-TOLARI-----ADSKDHVPVNDGFOA 166
DB 257 PLEYSDIVPADKA---GIIRYALGVDAFQEPFLKELNTIGSAPPQDHVFKGN-FAA 312
QY 167 LQGIHSLKK 177
DB 313 LRSTQRLQLEK 323

RESULT 6
US-08-482-293A-37
Sequence 37, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
APPLICATION NUMBER: US 08/286,889

[illegible]

Oy	57	PREQJLRQGLBEEBOKVLPGSDTYMHBEFBEASBQIYYENNQGYRTA-SVIALTLDELHED	115
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Oy	116	LFYFSE--REARSRDLAGIVYCVGVKD-FNE-TOLARI----ADSKDHVPFVNDGFOA	166
Db	257	PLEYSADVPAADKA---GIIRYALIGVDAPQEBETALKELNTIGSAPPDQHVFRVN-FAA	312
Oy	167	LOGIHSILKK	177
Db	313	LRSTQROLQEK	323

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RESULT 9
US-09-688-307A-37
Sequence 37, Application US/09688307A
Patent No. 6432404
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: No. 6432404el Human Beta-2
FILE REFERENCE: 27866/36646
CURRENT APPLICATION NUMBER: US/09/688,307A
PRIOR APPLICATION NUMBER: 2000-10-13
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 08/605,672
PRIOR FILING DATE: 1996-02-22
PRIOR APPLICATION NUMBER: 08/173,497
PRIOR FILING DATE: 1993-12-23
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR FILING DATE: 1994-08-05
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR FILING DATE: 1994-12-21
PRIOR APPLICATION NUMBER: 08/943,363
NUMBER OF FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
LENGTH: 1151
TYPE: PRT
ORGANISM: Rattus rattus
FEATURE:
NAME/KEY: misc_feature
LOCATION: 361
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 464
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 486
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 506
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 1117
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 1118
OTHER INFORMATION: Xaa = any or unknown amino acid
US-09-688-307A-37

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Query Match	15.0%;	Score 141.5;	DB 2;	Length 1151;
Best Local Similarity	27.7%;	Pred. No. 4.7e-07;		
Matches 53;	Conservative 38;	Mismatches 75;	Indels 25;	Gaps 10;

Qy 3 DLFLFLIDKSGSV-LHHMNIYFFVFLQALAKFSPOLRMSPLFVFSRGTGLMKLKE----- 56
 142 DIALFLDGGSSINQGRFQAKMDPVVALMGEFASSTLTSLMOYSNLTKEHTTFEPFNIL 201
 Qy 57 DREQIRQGLBELOKVLPGSDTYMHGFEFASQIYYENRQGRYA-SVIALTDGDELHED 115

Db 202 DPGSLVDPLVQIQ-----GLFTTALGIRTWEEELFHSNNGSRKSAKILLIVITDGGKYRD 256
 QY 116 LFFYGF--REANRSDLGAIYVCVGKD-FNE-TQLARI-----ADSKDHVFPYNDGFOA 166
 Db 257 PLEYSVIVIPAAKKA---GIIRYALGVGDAFOEPALKEMLNTIGSAPPQDHVFKGN-FAA 312
 QY 167 LOGIHSILKK 177
 Db 313 LRSIQKQLQEK 323

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RESULT 0
US-09-350-259-37
Sequence 37, Application US/09350259
Patent No. 6620915
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6620915el Human 2
FILE REFERENCE: 2766/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
LENGTH: 1151
TYPE: PRT
ORGANISM: Rattus rattus
US-09-350-259-37

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Query Match	15.0%;	Score 141.5;	DB 2;	Length 1151;
Best Local Similarity	27.7%;	Pred. No. 4.7e-07;		
Matches	53;	Conservative	38;	Mismatches 75;
			Indels	25;
			Gaps	10;

QY 3DIYFLLDSSGSV-LAHNMEIYFVEOLAHKISQLMSPIVSTROITLMKLE-----56
Db 142DIAPFLDSSGSINQNDPAQMDPVKALMGEPASISTLFSLMQYSNLKHTFTTEKKNIL201
QY 57DEBQIRQGLBELQKLVPGSDTYMHEGPERASEQIYENRQGYRTA-SVIALTDGELIHD115
Db 202DPQSLVDPIVQIQ-----GLTYTNTGTRTWMBELFHSKNSRSKAKILLVLITDQKYND256
QY 116LEFFYS--REANRSDLCALIVCYGVKD-FNE-TQLARI-----ADSKDHVPVNDGFOA166
Db 257PLEYSDVIPADKA---GIIRYALGVGDFAQEPALTELNTTIGSAPPDHFVKN-FAA312
QY 167LGGIHSILKK177
Db 313LRSIQROLQEK323

RESULT 11
 US-08-485-618-55
 ; Sequence 55, Application US/08485618
 ; Patent No. 5728533
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 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Gallatin, W. Michael
 ; APPLICANT: Van der Vlieten, Monica
 ; TITLE OF INVENTION: No. 5728533e1 Human 2 Integrin Alpha Subunit
 ; NUMBER OF SEQUENCES: 103
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSSEE: Marshall, O'Toole, Gerstein, Murray & Borun


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/
/   COMPUTER: IBM PC compatible
/   OPERATING SYSTEM: PC-DOS/MS-DOS
/   SOFTWARE: Patentin Release #1.0, Version #1.25
/   CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/08/605,672
/   FILING DATE:
/   CLASSIFICATION: 530
/   PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US 08/173,497
/   FILING DATE: 23-DEC-1993
/   PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US 08/286,889
/   FILING DATE: 5-AUG-1994
/   PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US 08/362,652
/   FILING DATE: 21-DEC-1994
/   ATTORNEY/AGENT INFORMATION:
/   NAME: Williams Jr., Joseph A.
/   REGISTRATION NUMBER: 38,659
/   REFERENCE/DOCKET NUMBER: 27866/32684
/   TELECOMMUNICATION INFORMATION:
/   TELEPHONE: 312-474-6300
/   TELEFAX: 312-474-0448
/   TELEX: 25-3856
/   INFORMATION FOR SEQ ID NO: 55:
/   SEQUENCE CHARACTERISTICS:
/   LENGTH: 1161 amino acids
/   TYPE: amino acid
/   TOPOLOGY: linear
/   MOLECULE TYPE: protein
/
US-08-605-672-55
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Query Match      15.0%; Score 141.5; DB 1; Length 1161;
Best Local Similarity 27.7%; Pred. No. 4.7e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

QY 3 DLYFIIDKSGSV-LHHNNEIYFVBOIAHKFISPOLMSPFVSTGCTLMKLT----- 56
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DB 152 DIAFLIDGSSINORDPAOKMDFKALMGEPASTSTLFSLMQYNNILKTHFTFEFNIL 211
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 57 DREQIRGLEELQVLPBGDTYHMEGPERASEQIYYENRQGYRTA-SVIALTDGELHED 115
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 212 DPSLVDPPIVOLQ-----GLTYATATGIRTYMELFHSKNGSRKSAKKILLVITDGOQYRD 266
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 LFPYSR--REANRSDIGAIVYCVGYND-FNE-TQLARI-----ADSKDHVPVNDGFOA 166
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 267 PLEYSVDIYPAADKA--GIIRYALGVDAFOEFTALKELNTIGSAPPQDHVFKVGN-FAA 322
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 167 LQGIHHSILKK 177
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DB 323 LRSTORQLQEK 333
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RESULT 14
US-08-482-293A-55
; Sequence 55, Application US/08482293A
; Patent No. 5831029
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5831029e1 Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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/
/   SOFTWARE: Patentin Release #1.0, Version #1.25
/   CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/08/482,293A
/   FILING DATE:
/   CLASSIFICATION: 530
/   PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US 08/173,497
/   FILING DATE: 23-DEC-1993
/   PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US 08/286,889
/   FILING DATE: 5-AUG-1994
/   PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US 08/362,652
/   FILING DATE: 21-DEC-1994
/   ATTORNEY/AGENT INFORMATION:
/   NAME: Williams Jr., Joseph A.
/   REGISTRATION NUMBER: 38,659
/   REFERENCE/DOCKET NUMBER: 27866/32684
/   TELECOMMUNICATION INFORMATION:
/   TELEPHONE: 312-474-6300
/   TELEFAX: 312-474-0448
/   TELEX: 25-3856
/   INFORMATION FOR SEQ ID NO: 55:
/   SEQUENCE CHARACTERISTICS:
/   LENGTH: 1161 amino acids
/   TYPE: amino acid
/   TOPOLOGY: linear
/   MOLECULE TYPE: protein
/
US-08-482-293A-55
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Query Match      15.0%; Score 141.5; DB 1; Length 1161;
Best Local Similarity 27.7%; Pred. No. 4.7e-07;
Matches 53; Conservative 38; Mismatches 75; Indels 25; Gaps 10;

QY 3 DLYFIIDKSGSV-LHHNNEIYFVBOIAHKFISPOLMSPFVSTGCTLMKLT----- 56
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 152 DIAFLIDGSSINORDPAOKMDFKALMGEPASTSTLFSLMQYNNILKTHFTFEFNIL 211
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 57 DREQIRGLEELQVLPBGDTYHMEGPERASEQIYYENRQGYRTA-SVIALTDGELHED 115
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 212 DPSLVDPPIVOLQ-----GLTYATATGIRTYMELFHSKNGSRKSAKKILLVITDGOQYRD 266
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 LFPYSR--REANRSDIGAIVYCVGYND-FNE-TQLARI-----ADSKDHVPVNDGFOA 166
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 267 PLEYSVDIYPAADKA--GIIRYALGVDAFOEFTALKELNTIGSAPPQDHVFKVGN-FAA 322
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 167 LQGIHHSILKK 177
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 323 LRSTORQLQEK 333
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RESULT 15
US-08-943-363-55
; Sequence 55, Application US/08943363
; Patent No. 5837478
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5837478e1 Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 11:18:07 ; Search time 54.5297 Seconds
(without alignments)
1386.897 Million cell updates/sec

Title: US-09-970-076-2_COPY_42_222

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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

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- 2: /cgn2_6/ptodaca/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodaca/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodaca/1/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	943	100.0	328	4 US-10-201-292-26	Sequence 26, Appl
3	943	100.0	333	3 US-09-796-753-12	Sequence 12, Appl
4	943	100.0	333	4 US-10-038-307-2	Sequence 2, Appl
5	943	100.0	333	4 US-10-201-292-2	Sequence 2, Appl
6	943	100.0	333	6 US-11-047-278-8	Sequence 8, Appl
7	943	100.0	342	4 US-10-038-307-22	Sequence 22, Appl
8	943	100.0	342	4 US-10-201-292-22	Sequence 22, Appl
9	943	100.0	345	4 US-10-038-307-24	Sequence 24, Appl
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12	943	100.0	403	3 US-09-833-245-621	Sequence 621, Appl
13	943	100.0	460	4 US-10-201-292-28	Sequence 28, Appl
14	943	100.0	479	4 US-10-201-292-32	Sequence 32, Appl
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19	943	100.0	564	3 US-09-918-715-187	Sequence 187, Appl
20	943	100.0	564	3 US-09-918-715-232	Sequence 232, Appl
21	943	100.0	564	4 US-10-038-307-20	Sequence 20, Appl
22	943	100.0	564	4 US-10-201-292-20	Sequence 20, Appl
23	943	100.0	564	4 US-10-301-822-199	Sequence 199, Appl
24	943	100.0	564	4 US-10-408-765A-1823	Sequence 1823, Appl
25	943	100.0	564	4 US-10-474-794-187	Sequence 187, Appl
26	943	100.0	564	4 US-10-474-794-232	Sequence 232, Appl
27	943	100.0	564	5 US-10-979-159-187	Sequence 187, Appl

28	943	100.0	564	5 US-10-979-159-232	Sequence 232, Appl
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38	922	97.8	534	4 US-10-038-307-12	Sequence 12, Appl
39	922	97.8	534	4 US-10-201-292-12	Sequence 12, Appl
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41	922	97.8	543	4 US-10-038-307-14	Sequence 14, Appl
42	922	97.8	543	4 US-10-038-307-16	Sequence 16, Appl
43	922	97.8	543	4 US-10-201-292-10	Sequence 10, Appl
44	922	97.8	543	4 US-10-201-292-14	Sequence 14, Appl
45	922	97.8	543	4 US-10-201-292-16	Sequence 16, Appl

ALIGNMENTS

```
RESULT 1
US-10-038-307-26
; Sequence 26, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALRY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038.307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-26

Query Match      100.0%; Score 943; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.7e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GFDLYFLDKSGSVLHHMNEIYFVEQLAKFISPOLRMSFIVPSTRGTTMLKLTEDREQ 60
Db      42  GFDLYFLDKSGSVLHHMNEIYFVEQLAKFISPOLRMSFIVPSTRGTTMLKLTEDREQ 101

QY      61  IROGLEBLQVLPBGDTYMHGEPERASEQIYENRQGYRTASVIALTDELHEDLFFYS 120
Db      102  IROGLEBLQVLPBGDTYMHGEPERASEQIYENRQGYRTASVIALTDELHEDLFFYS 161

QY      121  EREANNSRDIGAIYVCYGVQFNETQARLADSKDHVPVNDGFQALOGIHSILKKSCT 180
Db      162  EREANNSRDIGAIYVCYGVQFNETQARLADSKDHVPVNDGFQALOGIHSILKKSCT 221

QY      181  E 181
Db      222  E 222

RESULT 2
US-10-201-292-26
; Sequence 26, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
```

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; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-201-292-26

Query Match      100.0%; Score 943; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.7e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPDLYFILDKSGSVLHHMNEIYFVVEQLAHKFTSPQLRMSFVFSRGTTLMLKLTEDRQ 60
        |||
DB      42 GPDLYFILDKSGSVLHHMNEIYFVVEQLAHKFTSPQLRMSFVFSRGTTLMLKLTEDRQ 101
        |||

QY      61 IRQGLELOKVLPGSDTYHMEGFERASEQIYYENRQGYRTASVYIALTDGELHEDLFFYS 120
        |||
DB      102 IRQGLELOKVLPGSDTYHMEGFERASEQIYYENRQGYRTASVYIALTDGELHEDLFFYS 161
        |||

QY      121 EREANSRDLGAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSCT 180
        |||
DB      162 EREANSRDLGAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSCT 221
        |||

QY      181 E 181
        |
DB      222 E 222

RESULT 3
US-09-796-753-12
; Sequence 12, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
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; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 12
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-796-753-12

Query Match      100.0%; Score 943; DB 3; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPDLYFILDKSGSVLHHMNEIYFVVEQLAHKFTSPQLRMSFVFSRGTTLMLKLTEDRQ 60
        |||
DB      42 GPDLYFILDKSGSVLHHMNEIYFVVEQLAHKFTSPQLRMSFVFSRGTTLMLKLTEDRQ 101
        |||

QY      61 IRQGLELOKVLPGSDTYHMEGFERASEQIYYENRQGYRTASVYIALTDGELHEDLFFYS 120
        |||
DB      102 IRQGLELOKVLPGSDTYHMEGFERASEQIYYENRQGYRTASVYIALTDGELHEDLFFYS 161
        |||

QY      121 EREANSRDLGAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSCT 180
        |||
DB      162 EREANSRDLGAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIHSILKKSCT 221
        |||

QY      181 E 181
        |
DB      222 E 222

RESULT 4
US-10-038-307-2
; Sequence 2, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-038-307-2

Query Match      100.0%; Score 943; DB 4; Length 333;
```

Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTGTTLMKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTGTTLMKLTEDREQ 101
QY 61 IROGLELOKVLPGDVTYMHGEPERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 102 IROGLELOKVLPGDVTYMHGEPERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 161
QY 121 EREANRSRDIGAIYCVGVKDFNETOLARIADSKDHVPVNDGFOALOGIHSILKKSCT 180
DB 162 EREANRSRDIGAIYCVGVKDFNETOLARIADSKDHVPVNDGFOALOGIHSILKKSCT 221

QY 181 E 181
DB 222 E 222

RESULT 5

US-10-201-292-2
Sequence 2, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT FILING DATE: 2003-02-14
CURRENT APPLICATION NUMBER: US/10/201.292
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 333
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-2

Query Match 100.0%; Score 943; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTGTTLMKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTGTTLMKLTEDREQ 101
QY 61 IROGLELOKVLPGDVTYMHGEPERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 102 IROGLELOKVLPGDVTYMHGEPERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 161
QY 121 EREANRSRDIGAIYCVGVKDFNETOLARIADSKDHVPVNDGFOALOGIHSILKKSCT 180
DB 162 EREANRSRDIGAIYCVGVKDFNETOLARIADSKDHVPVNDGFOALOGIHSILKKSCT 221

QY 181 E 181
DB 222 E 222

RESULT 6

US-11-047-278-8
Sequence 8, Application US/11047278
Publication No. US20050196407A1
GENERAL INFORMATION:
APPLICANT: Young, John A. T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TITLE OF INVENTION: Anthrax Toxin Receptor
FILE REFERENCE: 960296.97745

CURRENT APPLICATION NUMBER: US/11/047.278
CURRENT FILING DATE: 2005-01-31
PRIOR APPLICATION NUMBER: US/09/970.076
PRIOR FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/251,481
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 333
TYPE: PRT
ORGANISM: Homo sapiens
US-11-047-278-8

Query Match 100.0%; Score 943; DB 6; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTGTTLMKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTGTTLMKLTEDREQ 101
QY 61 IROGLELOKVLPGDVTYMHGEPERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 102 IROGLELOKVLPGDVTYMHGEPERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 161
QY 121 EREANRSRDIGAIYCVGVKDFNETOLARIADSKDHVPVNDGFOALOGIHSILKKSCT 180
DB 162 EREANRSRDIGAIYCVGVKDFNETOLARIADSKDHVPVNDGFOALOGIHSILKKSCT 221

QY 181 E 181
DB 222 E 222

RESULT 7

US-10-038-307-22
Sequence 22, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT FILING DATE: 2002-06-28
CURRENT APPLICATION NUMBER: US/10/038.307
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 342
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-307-22

Query Match 100.0%; Score 943; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTGTTLMKLTEDREQ 60
DB 51 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTGTTLMKLTEDREQ 110
QY 61 IROGLELOKVLPGDVTYMHGEPERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 111 IROGLELOKVLPGDVTYMHGEPERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 170
QY 121 EREANRSRDIGAIYCVGVKDFNETOLARIADSKDHVPVNDGFOALOGIHSILKKSCT 180
DB 171 EREANRSRDIGAIYCVGVKDFNETOLARIADSKDHVPVNDGFOALOGIHSILKKSCT 230
QY 181 E 181

Db 231 E 231

RESULT 8

US-10-201-292-22

Sequence 22, Application US/10201292

Publication No. US20030144193A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/201,292

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 22

LENGTH: 342

TYPE: PRT

ORGANISM: Homo sapiens

US-10-201-292-22

Query Match

Best Local Similarity 100.0%; Score 943; DB 4; Length 342;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 60

Db 51 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 110

QY 61 IRQGLELOKVLPGGDTYHMEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYS 120

Db 111 IRQGLELOKVLPGGDTYHMEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYS 170

QY 121 EREANRSRDGAIVYCVGVDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKKSCT 180

Db 171 EREANRSRDGAIVYCVGVDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKKSCT 230

QY 181 E 181

Db 231 E 231

RESULT 9

US-10-038-307-24

Sequence 24, Application US/10038307

Publication No. US20030134766A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT FILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 24

LENGTH: 345

TYPE: PRT

ORGANISM: Homo sapiens

US-10-038-307-24

Query Match

Best Local Similarity 100.0%; Score 943; DB 4; Length 345;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 60

Db 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 101

QY 61 IRQGLELOKVLPGGDTYHMEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYS 120

Db 102 IRQGLELOKVLPGGDTYHMEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYS 161

QY 121 EREANRSRDGAIVYCVGVDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKKSCT 180

Db 162 EREANRSRDGAIVYCVGVDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKKSCT 221

QY 181 E 181

Db 222 E 222

RESULT 10

US-10-201-292-24

Sequence 24, Application US/10201292

Publication No. US20030144193A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/201,292

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 24

LENGTH: 345

TYPE: PRT

ORGANISM: Homo sapiens

US-10-201-292-24

Query Match

Best Local Similarity 100.0%; Score 943; DB 4; Length 345;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 60

Db 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 101

QY 61 IRQGLELOKVLPGGDTYHMEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYS 120

Db 102 IRQGLELOKVLPGGDTYHMEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYS 161

QY 121 EREANRSRDGAIVYCVGVDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKKSCT 180

Db 162 EREANRSRDGAIVYCVGVDFNETQLARIADSKDHFVPVNDGFQALOGIHSILKKSCT 221

QY 181 E 181

Db 222 E 222

RESULT 11

US-11-047-278-2

Sequence 2, Application US/11047278

Publication No. US20050196407A1

GENERAL INFORMATION:

APPLICANT: Young, John A.T.

APPLICANT: Bradley, Kenneth A.

APPLICANT: Collier, Robert J.

APPLICANT: Mogridge, Jeremy S.

TITLE OF INVENTION: Anthrax Toxin Receptor

FILE REFERENCE: 960296, 97745

CURRENT APPLICATION NUMBER: US/11/047,278

CURRENT FILING DATE: 2005-01-31

PRIOR APPLICATION NUMBER: US/09/970,076

PRIOR FILING DATE: 2001-10-03

PRIOR APPLICATION NUMBER: 60/251,481

PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 368
TYPE: PRT
ORGANISM: Homo sapiens
US-11-047-278-2

Query Match 100.0%; Score 943; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 2e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRTGTLTKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRTGTLTKLTEDREQ 101
QY 61 IROGLEELQKVLPGGDTYMHGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 102 IROGLEELQKVLPGGDTYMHGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 161
QY 121 ERENRSRDGAIVYCVGVDFNETQARIADSKDHVPVNDGFOALOGIHSILKKSCT 180
DB 162 ERENRSRDGAIVYCVGVDFNETQARIADSKDHVPVNDGFOALOGIHSILKKSCT 221
QY 181 E 181
DB 222 E 222

RESULT 12

US-09-833-245-621
Sequence 621, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: P5546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 621
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
US-09-833-245-621

Query Match 100.0%; Score 943; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 2.3e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRTGTLTKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRTGTLTKLTEDREQ 101
QY 61 IROGLEELQKVLPGGDTYMHGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 102 IROGLEELQKVLPGGDTYMHGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 161
QY 121 ERENRSRDGAIVYCVGVDFNETQARIADSKDHVPVNDGFOALOGIHSILKKSCT 180
DB 162 ERENRSRDGAIVYCVGVDFNETQARIADSKDHVPVNDGFOALOGIHSILKKSCT 221
QY 181 E 181
DB 222 E 222

RESULT 13

US-10-201-292-28
Sequence 28, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 460
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-28

Query Match 100.0%; Score 943; DB 4; Length 460;
Best Local Similarity 100.0%; Pred. No. 2.8e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRTGTLTKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRTGTLTKLTEDREQ 101
QY 61 IROGLEELQKVLPGGDTYMHGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 102 IROGLEELQKVLPGGDTYMHGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 161
QY 121 ERENRSRDGAIVYCVGVDFNETQARIADSKDHVPVNDGFOALOGIHSILKKSCT 180
DB 162 ERENRSRDGAIVYCVGVDFNETQARIADSKDHVPVNDGFOALOGIHSILKKSCT 221
QY 181 E 181
DB 222 E 222

RESULT 14

US-10-201-292-32
Sequence 32, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-32

Query Match 100.0%; Score 943; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.9e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRTGTLTKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRTGTLTKLTEDREQ 101

```

QY      61  IRQGLEELQKVLPGGDTYMHGEPERASEQIYYENRQGYRTASVYIALTDGELHEDLFFYS 120
      102  IRQGLEELQKVLPGGDTYMHGEPERASEQIYYENRQGYRTASVYIALTDGELHEDLFFYS 161
QY      121  EREANRSRDIGAIVYCVGVDFNETQIARIADSKDHVPVNDGFQALQGIHSHILKKSCT 180
      162  EREANRSRDIGAIVYCVGVDFNETQIARIADSKDHVPVNDGFQALQGIHSHILKKSCT 221
QY      181  E 181
      222  E 222
Db

```

```

RESULT 15
US-10-201-292-34
; Sequence 34, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-34

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Query Match      100.0%; Score 943; DB 4; Length 504;
Best Local Similarity 100.0%; Pred. No. 3.1e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  GFDLYFTLDKSGSVLHHMNEIYFVEQLAKFTSPQLRMSFIYFSTRGTTLMKLTEDPREQ 60
      42  GFDLYFTLDKSGSVLHHMNEIYFVEQLAKFTSPQLRMSFIYFSTRGTTLMKLTEDPREQ 101
QY      61  IRQGLEELQKVLPGGDTYMHGEPERASEQIYYENRQGYRTASVYIALTDGELHEDLFFYS 120
      102  IRQGLEELQKVLPGGDTYMHGEPERASEQIYYENRQGYRTASVYIALTDGELHEDLFFYS 161
Db      121  EREANRSRDIGAIVYCVGVDFNETQIARIADSKDHVPVNDGFQALQGIHSHILKKSCT 180
      162  EREANRSRDIGAIVYCVGVDFNETQIARIADSKDHVPVNDGFQALQGIHSHILKKSCT 221
QY      181  E 181
      222  E 222
Db

```

Search completed: December 14, 2005, 11:59:02
Job time : 55.6964 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 14, 2005, 11:18:48 : Search time 2.65999 Seconds
(without alignments)
458.218 Million cell updates/sec

Title: US-09-970-076-2_COPY_42_222

Perfect score: 943
Sequence: 1 GFLYFLIDKSGSVLHNMNE.....DGFQALQGIHSLKKSCT 181

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 51441 seqs, 6734002 residues

Total number of hits satisfying chosen parameters: 51441

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA New:

1: /cgn2_6/prodata/1/pubppae/US09_NEW_PUB pep: *
2: /cgn2_6/prodata/1/pubppae/US06_NEW_PUB pep: *
3: /cgn2_6/prodata/1/pubppae/US07_NEW_PUB pep: *
4: /cgn2_6/prodata/1/pubppae/US08_NEW_PUB pep: *
5: /cgn2_6/prodata/1/pubppae/PCT_NEW_PUB pep: *
6: /cgn2_6/prodata/1/pubppae/US10_NEW_PUB pep: *
7: /cgn2_6/prodata/1/pubppae/US11_NEW_PUB pep: *
8: /cgn2_6/prodata/1/pubppae/US60_NEW_PUB pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	943	100.0	564	US-11-186-284-199	Sequence 199, App
2	132.5	14.1	1152	US-11-186-284-199	Sequence 4, Appl
3	126.5	13.4	3063	US-11-186-284-26	Sequence 26, Appl
4	109	11.6	915	US-10-131-826A-294	Sequence 294, Appl
5	109	11.6	956	US-11-113-424-39	Sequence 39, Appl
6	108	11.5	1141	US-10-601-368-24	Sequence 24, Appl
7	108	11.5	1166	US-10-601-368-22	Sequence 22, Appl
8	108	11.5	1188	US-10-601-368-21	Sequence 21, Appl
9	105.5	11.2	739	US-11-057-047-2	Sequence 2, Appl
10	105.5	11.2	764	US-11-057-047-1	Sequence 1, Appl
11	105.5	11.2	798	US-10-821-234-1034	Sequence 1034, Ap
12	104	11.0	1141	US-10-601-368-6	Sequence 6, Appl
13	104	11.0	1166	US-10-601-368-4	Sequence 3, Appl
14	104	11.0	1188	US-10-601-368-3	Sequence 3, Appl
15	104	11.0	1188	US-11-000-463-338	Sequence 338, App
16	104	11.0	1188	US-11-000-463-810	Sequence 810, App
17	103.5	11.0	182	US-10-601-368-25	Sequence 25, Appl
18	100.5	10.7	828	US-10-995-561-983	Sequence 983, App
19	100.5	10.7	918	US-10-995-561-981	Sequence 981, App
20	100.5	10.7	1019	US-10-995-561-982	Sequence 982, App
21	99.5	10.6	182	US-10-601-368-7	Sequence 7, Appl
22	97.5	10.3	761	US-11-057-047-6	Sequence 6, Appl
23	95.5	10.1	1179	US-11-087-125-1	Sequence 1, Appl
24	95.5	10.1	1196	US-10-995-561-921	Sequence 921, App
25	94	10.0	678	US-11-102-240-34	Sequence 34, Appl

26	91.5	9.7	1167	US-11-097-125-2	Sequence 2, Appl
27	90	9.5	1167	US-10-601-368-18	Sequence 18, Appl
28	89.5	9.5	353	US-11-137-465-44	Sequence 44, Appl
29	89.5	9.5	448	US-11-137-465-45	Sequence 45, Appl
30	74	7.8	384	US-10-510-386-158	Sequence 158, App
31	73.5	7.8	509	US-10-793-626-2880	Sequence 2880, Ap
32	73	7.7	264	US-10-793-626-388	Sequence 388, App
33	73	7.7	292	US-10-793-626-2636	Sequence 2636, Ap
34	72	7.6	786	US-10-467-657-103	Sequence 103, App
35	70	7.4	488	US-10-467-657-5636	Sequence 5636, Ap
36	69.5	7.4	489	US-10-467-657-7846	Sequence 7846, Ap
37	69.5	7.4	629	US-10-467-657-250	Sequence 250, App
38	69.5	7.4	629	US-10-467-657-3084	Sequence 3084, App
39	69	7.3	242	US-10-467-657-7306	Sequence 7306, Ap
40	68.5	7.3	1734	US-11-192-867-6	Sequence 6, Appl
41	68.5	7.3	1734	US-11-193-715-6	Sequence 6, Appl
42	68	7.2	348	US-10-674-767-4	Sequence 4, Appl
43	66.5	7.1	1538	US-10-995-561-772	Sequence 772, App
44	66.5	7.1	1804	US-10-513-786-2	Sequence 2, Appl
45	66.5	7.1	3704	US-10-513-786-1	Sequence 1, Appl

ALIGNMENTS

```
RESULT 1
US-11-186-284-199
; Sequence 199, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangt
; APPLICANT: Kmetzger, Robert
; APPLICANT: Monahan, John B.
; APPLICANT: Tibbodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MEMO1-029P2RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-199

Query Match      100.0%; Score 943; DB 7; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GFLYFLIDKSGSVLHNMNEIYFVEQLAKHFPISPOLRMSFIVSTRGTTMLKLTEDREQ 60
DB 42 GFLYFLIDKSGSVLHNMNEIYFVEQLAKHFPISPOLRMSFIVSTRGTTMLKLTEDREQ 101
QY 61 IRGGLBELQKLVFGGDTYHMEGPERASBOIYNNRQGYRTASVITALLTDELEHDI.FFVS 120
DB 102 IRGGLBELQKLVFGGDTYHMEGPERASBOIYNNRQGYRTASVITALLTDELEHDI.FFVS 161
QY 121 EREANNSRDGALVYCVGVDFNETQLARIADSKDHVFPVNDGFLQGIHSLKKSCT 180

Db 162 ERANNSRDLGALVYCVGVDFNETOLARIADSKDHVFNPDGFOALGGIHSILKSCI 221

QY 181 E 181

Db 222 E 222

RESULT 2

US-11-080-026-4
; Sequence 4, Application US/11080026
; Publication No. US20050260192A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Shimooka, Motomu
; APPLICANT: Lu, Chaiten
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; FILE REFERENCE: CFBF-P02-021
; CURRENT APPLICATION NUMBER: US/11/080,026
; CURRENT FILING DATE: 2005-03-15
; PRIOR APPLICATION NUMBER: 09/945,265
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,700
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-026-4

Query Match 14.1%; Score 132.5; DB 7; Length 1152;
Best Local Similarity 26.3%; Pred. No. 3.1e-05;
Matches 52; Conservative 41; Mismatches 66; Indels 39; Gaps 11;

QY 3 DLYFILDKSGSVL-HHNNBIYFVEQLAHKFIISPOLMSFVSTRTGTTIMKLTDE-- 57
Db 150 DIFVLVDGSSYISIGIANFVYVRAFLVLYKSFISPRVQISLVQYSRDHTFTLKKFTK 139
QY 58 -----RSQIRQGLELEQKVLPGSDTYMHGFERASEQIYYENRQGYRTA-SVYIALT 108
Db 200 FTKEPQNNPNRSLVPIQLL--GRTHTATGIRKVVRELFNTNGARKQAFKILVIT 257
QY 109 DGEIHEHLFFYSE--REANNSRDLGALVYCVGVDFNETOLAR----IADS--KDHVP 159
Db 258 DGEKFGDPLGYEDVYIPADRE--GVIRYVIGVDARSEKRSQELNNTIASKEPRDHVFQ 314
QY 160 VNDGFOALGGIHSILK 177
Db 315 VNN-FEALKTIONOLREK 331

RESULT 3

US-11-186-284-26
; Sequence 26, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangt
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: BURGART, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPW01-029P2RMM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21

; PRIOR APPLICATION NUMBER: US/10/301,822

; PRIOR FILING DATE: 2002-11-21

; PRIOR APPLICATION NUMBER: US 60/339,971

; PRIOR FILING DATE: 2001-12-10

; PRIOR APPLICATION NUMBER: US 60/361,978

; PRIOR FILING DATE: 2002-03-05

; PRIOR APPLICATION NUMBER: US 60/381,988

; PRIOR FILING DATE: 2002-05-20

; NUMBER OF SEQ ID NOS: 228

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 26

; LENGTH: 3063

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-11-186-284-26

Query Match 13.4%; Score 126.5; DB 7; Length 3063;
Best Local Similarity 28.9%; Pred. No. 0.00042;
Matches 55; Conservative 38; Mismatches 74; Indels 23; Gaps 12;

QY 3 DLYFILDKSGSVL-HHNNBIYFVEQLAHKFIISPOLMSFVSTRTGTTIMKLTDE 56

Db 440 DIFVLVDGSSYISIGIANFVYVRAFLVLYKSFISPRVQISLVQYSRDHTFTLKKFTK 499

QY 57 DREQIRQGLELEQKVLPGSDTYMHGFERASEQIYYENRQGYRTA-SVYIALTDEL 112

Db 500 VEDII-----EAINFPYRGSGSTNGKAMTYVREKIFVPSK-GSRSNVPEKWIILTDGK- 552

QY 113 HEDLPFYSERANNSRDLGALVYCVGVDFNETOLARIAD--SKDHVFNPDGFOALGGI 170

Db 553 SSDAF---RDPAIKRNDSVDEIFAVGVKQAVRSELEAIASPAETHVTFVED-FDAFORI 608

QY 171 IHSILKSCI 180

Db 609 SPELTQSTCL 618

RESULT 4

US-10-131-826A-294
; Sequence 294, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Rivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RLC128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117

; PUBLICATION NO. US2
; GENERAL INFORMATION
;

```

1  APPLICANT: Pan, Yang
2  APPLICANT: Lora, Jose M.
3  TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
4  FILE REFERENCE: 07334-275001
5  CURRENT APPLICATION NUMBER: US/10/601,368
6  CURRENT FILING DATE: 2003-06-23
7  PRIOR APPLICATION NUMBER: US/09/561,263A
8  PRIOR FILING DATE: 2000-04-27
9  PRIOR APPLICATION NUMBER: US 09/322,790
10 PRIOR FILING DATE: 1999-05-28
11 NUMBER OF SEQ ID NOS: 40
12 SOFTWARE: FastSeq for Windows Version 3.0
13 SEQ ID NO 22
14 LENGTH: 1166
15 TYPE: prt
16 ORGANISM: Mus musculus
17 US-10-601-368-22

```

	Query Match	Similarity	11.5%	Score	108;	DB	6;	Length	1166;
	Best Local	Similarity	24.2%	Pred.	No.	0.0077;			
	Matches	Conservative	48;	Mismatches	84;	Indels	38;	Gaps	9
QY	3	DLYFLDYGSGVLAHMHNEIYYVEQLAKF-ISP-QLRMSFVFSTRGTTLMKLTJEDRQ	60						
	:	: : :	:	:	:	:	:	:	:
Db	142	DIVILVDPSNLS-YEMVEVOHFLINLKKFYIGPGIOVGIGDAVHEFH-LNDYRS	199						
	:	:	:	:	:	:	:	:	:
QY	61	IRQGEEELQKVLPGDDTYWHEGFE--RASQEIYENRGGYRTASYIALTGOELHED--	115						
	:	: : :	:	:	:	:	:	:	:
Db	200	VKDVEAASHIRGGTEETRTAFGLFPANSEAPQKGRRGAK-KMVIYTTOESHSDSD	257						
	:	:	:	:	:	:	:	:	:
QY	116	-----LEFYSEARNRSRDICAIYYCVGXD---FNQTOLARIA	151						
	:	: : :	:	:	:	:	:	:	:
Db	258	LKVIRQSEKDNVTREVAVALGYNNRRGINPETFLNEIKYIASDPDKHFVNUTDEAL-	316						
	:	:	:	:	:	:	:	:	:
QY	152	DSKHVPFVNDGFQALQG	169						
	:	: : :	:	:	:	:	:	:	:
Db	317	--KDIVDALGDRIFSLEG	332						

```

RESULT 8
US-10-601-368-21
; Sequence 21, Application US/10601368
; Publication NO. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 21
; LENGTH: 1188
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(22)
US-10-601-368-21

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	Query Match	11.5%	Score 108;	DB 6;	Length 1188;
	Best Local Similarity	24.2%;	Pred. No. 0.0079;		
Matches	48;	Conservative	26;	Mismatches	84; Indels 38; Gaps 9
Cy	3 DLPLPILDKGSGVLAHNNETYPVEQLAHNF-IIP-DLRMSFIYFSTRGTTLMLTEDREQ	60			
	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::				
Db	164 DIVIVLDGNSNI-YPPAVEVOHFILNITLTKFYISGGQIGVGIYOUGEDANHEPH-NIYRS	221			

Qy 61 IRGGEHELQXVPGDLYNHGEFE---RASQIYVENRGVTRASVIALTDGELHD-- 115
 Db 222 KQVDEASHIEQRGTEFRTAFGLFAPKSAAPQGGKRGAK--KMIIVITDDESHSDP 279
 Qy 116 -----LFFYSEREANRSRDGAIIVYCVGKD---FNETQLARIA 151
 Db 280 LEKVIRQSEKDNVTRKVAVALGYNRRKGINEFTPLNEIKYIASDPDDKHFPNVTDEAL- 358
 Qy 152 DSKDHVPVNDGFOALQG 169
 Db 339 --KQIVDALGDRIRFSLG 354

```

RESULT 9
US-11-057-047-2
; Sequence 2, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilkeson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; TITLE OR INVENTION: Methods Related Thereto
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057,047
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; PRIOR FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 739
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-057-047-2

```

[illegible]

```

RESULT 10
US-11-057-047-1
; Sequence 1, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Edwin
; APPLICANT: Gilkeson, Gary

```

```

/ TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
/ TITLE OF INVENTION: Methods Related Thereto
/ FILE REFERENCE: 2848-66
/ CURRENT APPLICATION NUMBER: US/11/057,047
/ PRIOR APPLICATION NUMBER: 60/543,594
/ PRIOR FILING DATE: 2004-02-10
/ PRIOR APPLICATION NUMBER: 60/636,239
/ PRIOR FILING DATE: 2004-12-14
/ PRIOR APPLICATION NUMBER: US04/015040
/ PRIOR FILING DATE: 2004-05-13
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1
/ LENGTH: 764
/ TYPE: PRN
/ ORGANISM: Homo sapiens
/ US-11-057-047-1

```

Query Match	11.2%	Score 105.5	DB 7	length 764
Best Local Similarity	22.6%	Pred. No. 0.0077		
Matches	48	Conservative	44	Mismatches 75; Indels 45; Gaps 10

QY	3	DLYITLDSKGSV-----LHHNNEIYFYVEQLAHKFIISPOLNMFVISTGCTTLMKLT-	56
Db	270	NIYVLPGSDSIGASNFPGAKKCLVNLIEKIASYVKR--RYGLVTYATYERIKWIKVSEA	327
QY	57	---DREGIPLGLEEL---OKVLPGGDITVYHMGFEPAESEOIYENR-----GGY-RTA	101
Db	328	DSSNADVWTKOLNINEINVEDHKLKSGTNT-----KKALQAVYISMMSSWDDVDPPEGMNFR	381
QY	102	SVIIALTGDG-----EDHEDLFYSEREANRSRLGAIIVYCVG--VYDFNETQ	146
Db	382	HVILMTDGLINMGDPITVVIDEIRDLLIYIGDRNCRPREDYLDVYFVGVLNVQVNNINA	441
QY	147	LARIADSKDHVFPYNDGFOALGIIHSLTKS	178
Db	442	LASKKNEQHFVKVD--MENLEDVFPYQIDDS	472

```

RESULT 11
US-10-821-234-1034
/ Sequence 1034, Application US/10821234
/ Publication No. US2005025511A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andermann, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pc_seq_genes Version 1.0
/ SEQ ID NO 1034
/ LENGTH: 798
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-821-234-1034

```

```

Query Match      11.2%  Score 105.5; DB 6; Length 799;
Best Local Similarity 22.6%  Pred. No. 0.0082;
Matches 48; Conservative 44; Mismatches 75; Indels 45; Gaps 10;

QY      3  DLYELDKSGSV-----LHHNNEYIYFVEQALAHKFIQPLMSPIVFSRTGTTMKLE- 56
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      304 NIVLVLDSDSISGASNFTGAKKCLVNLIEKVASGVKR--RYGLVYATYPRKIWWKSEA 361
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      57 ----DREQIRQLEEL-----QKVLDDGGDTYMHGEGFRASEQIYYENR-----QGY-RTA 101
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

```

Db      362  DSSNAWMYRKQINTEINVEDHKLKSGSTN-----KKALQAYSNMWSWDDVPPEGMNRT 415
Oy      102  SVTIATLDG-----ELHEDFPFYSEEARNSRDLGAIYCVG--VDFENETQ 146
Db      416  HVIIITMTDGLHNMGGDPIYVIDEINDDLVIQDKRKNPREVDLDVYVGVEGLVQNVINA 475
Oy      147  IARIADSKDHFEPVNDGFGALOGIHTSLKKS 178
Db      476  LASKDNEQGVKVKD-MENLEDVYQNIIDS 506

```

RESULT 12
US-10-601-368-6
Sequence 6, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lora, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
CURRENT APPLICATION NUMBER: US/10/601,368
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 1141
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(22)
US-10-601-368-6

	Query Match	11.0%	Score 104	DB 6	Length 1141
	Best Local Similarity	24.28	Pred. No. 0.018		
	Matches	48	Conservative	28	Mismatches 84; Indels 38; Gaps 9;
QY	3 DLYFILDKSGSVLHMHNEIYYEVEQLAKP-ISF-QLRMSFIVESTRGTTMLKLTEDREQ	60			
Db	164 DIVLVLEQNSNI--PPWVEVQHFLINILKKFYIGPGQIQVGGVGYGEDVHEFH--NDVR	221			
QY	61 IROGLEELQVLPGCDTVYHGEFE--RASEQIYYENRGVRTASVLIALDGLNHD-	115			
Db	222 VKDVVEASHIEORGTEETRTAFETIEFRASAPFGKRKA-KVMIVIDGSHSDPD	279			
QY	116 -----LFYSEREANRSRDGAIVYCVGKD-----FNFTOLARIA	151			
Db	280 LEKVITQOSEBDNTVRVAVALGYGNRRGINDETFINEIKYLASDPDDKHFPNVIDEAL-	338			
QY	152 DSKDHVPVVDGFOLQG	169			
Db	339 --KDIYDALGRIFPLEG	354			

RESULT 13
US-10-601-368-4
Sequence 4, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lora, Jose M.
TITLE OR INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-215001
CURRENT APPLICATION NUMBER: US/10/601,368
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28

```
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-601-368-4

Query Match      11.0%; Score 104; DB 6; Length 1166;
Best Local Similarity 24.2%; Pred. No. 0.019;
Matches 48; Conservative 28; Mismatches 84; Indels 38; Gaps 9;

QY 3 DLYFIIDKSGSVLHNNIEIYFVEQLAHKF-ISP-QLRMSFIVSTRGTTLMKLTEDREQ 60
   | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 164 DIVIVLDGNSNI-YPMVEVQHFLINILKKFYIGPGIQGVGVGQEDVHVEFHL-NDYRS 221
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 IROGLEBELQKVLPGDGTTHMEGFE--RASEQIYENRQGYRTASVITALTDEGLHED-- 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 222 VKDVEEAASHIEORGETETRTAFGIEFARSEAFQKGRKGA-KWMIVTDESHSDSPD 279
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 116 -----LFFYSREANRSRDLGAIYVCVVKD-----FNETOLARIA 151
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 280 LEKVIQOQSERDNTRYAVAVLGYNNRGINPEFTFLNEIKTIASDPDDKHFNVTDDEAL- 338
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 152 DSKDHVPVNDGFQALQG 169
   | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 317 --KDIVDALGDRIFSLG 332
   | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 14
US-10-601-368-3
; Sequence 3, Application US/10601368
; Publication No. US2005026702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1188
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(22)
US-10-601-368-3

Query Match      11.0%; Score 104; DB 6; Length 1188;
Best Local Similarity 24.2%; Pred. No. 0.019;
Matches 48; Conservative 28; Mismatches 84; Indels 38; Gaps 9;
```

```
DB 339 --KDIVDALGDRIFSLG 354

RESULT 15
US-11-000-463-338
; Sequence 338, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenhua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIPACN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 1188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-338

Query Match      11.0%; Score 104; DB 7; Length 1188;
Best Local Similarity 24.2%; Pred. No. 0.019;
Matches 48; Conservative 28; Mismatches 84; Indels 38; Gaps 9;

QY 3 DLYFIIDKSGSVLHNNIEIYFVEQLAHKF-ISP-QLRMSFIVSTRGTTLMKLTEDREQ 60
   | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 164 DIVIVLDGNSNI-YPMVEVQHFLINILKKFYIGPGIQGVGVGQEDVHVEFHL-NDYRS 221
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 IROGLEBELQKVLPGDGTTHMEGFE--RASEQIYENRQGYRTASVITALTDEGLHED-- 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 222 VKDVEEAASHIEORGETETRTAFGIEFARSEAFQKGRKGA-KWMIVTDESHSDSPD 279
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 116 -----LFFYSREANRSRDLGAIYVCVVKD-----FNETOLARIA 151
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 280 LEKVIQOQSERDNTRYAVAVLGYNNRGINPEFTFLNEIKTIASDPDDKHFNVTDDEAL- 338
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 152 DSKDHVPVNDGFQALQG 169
   | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 339 --KDIVDALGDRIFSLG 354
   | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Search completed: December 14, 2005, 11:59:30
Job time : 3.65999 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 11:11:02 ; Search time 215.58 Seconds
(without alignments)
1160.284 Million cell updates/sec

Title: US-09-970-076-2_COPY_42_222

Sequence: 943
1 GFDLYFILDKSGSVLHHMNE.....DGFQALQGIHSILKSKCIE 181

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

1: /cgn2_6/prodata/1/paa/US066_COMB.pep:*
2: /cgn2_6/prodata/1/paa/US067_COMB.pep:*
3: /cgn2_6/prodata/1/paa/US073_COMB.pep:*
4: /cgn2_6/prodata/1/paa/US074_COMB.pep:*
5: /cgn2_6/prodata/1/paa/US075_COMB.pep:*
6: /cgn2_6/prodata/1/paa/US076_COMB.pep:*
7: /cgn2_6/prodata/1/paa/US077_COMB.pep:*
8: /cgn2_6/prodata/1/paa/US078_COMB.pep:*
9: /cgn2_6/prodata/1/paa/US079_COMB.pep:*
10: /cgn2_6/prodata/1/paa/US080_COMB.pep:*
11: /cgn2_6/prodata/1/paa/US081_COMB.pep:*
12: /cgn2_6/prodata/1/paa/US082_COMB.pep:*
13: /cgn2_6/prodata/1/paa/US083_COMB.pep:*
14: /cgn2_6/prodata/1/paa/US084_COMB.pep:*
15: /cgn2_6/prodata/1/paa/US085_COMB.pep:*
16: /cgn2_6/prodata/1/paa/US086_COMB.pep:*
17: /cgn2_6/prodata/1/paa/US087_COMB.pep:*
18: /cgn2_6/prodata/1/paa/US088_COMB.pep:*
19: /cgn2_6/prodata/1/paa/US089_COMB.pep:*
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21: /cgn2_6/prodata/1/paa/US091_COMB.pep:*
22: /cgn2_6/prodata/1/paa/US092_COMB.pep:*
23: /cgn2_6/prodata/1/paa/US093_COMB.pep:*
24: /cgn2_6/prodata/1/paa/US094_COMB.pep:*
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26: /cgn2_6/prodata/1/paa/US096_COMB.pep:*
27: /cgn2_6/prodata/1/paa/US097_COMB.pep:*
28: /cgn2_6/prodata/1/paa/US098_COMB.pep:*
29: /cgn2_6/prodata/1/paa/US099_COMB.pep:*
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31: /cgn2_6/prodata/1/paa/US101_COMB.pep:*
32: /cgn2_6/prodata/1/paa/US102_COMB.pep:*
33: /cgn2_6/prodata/1/paa/US103_COMB.pep:*
34: /cgn2_6/prodata/1/paa/US104_COMB.pep:*
35: /cgn2_6/prodata/1/paa/US105_COMB.pep:*
36: /cgn2_6/prodata/1/paa/US106_COMB.pep:*
37: /cgn2_6/prodata/1/paa/US107_COMB.pep:*
38: /cgn2_6/prodata/1/paa/US108_COMB.pep:*
39: /cgn2_6/prodata/1/paa/US109_COMB.pep:*
40: /cgn2_6/prodata/1/paa/US110_COMB.pep:*
41: /cgn2_6/prodata/1/paa/US111_COMB.pep:*
42: /cgn2_6/prodata/1/paa/US112_COMB.pep:*
43: /cgn2_6/prodata/1/paa/US114_COMB.pep:*

Pred. No. is the number of results predicted by a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	943	100.0	274	1 PCT-US99-31025-50	Sequence 50, Appl
2	943	100.0	274	24 US-09-471-179-50	Sequence 50, Appl
3	943	100.0	293	49 US-60-561-086-16	Sequence 16, Appl
4	943	100.0	297	24 US-09-488-725A-2121	Sequence 2121, Ap
5	943	100.0	297	32 US-10-258-898A-2121	Sequence 2121, Ap
6	943	100.0	297	32 US-10-286-897-2121	Sequence 2121, Ap
7	943	100.0	301	1 PCT-US99-31025-132	Sequence 132, App
8	943	100.0	301	24 US-09-471-179-132	Sequence 132, App
9	943	100.0	306	1 PCT-US99-31025-30	Sequence 30, Appl
10	943	100.0	306	1 PCT-US99-31025-51	Sequence 51, Appl
11	943	100.0	306	24 US-09-471-179-30	Sequence 30, Appl
12	943	100.0	306	24 US-09-471-179-51	Sequence 51, Appl
13	943	100.0	328	30 US-10-038-307-26	Sequence 26, Appl
14	943	100.0	328	32 US-10-038-307-26	Sequence 26, Appl
15	943	100.0	328	32 US-10-201-229A-26	Sequence 26, Appl
16	943	100.0	333	1 PCT-US99-31025-9	Sequence 9, Appl
17	943	100.0	333	22 US-09-223-546-9	Sequence 9, Appl
18	943	100.0	333	24 US-09-471-179-9	Sequence 9, Appl
19	943	100.0	333	25 US-09-599-596-9	Sequence 9, Appl
20	943	100.0	333	27 US-09-796-753-12	Sequence 12, Appl
21	943	100.0	333	29 US-09-970-076-8	Sequence 8, Appl
22	943	100.0	333	30 US-10-038-307-2	Sequence 2, Appl
23	943	100.0	333	32 US-10-201-292-2	Sequence 2, Appl
24	943	100.0	333	32 US-10-201-292A-2	Sequence 2, Appl
25	943	100.0	333	40 US-11-047-224-8	Sequence 8, Appl
26	943	100.0	333	40 US-11-047-228-8	Sequence 8, Appl
27	943	100.0	333	49 US-60-568-073-741	Sequence 741, App
28	943	100.0	342	30 US-10-038-307-22	Sequence 22, Appl
29	943	100.0	342	32 US-10-201-292-22	Sequence 22, Appl
30	943	100.0	342	32 US-10-201-292A-22	Sequence 22, Appl
31	943	100.0	345	30 US-10-038-307-24	Sequence 24, Appl
32	943	100.0	345	32 US-10-201-292A-24	Sequence 24, Appl
33	943	100.0	345	32 US-10-201-292A-24	Sequence 24, Appl
34	943	100.0	368	29 US-09-970-076-2	Sequence 2, Appl
35	943	100.0	368	36 US-10-602-702-3	Sequence 3, Appl
36	943	100.0	368	36 US-10-602-727-3	Sequence 3, Appl
37	943	100.0	368	40 US-11-047-224-2	Sequence 2, Appl
38	943	100.0	368	40 US-11-047-228-2	Sequence 2, Appl
39	943	100.0	368	49 US-60-548-281-8	Sequence 8, Appl
40	943	100.0	403	1 PCT-US00-30045-94	Sequence 94, Appl
41	943	100.0	403	1 PCT-US01-11986-621	Sequence 621, App
42	943	100.0	403	28 US-09-833-245-621	Sequence 621, App
43	943	100.0	403	28 US-09-833-245A-621	Sequence 621, App
44	943	100.0	403	28 US-09-833-245B-621	Sequence 621, App
45	943	100.0	403	31 US-10-100-685-9107	Sequence 9107, Ap

ALIGNMENTS

RESULT 1
PCT-US99-31025-50
; Sequence 50, Application PC/TUS9931025
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.

```

; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
; FILE OF INVENTION: ENCODING THEM
; FILE REFERENCE: 7853-173-228
; CURRENT APPLICATION NUMBER: PCT/US99/31025
; CURRENT FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: 09/223,546
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US99-31025-50

Query Match          100.0%; Score 943; DB 1; Length 274;
Best Local Similarity 100.0%; Pred. No. 3.3e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 1 GPDLYFILDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVFSTRGTTLMKLTEDREQ 60
    |||||||
DB 15 GPDLYFILDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVFSTRGTTLMKLTEDREQ 74
    |||||||
QY 61 IRQGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVITALTDELHEDLFFYS 120
    |||||||
DB 75 IRQGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVITALTDELHEDLFFYS 134
    |||||||
QY 121 EREANRSRLGAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCSI 180
    |||||||
DB 135 EREANRSRLGAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCSI 194
    |||||||
QY 181 E 181
DB 195 E 195
```

```

RESULT 2
US-09-471-179-50
; Sequence 50, Application US/09471179
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas
; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 7853-173
; CURRENT APPLICATION NUMBER: US/09/471,179
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-471-179-50
```

```

Query Match          100.0%; Score 943; DB 24; Length 274;
Best Local Similarity 100.0%; Pred. No. 3.3e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 GPDLYFILDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVFSTRGTTLMKLTEDREQ 60
    |||||||
DB 15 GPDLYFILDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVFSTRGTTLMKLTEDREQ 74
    |||||||
QY 61 IRQGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVITALTDELHEDLFFYS 120
    |||||||
DB 75 IRQGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVITALTDELHEDLFFYS 134
    |||||||
QY 121 EREANRSRLGAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCSI 180
    |||||||
DB 135 EREANRSRLGAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCSI 194
    |||||||
QY 181 E 181
DB 195 E 195
```

```

DB 195 E 195

RESULT 3
US-60-561-086-16
; Sequence 16, Application US/60561086
; GENERAL INFORMATION:
; APPLICANT: Emtage, Peter
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods of Therapy and Diagnosis Using Targeting of Cells that Ex-
; FILE REFERENCE: NUVO-18
; CURRENT APPLICATION NUMBER: US/60/561,086
; CURRENT FILING DATE: 2004-04-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-60-561-086-16

Query Match          100.0%; Score 943; DB 49; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.6e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 GPDLYFILDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVFSTRGTTLMKLTEDREQ 60
    |||||||
DB 15 GPDLYFILDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVFSTRGTTLMKLTEDREQ 74
    |||||||
QY 61 IRQGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVITALTDELHEDLFFYS 120
    |||||||
DB 75 IRQGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVITALTDELHEDLFFYS 134
    |||||||
QY 121 EREANRSRLGAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCSI 180
    |||||||
DB 135 EREANRSRLGAIYVCVGVDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCSI 194
    |||||||
QY 181 E 181
DB 195 E 195
```

```

RESULT 4
US-09-488-725A-2121
; Sequence 2121, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_gene_b Versions 1.0
; SEQ ID NO 2121
; LENGTH: 298
; TYPE: PRT
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```

; ORGANISM: Homo sapiens
US-09-488-725A-2121

Query Match      100.0%; Score 943; DB 24; Length 297;
Best Local Similarity 100.0%; Pred. No. 3,7e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFTSPOLRMSPFVSTRGTTMLKLTEDREQ 60
DB      42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFTSPOLRMSPFVSTRGTTMLKLTEDREQ 101

QY      61 IROGLELEQVLPFGDVTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 120
DB      102 IROGLELEQVLPFGDVTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 161

QY      121 EREANRSRDIGAIVYCVGVDPFNETOLARIADSKDHVFPVNDGFQALOGIHSILKKSCT 180
DB      162 EREANRSRDIGAIVYCVGVDPFNETOLARIADSKDHVFPVNDGFQALOGIHSILKKSCT 221

QY      181 E 181
DB      222 E 222
```

```

RESULT 5
US-10-258-898A-2121
; Sequence 2121, Application US/10258898A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/10/258,898A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7143
; SOFTWARE: pc_FL_genes_b Versions 1.0
; SEQ ID NO 2121
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-898A-2121
```

```

Query Match      100.0%; Score 943; DB 32; Length 297;
Best Local Similarity 100.0%; Pred. No. 3,7e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFTSPOLRMSPFVSTRGTTMLKLTEDREQ 60
DB      42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFTSPOLRMSPFVSTRGTTMLKLTEDREQ 101

QY      61 IROGLELEQVLPFGDVTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 120
DB      102 IROGLELEQVLPFGDVTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 161

QY      121 EREANRSRDIGAIVYCVGVDPFNETOLARIADSKDHVFPVNDGFQALOGIHSILKKSCT 180
DB      162 EREANRSRDIGAIVYCVGVDPFNETOLARIADSKDHVFPVNDGFQALOGIHSILKKSCT 221
```

```

QY      181 E 181
DB      222 E 222
```

```

RESULT 6
US-10-286-897-2121
; Sequence 2121, Application US/10286897
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/10/286,897
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US/09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US/09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US/09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US/09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US/09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US/09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7143
; SOFTWARE: pc_FL_genes_b Versions 1.0
; SEQ ID NO 2121
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-897-2121
```

```

Query Match      100.0%; Score 943; DB 32; Length 297;
Best Local Similarity 100.0%; Pred. No. 3,7e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFTSPOLRMSPFVSTRGTTMLKLTEDREQ 60
DB      42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFTSPOLRMSPFVSTRGTTMLKLTEDREQ 101

QY      61 IROGLELEQVLPFGDVTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 120
DB      102 IROGLELEQVLPFGDVTYMHGEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 161

QY      121 EREANRSRDIGAIVYCVGVDPFNETOLARIADSKDHVFPVNDGFQALOGIHSILKKSCT 180
DB      162 EREANRSRDIGAIVYCVGVDPFNETOLARIADSKDHVFPVNDGFQALOGIHSILKKSCT 221

QY      181 E 181
DB      222 E 222
```

```

RESULT 7
PCT-US99-31025-132
; Sequence 132, Application PC/TUS9931025
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: 7853-173-228
; CURRENT APPLICATION NUMBER: PCT/US99/31025
; CURRENT FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 132
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-31025-132
```

```
Query Match          100.0%; Score 943; DB 1; Length 301;
Best Local Similarity 100.0%; Pred. No. 3.8e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 101
QY 61 IROGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 102 IROGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 161
QY 121 EREANSRDLGAIYCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSLKKSCT 180
DB 162 EREANSRDLGAIYCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSLKKSCT 221
```

```
QY 181 E 181
DB 222 E 222
```

```
RESULT 8
US-09-471-179-132
; Sequence 132, Application US/09471179
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas
; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 7853-173
; CURRENT APPLICATION NUMBER: US/09/471.179
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-179-132
```

```
Query Match          100.0%; Score 943; DB 24; Length 301;
Best Local Similarity 100.0%; Pred. No. 3.8e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 60
DB 42 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 101
QY 61 IROGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 102 IROGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 161
QY 121 EREANSRDLGAIYCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSLKKSCT 180
DB 162 EREANSRDLGAIYCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSLKKSCT 221
QY 181 E 181
DB 222 E 222
```

```
RESULT 9
PCT-US99-31025-30
; Sequence 30, Application PC/TUS9931025
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
```

```
; TITLE OF INVENTION: ENCODING THEM
; FILE REFERENCE: 7853-173-228
; CURRENT APPLICATION NUMBER: PCT/US99/31025
; CURRENT FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: 09/223,546
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-31025-30
```

```
Query Match          100.0%; Score 943; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 3.9e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 60
DB 15 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 74
QY 61 IROGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 75 IROGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 134
QY 121 EREANSRDLGAIYCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSLKKSCT 180
DB 135 EREANSRDLGAIYCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSLKKSCT 194
```

```
QY 181 E 181
DB 195 E 195
```

```
RESULT 10
PCT-US99-31025-51
; Sequence 51, Application PC/TUS9931025
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: 7853-173-228
; CURRENT APPLICATION NUMBER: PCT/US99/31025
; CURRENT FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: 09/223,546
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-31025-51
```

```
Query Match          100.0%; Score 943; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 3.9e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 60
DB 15 GFDLYFLDKSGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQ 74
QY 61 IROGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 120
DB 75 IROGLEELQKVLPGGDTYMHGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYS 134
QY 121 EREANSRDLGAIYCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSLKKSCT 180
DB 135 EREANSRDLGAIYCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSLKKSCT 194
QY 181 E 181
```



```
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFI SPQLRMSFIYFSTRTTLMKLTEDREQ 60
Db 42 GFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFI SPQLRMSFIYFSTRTTLMKLTEDREQ 101
QY 61 IROGLEBELQKVLPGGDTYMHGEPERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 120
Db 102 IROGLEBELQKVLPGGDTYMHGEPERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 161
QY 121 EREANRSRDLGAIYVCVGDENETOLARIADSKDHVPVNDGFQALOGIHSILKSCI 180
Db 162 EREANRSRDLGAIYVCVGDENETOLARIADSKDHVPVNDGFQALOGIHSILKSCI 221
QY 181 E 181
Db 222 E 222

RESULT 15
US-10-201-292A-26
; Sequence 26, Application US/10201292A
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: James B. Rottman
; APPLICANT: Theresa L. O'Keefe
; APPLICANT: Englin Ozkaynak
; APPLICANT: Judith J. Healey
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: MP101-307CPLM
; CURRENT APPLICATION NUMBER: US/10/201,292A
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 10/038,307
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-201-292A-26

Query Match 100.0%; Score 943; DB 32; Length 328;
Best Local Similarity 100.0%; Pred. No. 4.3e-92;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFI SPQLRMSFIYFSTRTTLMKLTEDREQ 60
Db 42 GFDLYFIIDKSGSVLHHMNEIYFVEQLAHKFI SPQLRMSFIYFSTRTTLMKLTEDREQ 101
QY 61 IROGLEBELQKVLPGGDTYMHGEPERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 120
Db 102 IROGLEBELQKVLPGGDTYMHGEPERASEQIYENRQGYRTASVIALTDGELHEDLFFYS 161
QY 121 EREANRSRDLGAIYVCVGDENETOLARIADSKDHVPVNDGFQALOGIHSILKSCI 180
Db 162 EREANRSRDLGAIYVCVGDENETOLARIADSKDHVPVNDGFQALOGIHSILKSCI 221
QY 181 E 181
Db 222 E 222
```

Search completed: December 14, 2005, 11:50:58
Job time : 216.58 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: December 18, 2005, 07:35:12 / Search time 579.877 Seconds
(without alignments)
2581.163 Million cell updates/sec

Title: US-09-970-076-2_COPY_42_222

Perfect score: 943

Sequence: 1 GFDLYFLIDSGSVLHMNE.....DGFQALQGIHSLKSKSCIE 181

Scoring table:

BLSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame_p2n.model -DEV=xlh
-Q=/cg2_1/USFTO.spool/US0970076/runat_14122005_11852_21035/app_query.fasta.1.2410
-DB=published.Applications.NA.Main -QPM=fastcap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCD=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blsum62
-TRANS=human40.csl -LIST=45 -LOCAL=LOCAL=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US0970076 @CGN_1.1.2715 @runat_14122005_11852_21035
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications.NA.Main.*

1: /cg2_6/ptodaca/1/pubpna/US07_PUBCOMB.seq.*
2: /cg2_6/ptodaca/1/pubpna/US08_PUBCOMB.seq.*
3: /cg2_6/ptodaca/1/pubpna/US09_PUBCOMB.seq.*
4: /cg2_6/ptodaca/1/pubpna/US09B_PUBCOMB.seq.*
5: /cg2_6/ptodaca/1/pubpna/US10A_PUBCOMB.seq.*
6: /cg2_6/ptodaca/1/pubpna/US10B_PUBCOMB.seq.*
7: /cg2_6/ptodaca/1/pubpna/US10C_PUBCOMB.seq.*
8: /cg2_6/ptodaca/1/pubpna/US10D_PUBCOMB.seq.*
9: /cg2_6/ptodaca/1/pubpna/US10E_PUBCOMB.seq.*
10: /cg2_6/ptodaca/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	943	100.0	1008	US-10-038-307-25	Sequence 25, Appl
2	943	100.0	1008	US-10-201-292-25	Sequence 25, Appl
3	943	100.0	1047	US-10-038-307-21	Sequence 21, Appl
4	943	100.0	1047	US-10-201-292-21	Sequence 21, Appl
5	943	100.0	1056	US-10-038-307-23	Sequence 23, Appl
6	943	100.0	1056	US-10-201-292-23	Sequence 23, Appl
7	943	100.0	1401	US-10-201-292-27	Sequence 27, Appl
8	943	100.0	1401	US-10-201-292-29	Sequence 29, Appl

9	943	100.0	1414	US-11-047-278-1	Sequence 1, Appl1
10	943	100.0	1436	US-11-047-278-9	Sequence 9, Appl1
11	943	100.0	1454	US-10-133-937-58	Sequence 58, Appl1
12	943	100.0	1454	US-10-159-563-58	Sequence 58, Appl1
13	943	100.0	1464	US-10-201-292-31	Sequence 31, Appl1
14	943	100.0	1534	US-10-201-292-33	Sequence 33, Appl1
15	943	100.0	1608	US-10-201-292-35	Sequence 35, Appl1
16	943	100.0	1609	US-10-037-270-8	Sequence 8, Appl1
17	943	100.0	1609	US-10-117-222-8	Sequence 8, Appl1
18	943	100.0	1609	US-10-122-851-8	Sequence 8, Appl1
19	943	100.0	1623	US-10-038-307-11	Sequence 11, Appl1
20	943	100.0	1623	US-10-201-292-11	Sequence 11, Appl1
21	943	100.0	1650	US-10-038-307-9	Sequence 9, Appl1
22	943	100.0	1650	US-10-038-307-13	Sequence 13, Appl1
23	943	100.0	1650	US-10-038-307-15	Sequence 15, Appl1
24	943	100.0	1650	US-10-201-292-9	Sequence 9, Appl1
25	943	100.0	1650	US-10-201-292-13	Sequence 13, Appl1
26	943	100.0	1650	US-10-201-292-15	Sequence 15, Appl1
27	943	100.0	1674	US-10-038-307-17	Sequence 17, Appl1
28	943	100.0	1674	US-10-201-292-17	Sequence 17, Appl1
29	943	100.0	1713	US-10-038-307-19	Sequence 19, Appl1
30	943	100.0	1713	US-10-201-292-19	Sequence 19, Appl1
31	943	100.0	1718	US-10-357-930-30300	Sequence 30300, A
32	943	100.0	2112	US-11-047-278-7	Sequence 7, Appl1
33	943	100.0	2272	US-09-796-753-11	Sequence 11, Appl1
34	943	100.0	2272	US-10-038-307-1	Sequence 1, Appl1
35	943	100.0	2272	US-10-201-292-1	Sequence 1, Appl1
36	943	100.0	2235	US-10-198-846-9957	Sequence 9957, Ap
37	943	100.0	5540	US-09-918-715-176	Sequence 176, App
38	943	100.0	5540	US-09-918-715-231	Sequence 231, App
39	943	100.0	5540	US-10-301-822-198	Sequence 198, App
40	943	100.0	5540	US-10-474-794-176	Sequence 176, App
41	943	100.0	5540	US-10-474-794-231	Sequence 231, App
42	943	100.0	5540	US-10-979-159-176	Sequence 176, App
43	943	100.0	5540	US-10-979-159-231	Sequence 231, App
44	943	100.0	5540	US-11-047-278-5	Sequence 5, Appl1
45	934	99.0	5220	US-09-918-715-186	Sequence 186, App

ALIGNMENTS

RESULT 1
US-10-038-307-25
; Sequence 25, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OR INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-25

Alignment Scores:

Pred. No.: 1,71e-116
Score: 943.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6
Length: 1008
Matches: 181
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-038-307-25 (1-1008)

QY 1 GlyPhAspleuYrthetleuAsplySserGlySerValleuIshietrPaenglu 20

DB 136 GGAATTGACCTGACTTATTTGGACAAATCGAAGTGTGTCACCACTGGATGAA 195
|||
QY 21 ILETYTYRPhenValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMetSer 40
|||
DB 196 ATCTATTACTTGTGGAAACAGTTGGCTCACAATAATTCATGACCCACAGTGAATAATGTC 255
|||
QY 41 PheIleValPheSerThrArgGlyThrThrLeuMetIleSerThrGluAspArgGluGln 60
|||
DB 256 TTTATTGTTTCTCCACCCGAGAACACTTAATGAACTGCACAGAAACAGAGAAACA 315
|||
QY 61 ILeArgGlnGlyLeuGlnGluLeuGlnIleValLeuProGlyGlyAspThrIleMetHis 80
|||
DB 316 ATCCGTCAAGCCCTAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACACTTACATGCAT 375
|||
QY 81 GluGlyPheGluArgAlaSerGluGlnIleIleTYTYRGLuAspArgGlnGlyTYRArgThr 100
|||
DB 376 GAAGGATTTGAAAGGGCCAGTGAAGCATTTATTATGAAACAGACAAAGGTCAGAGACA 435
|||
QY 101 AlaSerValIleIleAlaLeuThrArgGlyGluLeuHisGluAspLeuPhePheTYRser 120
|||
DB 436 GCCAGGCTCATCTGCTGTTGACTGATGAGAACTCCATGAAATCTCTTTTCTATTCA 495
|||
QY 121 GluArgGluAlaAspArgSerArgAspLeuGlyAlaIleValTYRcySValGlyValIys 140
|||
DB 496 GAGAGGAGGCTAATAGTCTCCGAGATCTTGCGCAATTTGTTACTGTGTGGTGAGAA 555
|||
QY 141 AspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerIleAspHisValPheProVal 160
|||
DB 556 GATTTCATAGACACACAGCTGGCCGGATTCGGACAGTAAGATCATGTGTTCCCGTG 615
|||
QY 161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIleIysSerCysIle 180
|||
DB 616 AATGACGCTTTCAGGCTCTGCAAGGCAATCCATCTCAATTTTGAAGAAGTCTGCATC 675
|||
QY 181 Glu 181
|||
DB 676 GAA 678

RESULT 2
US-10-201-292-25
; Sequence 25, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-25

Alignment Scores:
Pred. No.: 1,716-116 Length: 1008
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-201-292-25 (1-1008)

QY 1 GlyPheAspLeuTYRPhenIleLeuAspIleSerGlySerValLeuHisIleSTPAsnGlu 20
|||
DB 136 GGAATTGACCTGACTTATTTGGACAAATCGAAGTGTGTCACCACTGGATGAA 195

QY 21 ILETYTYRPhenValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMetSer 40
|||
DB 196 ATCTATTACTTGTGGAAACAGTTGGCTCACAATAATTCATGACCCACAGTGAATAATGTC 255
|||
QY 41 PheIleValPheSerThrArgGlyThrThrLeuMetIleSerThrGluAspArgGluGln 60
|||
DB 256 TTTATTGTTTCTCCACCCGAGAACACTTAATGAACTGCACAGAAACAGAGAAACA 315
|||
QY 61 ILeArgGlnGlyLeuGlnGluLeuGlnIleValLeuProGlyGlyAspThrIleMetHis 80
|||
DB 316 ATCCGTCAAGCCCTAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGAGACACTTACATGCAT 375
|||
QY 81 GluGlyPheGluArgAlaSerGluGlnIleIleTYTYRGLuAspArgGlnGlyTYRArgThr 100
|||
DB 376 GAAGGATTTGAAAGGGCCAGTGAAGCATTTATTATGAAACAGACAAAGGTCAGAGACA 435
|||
QY 101 AlaSerValIleIleAlaLeuThrArgGlyGluLeuHisGluAspLeuPhePheTYRser 120
|||
DB 436 GCCAGGCTCATCTGCTGTTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTATTCA 495
|||
QY 121 GluArgGluAlaAspArgSerArgAspLeuGlyAlaIleValTYRcySValGlyValIys 140
|||
DB 496 GAGAGGAGGCTAATAGTCTCCGAGATCTTGCGCAATTTGTTACTGTGTGGTGAGAA 555
|||
QY 141 AspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerIleAspHisValPheProVal 160
|||
DB 556 GATTTCATAGACACACAGCTGGCCGGATTCGGACAGTAAGATCATGTGTTCCCGTG 615
|||
QY 161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIleIysSerCysIle 180
|||
DB 616 AATGACGCTTTCAGGCTCTGCAAGGCAATCCATCTCAATTTTGAAGAAGTCTGCATC 675
|||
QY 181 Glu 181
|||
DB 676 GAA 678

RESULT 3
US-10-038-307-21
; Sequence 21, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-21

Alignment Scores:
Pred. No.: 1,826-116 Length: 1047
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-038-307-21 (1-1047)

QY 1 GlyPheAspLeuTYRPhenIleLeuAspIleSerGlySerValLeuHisIleSTPAsnGlu 20
|||
DB 163 GGAATTGACCTGACTTATTTGGACAAATCGAAGTGTGTCACCACTGGATGAA 222
|||
QY 21 ILETYTYRPhenValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMetSer 40

```
|||||
Db 223 ATCATTAATTGTTGGAAACAGTTGGCTCACAAATTCACGCCACAGTTGAGAAATGTC 282
Qy 41 PheIIeValPheSerThrArgIleuThrThrLeuMetLysLeuThrGluAspArgGluGln 60
Db 283 TTTATTGTTTTCTCCACCCGAGAACACTTAATGAACCTGACAGAACAGACAGAACAA 342
Qy 61 IleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyIleAspThrTyrMetHis 80
Db 343 ATCCGTAAAGCCCTAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATCAT 402
Qy 81 GluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThr 100
Db 403 GAAGGATTGMAAGGGCCAGTGAAGCAGATTATTAAGAAACAGAACAGGTTACAGACA 462
Qy 101 AlasSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSer 120
Db 463 GCCAGCTCATCATCTGCTTTGACTGATGAGAGAACTCCATGAAATCTTTTCTATTCA 522
Qy 121 GluArgGluAlaAsnArgSerArgAspLeuGlyValIleValTyrCysValGlyValLys 140
Db 523 GAGAGGAGGCTAATAGCTCTCGAGATCTTGTCATATGTTACTGTGTGGTGAAA 582
Qy 141 AspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPheProVal 160
Db 583 GATTTCATAGACACACAGCTGCGCCGATTCGGACAGTAAGATCATGTGTTCCCGTG 642
Qy 161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCysIle 180
Db 643 AATGACCGCTTTCAGGCTTGCAAGGCATCATCAATTTTGAAGAGTCTCGATC 702
Qy 181 Glu 181
Db 703 GAA 705

RESULT 4
US-10-201-292-21
; Sequence 21, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-21

Alignment Scores:
Pred. No.: 1,82e-116 Length: 1047
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-201-292-21 (1-1047)
Qy 1 G1YPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleSTPAAnglu 20
Db 163 GGAATTGACCTGTAATCTTATTTGGACAAATCAAGAAAGTGCTGCAACCACTGGAATGAA 222
Qy 21 IleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSer 40
Db 223 ATCATTAATTGTTGGAAACAGTTGGCTCACAAATTCACGCCACAGTTGAGAAATGTC 282
```

```
Qy 41 PheIIeValPheSerThrArgIleuThrThrLeuMetLysLeuThrGluAspArgGluGln 60
Db 283 TTTATTGTTTTCTCCACCCGAGAACACTTAATGAACCTGACAGAACAGACAGAACAA 342
Qy 61 IleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyIleAspThrTyrMetHis 80
Db 343 ATCCGTAAAGCCCTAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATCAT 402
Qy 81 GluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThr 100
Db 403 GAAGGATTGMAAGGGCCAGTGAAGCAGATTATTAAGAAACAGAACAGGTTACAGACA 462
Qy 101 AlasSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSer 120
Db 463 GCCAGCTCATCATCTGCTTTGACTGATGAGAGAACTCCATGAAATCTTTTCTATTCA 522
Qy 121 GluArgGluAlaAsnArgSerArgAspLeuGlyValIleValTyrCysValGlyValLys 140
Db 523 GAGAGGAGGCTAATAGCTCTCGAGATCTTGTCATATGTTACTGTGTGGTGAAA 582
Qy 141 AspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPheProVal 160
Db 583 GATTTCATAGACACACAGCTGCGCCGATTCGGACAGTAAGATCATGTGTTCCCGTG 642
Qy 161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCysIle 180
Db 643 AATGACCGCTTTCAGGCTTGCAAGGCATCATCAATTTTGAAGAGTCTCGATC 702
Qy 181 Glu 181
Db 703 GAA 705

RESULT 5
US-10-038-307-23
; Sequence 23, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-23

Alignment Scores:
Pred. No.: 1,84e-116 Length: 1056
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-038-307-23 (1-1056)
Qy 1 G1YPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleSTPAAnglu 20
Db 136 GGAATTGACCTGTAATCTTATTTGGACAAATCAAGAAAGTGCTGCAACCACTGGAATGAA 195
Qy 21 IleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSer 40
Db 196 ATCATTAATTGTTGGAAACAGTTGGCTCACAAATTCACGCCACAGTTGAGAAATGTC 255
Qy 41 PheIIeValPheSerThrArgIleuThrThrLeuMetLysLeuThrGluAspArgGluGln 60
```



```
Db 316 ATCCGTCAGGCGCTAGAAAGAACTCCAGAAAGTTCTGCAGAGGAGACACTTACATCAT 375
Qy 81 GUGUlypHeGluuAgaAlaSerGluGlnlIeTyTyrgLuuAaArgGlnGlyTyraGThr 100
Db 376 GAAGGATTTTGAAGGGCCAGTGGACAGATTATTAAGAAACAGACAGAGGTACAGACA 435
Qy 101 AlaserValIleIleAlaLeuThrAspGlyGluLeuHISgluAaPheLeuPheTySer 120
Db 436 GCCAGGCTCATCTTGTCTTGCATGATGAGAACTCCATGAAAGATCTCTTTTCTATTCA 495
Qy 121 GUAArgLuuAlaAaArgSerArgAspLeuGlyAlaIleValTyrcysValGlyValIys 140
Db 496 GAGAGGAGGCTAATAGCTCTCGAGATCTTGTCGAATTGTTACTGTGTGGTGTA 555
Qy 141 AspPheAaGluThrGlnLeuAlaArgIleAlaAspSerIysAaPheIleValPheProVal 160
Db 556 GATTTCAATGACACAGCTGGCCCGATGGCAGACAGTAAAGATCATGTGTTCCCGTG 615
Qy 161 AaAaSpGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuYsIysSerCysIle 180
Db 616 AATGACGGCTTTTCAGGCTCTGCAGAGGATCATCTCAATTTTGAAGAAAGTCTGCATC 675
Qy 181 Glu 181
Db 676 GAA 678
```

RESULT 8

```
US-10-201-292-29
; Sequence 29, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZAYANAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201.292
; PRIORITY FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-201-292-29
```

Alignment Scores:

```
Pred. No.: 2 846-116 Length: 1401
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
```

US-09-970-076-2_COPY_42_222 (1-181) x US-10-201-292-29 (1-1401)

```
Qy 1 GlyPheAaPleuTyrrPheIleLeuAaPlySerGlySerValIleuHISgluPaanglu 20
Db 136 GGAATTGACCTGTACTTTCATTTTGGACAATCAGAGAGTGTGTGCACTGGAATGAA 195
Qy 21 ILeTyTyrrPheValGluGlnLeuAlaHISlyPheIleSerProGlnLeuArgMetSer 40
Db 196 ATCTATTACTTGTGGAAAGTTGGCTCACAAATTCATCAGCCCAAGTGGAGATGTCC 255
Qy 41 PheIleValPheSerThrArgGlyThrThrLeuMetIysLeuThrGluAaPargGluGln 60
Db 256 TTTTATTCTTTCTCCACCCAGACAACTTATTAAGAACTGACAGACAGACAGACAA 315
Qy 61 ILeArgGlnGlyLeuGlnGluLeuGlnIysValIleuProGlyIaSerThrTyMetHis 80
Db 316 ATCCGTCAAGGCGCTAGAAAGAACTCCAGAAAGTTCTGCAGAGGAGACACTTACATCAT 375
```

```
Qy 81 GUGUlypHeGluuAgaAlaSerGluGlnlIeTyTyrgLuuAaArgGlnGlyTyraGThr 100
Db 376 GAAGGATTTTGAAGGGCCAGTGGACAGATTATTAAGAAACAGACAGAGGTACAGACA 435
Qy 101 AlaserValIleIleAlaLeuThrAspGlyGluLeuHISgluAaPheLeuPheTySer 120
Db 436 GCCAGGCTCATCTTGTCTTGCATGATGAGAACTCCATGAAAGATCTCTTTTCTATTCA 495
Qy 121 GUAArgLuuAlaAaArgSerArgAspLeuGlyAlaIleValTyrcysValGlyValIys 140
Db 496 GAGAGGAGGCTAATAGCTCTCGAGATCTTGTCGAATTGTTACTGTGTGGTGTA 555
Qy 141 AspPheAaGluThrGlnLeuAlaArgIleAlaAspSerIysAaPheIleValPheProVal 160
Db 556 GATTTCAATGACACAGCTGGCCCGATGGCAGACAGTAAAGATCATGTGTTCCCGTG 615
Qy 161 AaAaSpGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuYsIysSerCysIle 180
Db 616 AATGACGGCTTTTCAGGCTCTGCAGAGGATCATCTCAATTTTGAAGAAAGTCTGCATC 675
Qy 181 Glu 181
Db 676 GAA 678
```

RESULT 9

```
US-11-047-278-1
; Sequence 1, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047.278
; PRIORITY FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970.076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251.481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)..(1207)
; US-11-047-278-1
```

Alignment Scores:

```
Pred. No.: 2 886-116 Length: 1414
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
```

US-09-970-076-2_COPY_42_222 (1-181) x US-11-047-278-1 (1-1414)

```
Qy 1 GlyPheAaPleuTyrrPheIleLeuAaPlySerGlySerValIleuHISgluPaanglu 20
Db 227 GGAATTGACCTGTACTTTCATTTTGGACAATCAGAGAGTGTGTGCACTGGAATGAA 286
Qy 21 ILeTyTyrrPheValGluGlnLeuAlaHISlyPheIleSerProGlnLeuArgMetSer 40
Db 287 ATCTATTACTTGTGGAAAGTTGGCTCACAAATTCATCAGCCCAAGTGGAGAAATGTCC 346
Qy 41 PheIleValPheSerThrArgGlyThrThrLeuMetIysLeuThrGluAaPargGluGln 60
```

Db 347 TTTATTGTTTCTCCACCCGAGAGAACCTTAATGAACTGACAGAGACAGAGAACAA 406
QY 61 TLeaRGlnGlyLeuGlnGlyLeuGlnGlyValLeuProGlyGlyAspThrTyrimethis 80
Db 407 ATCCGTCAAGGCTTAAGAAATCCAGAAAGTTCTGCGAGAGAGACACTTACATGCAAT 466
QY 81 GlnGlyPheGlnuArgAlaSerGlnGlnIleTyTyTyGlnuAsnArgGlnGlyTyraGthr 100
Db 467 GAAGATTGAAAGGCGCAATGAGCAATTTATGAAAGACAGACAGGATCAGAGACA 526
QY 101 AlaSerValIleIleAlaLeuThrAspGlyGlnuLeuHisGlnuAspLeuPhePheTySer 120
Db 527 GCCAGGCTCATCTGCTTGAATGAGAACTCCATGAACTCTCTTTTCTATCA 586
QY 121 GlnuArgGlnuAlaAsnArgSerArgAspLeuGlyAlaIleValTyTyCysValGlyValLys 140
Db 587 GAGAGGAGGCTTAATAGGTCTGAGATCTTGAGCAATTTTACTGTTGATGAGAA 646
QY 141 AspPheAsnGlnuThrGlnuLeuAlaArgIleAlaAspSerLysAspHisValPheProVal 160
Db 647 GATTTCATGAGACACAGCTGCGCGGATTCGCGAGACGTAAGATCATGTTTCCCGTG 706
QY 161 AsnAspGlyPheGlnuAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCysIle 180
Db 707 AATGACGGCTTTCAGGCTCTGCAAGGCATCATCCTCAATTTTGAAGAAAGTCTGCATC 766
QY 181 Gln 181
Db 767 GAA 769

RESULT 10

US-11-047-278-9
Sequence 9, Application US/11047278
Publication No. US20050196407A1
GENERAL INFORMATION:
APPLICANT: Young, John A.T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TITLE OF INVENTION: Anthrax Toxin Receptor
FILE REFERENCE: 960296.97745
CURRENT APPLICATION NUMBER: US/11/047, 278
CURRENT FILING DATE: 2005-01-31
PRIOR APPLICATION NUMBER: US/09/970, 076
PRIOR FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 1436
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (380)..(1033)
US-11-047-278-9

Alignment Scores:
Pred. No.: 2,95e-116 Length: 1436
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-11-047-278-9 (1-1436)

QY 1 GlnPheAspLeuTyTyPheIleLeuAspLysSerGlySerValLeuHisIleTPaenglu 20
Db 266 GGATTGACCTGTAATCTTATTTGACAAATCAGAAAGTGTGCGACCACTGGAAATGAA 325
QY 21 IleTyTyTyPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSer 40

Db 326 ATCTATTACTTTGTGGAACAGTTGGCTCAAAATTCATCAGGCCACAGTTGGAATGTC 385
QY 41 PheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGlnuAspArgGln 60
Db 386 TTTATTGTTTCTCCACCCGAGAGAACCTTAATGAAACTGACAGAAACAGAGAACAA 445
QY 61 TLeaRGlnGlyLeuGlnuLeuGlnuLysValLeuProGlyGlyAspThrTyrimethis 80
Db 446 ATCCGTCAAGGCTTAAGAAATCCAGAAAGTTCTGCGAGAGAGACACTTACATGCAAT 505
QY 81 GlnGlyPheGlnuArgAlaSerGlnGlnIleTyTyTyGlnuAsnArgGlnGlyTyraGthr 100
Db 506 GAAGATTGAAAGGCGCAATGAGCAATTTATGAAAGACAGAGGATCAGAGACA 565
QY 101 AlaSerValIleIleAlaLeuThrAspGlyGlnuLeuHisGlnuAspLeuPhePheTySer 120
Db 566 GCTAGCGCTCATCTGCTTGAATGAGAACTCCATGAAATCTCTTTTCTATTC 625
QY 121 GlnuArgGlnuAlaAsnArgSerArgAspLeuGlyAlaIleValTyTyCysValGlyValLys 140
Db 626 GAGAGGAGGCTTAATAGGTCTGAGATCTTGTCATATTGTTTACTGTTGATGAGAA 685
QY 141 AspPheAsnGlnuThrGlnuLeuAlaArgIleAlaAspSerLysAspHisValPheProVal 160
Db 686 GATTTCATGAGACACAGCTGCGCGGATTCGCGAGACGTAAGATCATGTTTCCCGTG 745
QY 161 AsnAspGlyPheGlnuAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCysIle 180
Db 746 AATGACGGCTTTCAGGCTCTGCAAGGCATCATCCTCAATTTTGAAGAAAGTCTGCATC 805
QY 181 Gln 181
Db 806 GAA 808

RESULT 11

US-10-133-937-58
Sequence 58, Application US/10133937
Publication No. US20030207278A1
GENERAL INFORMATION:
APPLICANT: Khan, Javed
APPLICANT: Ringner, Markus
APPLICANT: Peterson, Carsten
APPLICANT: Meltzer, Paul
TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
TITLE OF INVENTION: OTHER BIOLOGICAL STRATES
FILE REFERENCE: 11613.56US01
CURRENT APPLICATION NUMBER: US/10/133, 937
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58
LENGTH: 1454
TYPE: DNA
ORGANISM: Homo sapiens
US-10-133-937-58

Alignment Scores:
Pred. No.: 3e-116 Length: 1454
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-133-937-58 (1-1454)

QY 1 GlnPheAspLeuTyTyPheIleLeuAspLysSerGlySerValLeuHisIleTPaenglu 20
Db 267 GGATTGACCTGTAATCTTATTTGACAAATCAGAAAGTGTGCGACCACTGGAAATGAA 326
QY 21 IleTyTyTyPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSer 40

DB 327 ATCTATTACTTTGGAAACAGTTGGCTCACAAATTCATCAGCCACAGTTGAGATGTCC 386
QY 41 PheIIeValPheSerThrArgGlyThrThreumetylserLeuThrgluaspArgGluIn 60
DB 387 TTTATTTGTTTCTTCACCCGAGAACACTTAATGAAGTGAACAGACAGAACAA 446
QY 61 IleArgIngluLeuGluGluLeuGlnIleValLeuProGlyGlyAspThrTyrMetHis 80
DB 447 ATCCGTAAAGGCTTGAAGAACTCCAGAACTTCCAGAGAGAGACACTTACATCAT 506
QY 81 GluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThr 100
DB 507 GAAGGATTTGAAAGGCGCAGTGAAGCATTTATATGAAACAGACAGAGGTACAGACA 566
QY 101 AlAsSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSer 120
DB 567 GCCAGCGTCATCATTTGCTTGTGACTGATGAGAACTCCATGAAAGATCTTTTCTTATTTCA 626
QY 121 GluArgGluAlaAsnArgSerArgAspLeuGlyValIleValTyrCysValGlyValIys 140
DB 627 GAGAGGAGGCTTAATAGTCTCGAGATCTTGTCATTTGTTACTGTGTGGTGAA 686
QY 141 AspPheAsnGluThrgluLeuAlaArgIleAlaAspSerIysAspHisValPheProVal 160
DB 687 GATTTCAATGACACACAGCTGGCCGGATTGCGACAGTAAGATCATGTGTTCCCGTG 746
QY 161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisserIleLeuIlylsSerCysIle 180
DB 747 AATGACGGCTTTTCAGGCTTGCAAGGATCATCATCAATTTTGAAGAGTCTGCATC 806
QY 181 Glu 181
DB 807 GAA 809

RESULT 12

US-10-159-563-58
; Sequence 58, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Metzger, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-58

Alignment Scores:

Pred. No.: 3e-116
Score: 943.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6

Length: 1454
Matches: 181
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-159-563-58 (1-1454)

QY 1 GlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTTPaenglu 20
DB 267 GGATTGACCTGACTTCAATTTGGACAAATCAGAAAGTGTGTCACCACTGGAATGAA 326

QY 21 IleTyrPheValGluGlnLeuAlaHisIysPheIleSerProGlnLeuArgMetSer 40
DB 327 ATCTATTACTTTGGAAACAGTTGGCTCACAAATTCATCAGCCACAGTTGAGATGTCC 386
QY 41 PheIIeValPheSerThrArgGlyThrThreumetylserLeuThrgluaspArgGluIn 60
DB 387 TTTATTTGTTTCTTCACCCGAGAACACTTAATGAAGTGAACAGACAGAACAA 446
QY 61 IleArgIngluLeuGluGluLeuGlnIleValLeuProGlyGlyAspThrTyrMetHis 80
DB 447 ATCCGTAAAGGCTTGAAGAACTCCAGAACTTCCAGAGAGAGACACTTACATCAT 506
QY 81 GluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThr 100
DB 507 GAAGGATTTGAAAGGCGCAGTGAAGCATTTATATGAAACAGACAGAGGTACAGACA 566
QY 101 AlAsSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSer 120
DB 567 GCCAGCGTCATCATTTGCTTGTGACTGATGAGAACTCCATGAAAGATCTTTTCTTATTTCA 626
QY 121 GluArgGluAlaAsnArgSerArgAspLeuGlyValIleValTyrCysValGlyValIys 140
DB 627 GAGAGGAGGCTTAATAGTCTCGAGATCTTGTCATTTGTTACTGTGTGGTGAA 686
QY 141 AspPheAsnGluThrgluLeuAlaArgIleAlaAspSerIysAspHisValPheProVal 160
DB 687 GATTTCAATGACACACAGCTGGCCGGATTGCGACAGTAAGATCATGTGTTCCCGTG 746
QY 161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisserIleLeuIlylsSerCysIle 180
DB 747 AATGACGGCTTTTCAGGCTTGCAAGGATCATCATCAATTTTGAAGAGTCTGCATC 806
QY 181 Glu 181
DB 807 GAA 809

RESULT 13

US-10-201-292-31
; Sequence 31, Application US/10201292
; Publication No. US2003014193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALRY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-31

Alignment Scores:

Pred. No.: 3.04e-116
Score: 943.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6

Length: 1464
Matches: 181
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-201-292-31 (1-1464)

QY 1 GlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTTPaenglu 20
DB 136 GGATTGACCTGACTTCAATTTGGACAAATCAGAAAGTGTGTCACCACTGGAATGAA 195
QY 21 IleTyrPheValGluGlnLeuAlaHisIysPheIleSerProGlnLeuArgMetSer 40

Db 196 ATCTATTACTTTGTGGACAGTTGGCTCAAAATTCATCCAGCCACAGTTGAGAAATGTC 255
Qy 41 PheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGluGln 60
Db 256 TTTATTGTTTCTTCACCCGAGAAACAACCTTAATGAACCTGACAGAAAGACAGAGAACAA 315
Qy 61 IleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMetHis 80
Db 316 ATCCGTCAAGGCTTAAGAAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATGCAAT 375
Qy 81 GluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThr 100
Db 376 GAAGAGATTGAAAGGCGCAGTGAAGATTTATGAAAACAGACAGAGGTTACAGAC 435
Qy 101 AlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSer 120
Db 436 GCCAGGCTCATCTGCTTTGACTGATGAGAACTCCATGAATCTCTTTTCATATCA 495
Qy 121 GluArgGluAlaAsnArgSerArgAspLeuGlyValIleValTyrCysValGlyValLys 140
Db 496 GAAGGAGAGGCTTAATAGCTCTCGAGATCTTGCGCAATTTCTTACTGTGTGGTGA 555
Qy 141 AspPheAsnGlyThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPheProVal 160
Db 556 GATTTCATATGACACACAGCTGCGCCGATTCGCGACAGTAAGATCATCTGTCCCGTG 615
Qy 161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCysIle 180
Db 616 AATGACGGCTTTCAGGCTCTGCAAGGATCATCATCAATTTTGAAGAACTCTGCAATC 675
Qy 181 Glu 181
Db 676 GAA 678

RESULT 14
US-10-201-292-33
; Sequence 33, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 1534
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-33

Alignment Scores:
Pred. No.: 3,26e-116 Length: 1534
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-201-292-33 (1-1534)

Qy 1 GlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisHisIleTPAsnGlu 20
Db 136 GGAATTGACCTGTACTTCAATTTGGACAATAACAGAAAGTGTGCTGCAACCACTGGAATGAA 195
Qy 21 IleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSer 40
Db 196 ATCTATTACTTTGTGGACAGTTGGCTCAAAATTCATCAAGCCACAGTTGAGAAATGTC 255

Qy 41 PheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGluGln 60
Db 256 TTTATTGTTTCTTCACCCGAGAAACAACCTTAATGAACCTGACAGAAAGACAGAGAACAA 315
Qy 61 IleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMetHis 80
Db 316 ATCCGTCAAGGCTTAAGAAACTCCAGAAAGTTCTGCGAGAGAGACACTTACATGCAAT 375
Qy 81 GluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThr 100
Db 376 GAAGAGATTGAAAGGCGCAGTGAAGATTTATGAAAACAGACAGAGGTTACAGAC 435
Qy 101 AlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSer 120
Db 436 GCCAGGCTCATCTGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTCATATCA 495
Qy 121 GluArgGluAlaAsnArgSerArgAspLeuGlyValIleValTyrCysValGlyValLys 140
Db 496 GAAGGAGAGGCTTAATAGCTCTCGAGATCTTGCGCAATTTCTTACTGTGTGGTGA 555
Qy 141 AspPheAsnGlyThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPheProVal 160
Db 556 GATTTCATATGACACACAGCTGCGCCGATTCGCGACAGTAAGATCATCTGTCCCGTG 615
Qy 161 AsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCysIle 180
Db 616 AATGACGGCTTTCAGGCTCTGCAAGGATCATCATCAATTTTGAAGAACTCTGCAATC 675
Qy 181 Glu 181
Db 676 GAA 678

RESULT 15
US-10-201-292-35
; Sequence 35, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 1608
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-35

Alignment Scores:
Pred. No.: 3,51e-116 Length: 1608
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-970-076-2_COPY_42_222 (1-181) x US-10-201-292-35 (1-1608)

Qy 1 GlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisHisIleTPAsnGlu 20
Db 136 GGAATTGACCTGTACTTCAATTTGGACAATAACAGAAAGTGTGCTGCAACCACTGGAATGAA 195
Qy 21 IleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSer 40
Db 196 ATCTATTACTTTGTGGACAGTTGGCTCAAAATTCATCAAGCCACAGTTGAGAAATGTC 255
Qy 41 PheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGluGln 60

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Db      256 TTTATTGTTTCTCCACCCGAGAACACTTAATGAACAGACAGAAACAA 315
Qy      61  |||
Db      316 ATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGCAT 375
Qy      81  |||
Db      376 GAAGGATTGTGAAAGGCCACGTGACACAGATTATTTGAAAACAGACAAAGGTACAGACA 435
Qy      101 AlAservAlIleIleAlLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSer 120
Db      436 GCCAGCGTCATCATTTGCTTGTGATGAGAACTCCATGAAGATCTCTTTCTCATTTCA 495
Qy      121 GluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValLys 140
Db      496 GAGAGGGAGGCTTAATAGGTCCTCGAGATCTTGTCMAATGTTTACTGTGTGTGAGAA 555
Qy      141 AspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPheProVal 160
Db      556 GATTTCATAGACACACAGCTGCCCCGATTCGGAACAGTAAAGATCATGTGTTCCCGTG 615
Qy      161 AsnAspGlyPheGlnAlaLeuGlnGlyTleIleHisSerIleLeuLysSerCysIle 180
Db      616 AATGACGGCTTTCAGGCTCTGCAAGGATCATCCACTCAATTTGAAGAAGTCTGCATC 675
Qy      181 Glu 181
Db      676 GAA 678
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Search completed: December 19, 2005, 02:10:36
Job time : 586.877 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:41:36 ; Search time 146.057 Seconds
(without alignments)
607.449 Million cell updates/sec

Title: US-09-970-076-2_COPY_42_222

Perfect score: 943

Sequence: 1 GFDLYFLIDKSGSVLHMNE.....DGFQALGGIHSILKKSCTE 181

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications NA New -QEMT=fastcap -SUFFIX=rnbn -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62
-TRANS=human0.cdt -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076.@CGN_1_1_675@runat_14122005_11853_21065
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-Fgapop=6 -Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:*

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2: /cg2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cg2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
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6: /cg2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
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8: /cg2_6/prodata/1/pubpna/US11_NEW_PUB.seq2:*
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10: /cg2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	943	100.0	5540	7 US-11-186-284-198	Sequence 198, App
2	132.5	14.1	4740	7 US-11-080-026-3	Sequence 3, Appl
3	126.5	13.4	11447	7 US-11-186-284-25	Sequence 35, Appl
4	122	12.9	2834	6 US-10-750-185-39040	Sequence 39040, A
5	109	11.6	3449	6 US-10-131-826A-293	Sequence 293, App
6	108	11.5	3564	6 US-10-601-368-20	Sequence 19, Appl
7	108	11.5	4858	6 US-10-601-368-19	Sequence 19, Appl
8	107	11.3	1325	6 US-10-750-185-56394	Sequence 56394, A

C	9	105.5	11.2	2501	6 US-10-821-234-182	Sequence 182, App
	10	104	11.0	3564	6 US-10-601-368-2	Sequence 2, Appl
	11	104	11.0	3967	7 US-11-000-463-574	Sequence 574, App
	12	104	11.0	3969	7 US-11-000-463-102	Sequence 102, App
	13	104	11.0	5042	6 US-10-601-368-1	Sequence 1, Appl
	14	103.5	11.0	3175	6 US-10-995-561-464	Sequence 464, App
	15	103.5	11.0	3464	6 US-10-995-561-465	Sequence 465, App
	16	103.5	11.0	3468	6 US-10-995-561-466	Sequence 466, App
	17	101.5	10.8	47572	6 US-10-995-561-13356	Sequence 13356, A
	18	95.5	10.1	3868	6 US-10-995-561-404	Sequence 404, App
	19	95	10.1	3884	6 US-10-601-368-17	Sequence 17, Appl
	20	94	10.0	2773	7 US-11-102-240-33	Sequence 33, Appl
	21	89.5	9.5	1062	7 US-11-137-465-11	Sequence 11, Appl
	22	89.5	9.5	1347	7 US-11-137-465-12	Sequence 12, Appl
C	23	79.5	8.4	3366	6 US-10-467-657-6111	Sequence 6111, App
	24	75	8.0	3435	6 US-10-793-626-3648	Sequence 3648, App
	25	74	7.8	1688	6 US-10-510-386-157	Sequence 157, App
C	26	73.5	7.8	1530	6 US-10-793-626-2879	Sequence 2879, App
	27	73.5	7.8	2996	6 US-10-793-626-3563	Sequence 3563, App
C	28	73.5	7.8	3092	6 US-10-793-626-3559	Sequence 3559, App
	29	73.5	7.8	3900	6 US-10-793-626-4177	Sequence 4177, App
	30	73	7.7	795	6 US-10-793-626-387	Sequence 387, App
	31	73	7.7	876	6 US-10-793-626-2635	Sequence 2635, App
	32	73	7.7	2657	6 US-10-793-626-3472	Sequence 3472, App
C	33	73	7.7	3281	6 US-10-793-626-4324	Sequence 4324, App
	34	73	7.7	3290	6 US-10-793-626-3960	Sequence 3960, App
	35	73	7.7	3633	6 US-10-793-626-4307	Sequence 4307, App
	36	72	7.6	2361	6 US-10-467-626-102	Sequence 102, App
C	37	70	7.4	1305	6 US-10-467-657-5693	Sequence 5693, App
	38	70	7.4	1404	6 US-10-467-657-5695	Sequence 5695, App
	39	70	7.4	96988	7 US-11-117-187-196	Sequence 196, App
	40	69.5	7.4	730	6 US-10-750-185-61019	Sequence 61019, A
	41	69.5	7.4	1467	6 US-10-467-657-7845	Sequence 7845, App
	42	69.5	7.4	1887	6 US-10-467-657-249	Sequence 249, App
	43	69.5	7.4	1887	6 US-10-467-657-3083	Sequence 3083, App
	44	69	7.3	726	6 US-10-467-657-7305	Sequence 7305, App
C	45	69	7.3	786	6 US-10-467-657-7299	Sequence 7299, App

ALIGNMENTS

RESULT 1
US-11-186-284-198
; Sequence 198, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceutical, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MEMO1-029P2RM
; CURRENT APPLICATION NUMBER: US/11186,284
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 5540
; TYPE: DNA

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; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144) ... (1838)
US-11-186-284-198

Alignment Scores:
Pred. No.: 1,156-113 Length: 5540
Score: 943.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

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Db 267 GGATTTGACCTGACTTCACTTTTGGACAATACAGAAAGTGTCTGCACCACTGGAAATGAA 326
QY 21 I1eTyTyPheValGlugluLeuAlAh1bLyPheI1eSerTyroGluLeuA1gMetSer 40
Db 327 ATCTATTACTTTGTGGAAACAGTTGGCTGCACAAATTATCATCGCCACAGTTGAAATGTCC 386
QY 41 PheI1eValPheSerThrArrog1yThrThrIeMetLyLeuThrgluAspArGg1uglu 60
Db 387 TTTATTGTTTCTCCACCCGAGGACAACTTATGAACTGACAGACGACAGAACAA 446
QY 61 I1eArG1ng1yLeugluGluLeugluLyValIeuproG1ygl1AspThrTyMetHis 80
Db 447 ATCCGTCMAAGCCTTGAAAGAACTCCAGAAAGTTCTGCGACGAGAGACCTTACATGCAT 506
QY 81 Glug1yPhegluArgAlaSerGluGluI1eTyTyGluAsnArG1ng1yTyArgThr 100
Db 507 GAAGGATTGAAAGGCGCCAGTGCAGATTATTAAGAAACAGACAGGTAACAGACA 566
QY 101 AlaSerVal1Ie1IeAlaLeuThrArpG1ygluLeuH1eGluAspLeuPhePheTySer 120
Db 567 GCCACGCTATCATCTGCTTGAAGTGAAGAACTCCATGAAATCTCTTTTCTATCA 626
QY 121 GluArG1uAlaAsnArGseArGAspLeuG1yAl1eValTyTyCyVal1G1yVallys 140
Db 627 GAGAGGGAAGGCTRAATAGCTGTGCAGATCTTGCGCAATTTTAACTGTGTGGGTGAAA 666
QY 141 AspPheAsnGluThrgluLeuAlaArg1IeAlaAspSerLyAspHisVal1PheProVal 160
Db 687 GATTTCATGAGACACAGCTGCGCCGAGATGCGGACAGTAAGATCATGTGTTCCCGTG 746
QY 161 AsnAspGlyPheGluAlaLeugluG1y1Ie1IeHisSer1IeLeuLybLySerCyb1Ie 180
Db 747 AATGACGGCTTTCAGGCTCTGCMAAGCATCATCATCAATTTTGAAGAAGTCTGTGATC 806
QY 181 Glu 181
Db 807 GAA 809

RESULT 2
US-11-080-026-3
; Sequence 3, Application US/11080026
; Publication No. US20050260192A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy A.
; APPLICANT: Shimooka, Motomu
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
; TITLE OF INVENTION: DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: CFBF-P02-021
; CURRENT APPLICATION NUMBER: US/11/080,026
; CURRENT FILING DATE: 2005-03-15
; PRIOR APPLICATION NUMBER: 09/945,265
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,700
; PRIOR FILING DATE: 2000-09-01

```

```

; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-080-026-3

Alignment Scores:
Pred. No.:      3.15e-06      Length:      4740
Score:          132.50       Matches:     52
Percent Similarity: 46.97%   Conservative: 41
Best Local Similarity: 26.26% Mismatches:    39
Query Match:     14.05%     Indels:        36
DB:              7          Gaps:         11

US-09-970-076-2_COPY_42_222 (1-181) x US-11-080-026-3 (1-4740)
QY      3 AspleuTyRPreIleLeuAapLySeSerGjSeryValieu--HsiHisTRPaenGlutIle 21
           |||::: |||:::|||||||:::|||||:::|||||:::|||||:::|||||:::
Db      520 GACATTCGCCTTCTTGATTGATGTAGCGCTCTGGTAAGCATCCACATCACTTGGCGGATG 579
QY      22 TytTyRPhyAlaGlutInLeuAlaHlaLysPheHlleSerProGlnLeuArgMetSerPhe 41
           |||::: |||:::|||||||:::|||||:::|||||:::|||||:::|||||:::
Db      580 AAGGAGTTGTGTCTCACT-----GTATGAGCAGCATTAATAAAAGTCCAAA 624
QY      42 IleValPheSerThrArgGlyThrThLeuMetLysLysLeuThrGluAsp----- 57
           ::|||::: |||:::|||||||:::|||||:::|||||:::|||||:::|||||:::
Db      625 ACCTGTGTCTCT-----TTGATGACAGTACTGTGAAGAATTCGCCGATTCAAC 669
QY      58 -----ArgGlnGlnIleArgGlnGlyLeuGlnGluLeuGln 69
           |||::: |||:::|||||||:::|||||:::|||||:::|||||:::|||||:::
Db      670 TTTCACCTTCAAAGAGTTCACAGAACACCCTAACCCAAAGATCATCTGGTAGAACCCATTAAC 729
QY      70 LysValLeuProGlyGlyAspThrTyTMeHiSGlGlyPheGluArgAlaSerGluGln 89
           ::|||::: |||:::|||||||:::|||||:::|||||:::|||||:::|||||:::
Db      730 CAGCTGCCT-----GGGCGGACACACACCGGCCACGGGATCCGCAAAGTGTCAGAGAG 783
QY      90 IleTyTyRGluAsnArgGlnGlyTyArgThrAla---SerValIleIleAlaLeuThr 108
           ::|||::: |||:::|||||||:::|||||:::|||||:::|||||:::|||||:::
Db      784 CTGTTTAACAATCACCAACCGAGCCCGGAAGATGCTTTAAGATCTTAAGATCTTAAGTGCATCAGC 843
QY      109 AspGlyGlyLeuHISgluAerLeuPhePheTySerGlu-----ArgGluAlaAsnArg 126
           |||::: |||:::|||||||:::|||||:::|||||:::|||||:::|||||:::
Db      844 GATGGAGAGAAAGTTGGCGGATCCCTTGGAGATGAGAGATGTCATCCCTGAGGCGACAGAGA 903
QY      127 SerArgAerLeuGlyAlaIleValTyTcySvalAlaGlyValLysAerPheAsnGluThrGln 146
           |||::: |||:::|||||||:::|||||:::|||||:::|||||:::|||||:::
Db      904 GAG-----GAGATCATTCGGTACGTGATATGGGTGGGAGATGCGCTCCGAGTGAAG 954
QY      147 LeuAlaArg-----IleAlaSpSer-----LysAerPHisValPhePro 159
           ::|||::: |||:::|||||||:::|||||:::|||||:::|||||:::|||||:::
Db      955 AAATCCCGCCAAGAGCTTAATACATCGCATCCCAAGCCGCTCGATATCACTTCCAG 1014
QY      160 ValAsnAerGlyPheGlnAlaLeuGlnGlyIleIleHisserIleLeuLysValys 177
           |||::: |||:::|||||||:::|||||:::|||||:::|||||:::|||||:::
Db      1015 GTGATAATAC--TTTGAGGCTGTGAAGACCATTCAGAACAGCTTGGGAGAGAG 1065

RESULT 3
US-11-186-284-25
; Sequence 25, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS AND
; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
```

TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MEM01-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: ParseSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 11447
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(9192)
US-11-186-284-25

Alignment Scores:
Pred. No.: 7,186-05 Length: 11447
Score: 126.50 Matches: 55
Percent Similarity: 48.95% Conservative: 38
Best Local Similarity: 28.95% Mismatches: 74
Query Match: 13.41% Indels: 23
Gaps: 12

US-09-970-076-2_COPY_42_222 (1-181) x US-11-186-284-25 (1-11447)

QY 3 AspleuTyRheleuAerlySerGlySerVal---LeuHisStrPaenglu 21
DB 1318 GATATTCGTTTGGTTGATGCTCTATGATGCGATGCGAATCTTTGTTAAAGTT 1377
QY 22 TyTyTyRheValGluGlnLeuAlaHisLeuPhe---LleSerPro---GlnLeuAArgMet 39
DB 1378 AGAGCCCTTTTGGAGGTTCTGTGTAATAAGTTGAAATTTACCAATAAGGCTCCAGATT 1437
QY 40 SerPheleValPheSerThr-----ArgGlyThrRheuMetLysLeuThrGlu 56
DB 1438 AGCTTGTGCAATACAGCCCGGATCTCATACGATGCTTGTGAAAAAATTCACCAAA 1497
QY 57 AsparGluGlnIleArgGlnGlyLeuGluGlnLeuGlnLysValLeuPro-----Gly 74
DB 1498 GTTGAAGATATAATT-----GAAGCAATAAACAACCTTCCTTACAGAGA 1542
QY 75 GlyAspThrTyRheHisGluGlyPheGluArgAlaSerGluGlnIleTyTyTyGluAsn 94
DB 1543 GGATCTTACAAATACCTGGCAAGCAATGATTAATGTCAGAGAAATAATTTGTGCCATGC 1602
QY 95 ArgGlnGlyTyRArgThr-----AlaSerValIleleAlaLeuThrAspGlyGluLeu 112
DB 1603 AAG---CGATCAAGAACCAATGTCGCAAGATGATTTCTTATCAGCGATGGAAA--- 1556
QY 113 HisGluAspLeuPhePheTyRSerGluArgGlnAlaAsnArgSerArgAspLeuGlyAla 132
DB 1657 TCATCGATGCTTTC-----AGAGATCTCGCGATAAAGTCAGAGAAATCAGATGTT 1707
QY 133 IleValTyRcyValGlyValLysAspPheAsnGluThrGlnLeuAlaArgIleAlaAsp 152
DB 1708 GAATCTTTGCGATGTTGTTGAGAGATGCCGTTGCGCAATTTGAAAGCTATTTGCCCTCT 1767
QY 153 -----SerLysAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGlyIle 170
DB 1768 CTCCTCGACAGACCACTGTTTTCACAGTGGAGAT---TTTATGCTTTTTCAGAGATA 1824
QY 171 IleHisSerIleLeuLysLysSerCysIle 180
DB 1825 TCTTTGAACTCACACAGTCTATCTGCTT 1854

RESULT 4

US-10-750-185-39040/c
Sequence 39040, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 39040
LENGTH: 2834
TYPE: DNA
ORGANISM: Bovine 19866880867914
US-10-750-185-39040

Alignment Scores:
Pred. No.: 3,666-05 Length: 2834
Score: 122.00 Matches: 54
Percent Similarity: 50.00% Conservative: 39
Best Local Similarity: 29.03% Mismatches: 71
Query Match: 12.94% Indels: 24
Gaps: 10

US-09-970-076-2_COPY_42_222 (1-181) x US-10-750-185-39040 (1-2834)

QY 3 AspleuTyRheleuAerlySerGlySerValLeuHisStrPaenglu----- 20
DB 2115 GACATTTACTCTTTTATGACGGGCTTGGCAGTACC-----CACCAAGCAGCTTTCTC 2062
QY 21 ---IleTyTyRheValGluGlnLeuAlaHisLeuPhe---LleSerProGlnLeuArg 38
DB 2061 GCGATGAAGGTGTTCAATGATAGTGAATTAAGATGTTCCAGCTGGACCGAAC---AGA 2005
QY 39 MetSerPheIleVal-PheSerThrArgGlyThrRheuMetLysLeuThrGluAsp 58
DB 2004 GTCCAGTTTGGAGTCCGTTCTGATCGGATGAAGTCAAGTCCCAAGTTTACCTCAGCCAG 1945
QY 58 GlnGlnIleArgGlnGlyLeuGlu-----GlnLeuGlnLysValLeuProG 74
DB 1944 CACTCCAGTGTGGCAGGGGCTTGGAGGTAGCCGTTGACAGCATCCAGCAG---AAGGG 1891
QY 74 YGlyAspThrTyRheHisGluGlyPheGluArgAlaSerGluGlnIleTyTyTyGluAsn 94
DB 1890 AGGGGGACCAAGATGGGTGAGGCCG---GGCAGACATGATCCAGGTCTTTCAGACTC 1834
QY 94 nArgGlnGlyTyRArgThrAlaSerValIleleAlaLeuThrAspGlyGluLeuHisG 114
DB 1833 TGCTCCAGCAA-CGTGCCCTT-CGTATCTCATTTGTTGTACATCGAGCGCAATCTATGGA 1776
QY 114 uAspLeuPhePheTyRSerGluArgGlnAlaAsnArgSerArgAspLeuGlyAlaIleVal 134
DB 1775 CCGCGTG-----GCTGATCTGACAGCGGCTGAGGGGCGCATGAGATCACCAT 1728
QY 134 TyTyCysValGlyValLysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLys 154
DB 1727 TTATGCAAGTTGAGATGAGATGCTAATATGCTGAGCTTCAAGATTTGCTGAA----- 1673
QY 154 AspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerI 174
DB 1672 -GACAGAAATGTTTTTGTGCTGATGAT---TTTATGCTCTTGAAGACATCCACACAGAAAT 1617
QY 174 eleuLysLysSerCys 179

```
Db      1616 GGTACAAGACATCTGT 1601
      :
      :
RESULT 5
US-10-131-826A-293
/ Sequence 293, Application US/10131826A
/ Publication No. US20050245730A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: Deforge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerltsen, Maty B.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3330R1C128
/ CURRENT APPLICATION NUMBER: US/10/131,826A
/ PRIOR FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: 60/049911
/ PRIOR FILING DATE: 1997-06-18
/ PRIOR APPLICATION NUMBER: 60/056974
/ PRIOR FILING DATE: 1997-08-26
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059115
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059117
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059122
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059184
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059352
/ PRIOR FILING DATE: 1997-09-19
/ PRIOR APPLICATION NUMBER: 60/059588
/ PRIOR FILING DATE: 1997-09-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 293
/ LENGTH: 3449
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-131-826A-293

Alignment Scores:
Pred. No.:      0.00259      Length:      3449
Score:          109.00      Matches:      46
Percent Similarity: 46.35%      Conservative: 43
Best Local Similarity: 23.96%      Mismatches: 77
Query Match:    11.56%      Indels:      26
DB:             6          Gaps:      10

US-09-970-076-2_COPY_42_222 (1-181) x US-10-131-826A-293 (1-3449)

QY      3 AspLeuTyrrPheIleuAspIysSerGlySerVal---LeuHisHisTrpAsnGluIle 21
      |||||
Db      372 GACCTGGTTTTCATTCAGACGCTTCGCAGTGCAACACCCATGACTATGCAAAAGGTC 431
      |||||

QY      22 TyrrTyrrPhe---ValGluGlnLeuAlaHisIlySerPheIleSerProGlnLeu---ArgMet 39
      |||||
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```
Db      433 AAGAGTTTCATGCTGACATCTTGCATTTCTTGACATTTGCTCGATGTCACCCGAGTG 491
      |||
QY      40 SerPheIleValPheSerThrArgGlyThrThrLeu-----MetIyValau 54
      :
Db      492 GGCCTGCTCAATAT-----GGCAGACATGTTCAGAAATGATGTCCTCCCAAGAC 542
      :
QY      55 ThrGluAspArgGluGlnIleArgGlnIyLeuGlnIyLeuGlnIyValLeuProGly 74
      :
Db      543 TTCAGAGGAGAGTCCGAGGTGAGCGTGTCTCAAGAGAGATCGGCATGTTCACGGGC 602
      :
QY      75 GlyAspThrTyrrMechIseGluGlyPheGluArgAlaSerGlnIleTyrrGlyuAn 94
      :
Db      603 ACCATGACTGGGCTGGCCATCCAGATAT-----GCCCTGAACATGCCATTTCTCAGAA 653
      :
QY      95 ArgGlnIyTyrrArg-----ThrAlaSerValIleIleAlaLeuThrAsp 109
      :
Db      654 GCAGAGGGGGCCCGCCCTGAGAGGAAATGTGCCAGGGGTCTATATGATCGTCAACAT 713
      :
QY      110 GlyGluLeuHisGluAspLeuPheTyrrSerGluArgGluAlaAsnArgSerArgAsp 129
      :
Db      714 GGGAGACCTCAGAGACTCCGTG-----GCCGAGGTGGCTGTCAAGCAGCGGAC 761
      :
QY      130 LeuGlyAlaIleValTyrrCySerValGlyVal-----LysAspPheAsnGlnIyThrGlnLeu 147
      :
Db      762 ACCGGCATCTATATCTTGCATTTGCTGGCCAGGTAGACTTCAACACCTTGAAGTCC 821
      :
QY      148 AlaArgIleAlaAspSerIyAspHisValPheProValAsnAspIyPheGlnIleAlaLeu 167
      :
Db      822 ATTTGGAGTGAAGCCCATAGAGACATGCTCTTCTTGCGCAAT---TTCAACCGAGATT 878
      :
QY      168 gInGlyIleIleHisSerIleLeuIyIySerCyS 179
      :
Db      879 GAGACGCTGACCTCCGTGTTCCAGAGAGATTGTGC 914
      :

RESULT 6
US-10-601-368-20
/ Sequence 20, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 07334-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 20
/ LENGTH: 3564
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(3564)
US-10-601-368-20

Alignment Scores:
Pred. No.:      0.00369      Length:      3564
Score:          108.00      Matches:      48
Percent Similarity: 38.38%      Conservative: 28
Best Local Similarity: 24.24%      Mismatches: 84
Query Match:    11.45%      Indels:      38
DB:             6          Gaps:      9

US-09-970-076-2_COPY_42_222 (1-181) x US-10-601-368-20 (1-3564)

QY      3 AspLeuTyrrPheIleuAspIysSerGlySerValLeuHisHisTrpAsnGluIleTyrr 22
      |||||
```


Db 490 GACATCGTCATTTGTTAGATGCTCCAGACAGCATC---TACCCCTGGGTGGAGCTCAA 546
Qy 23 TyrPheValIgluInLeuAlaHisIleValPhe---IleSerPro---GlnLeuArgMetSer 40
Db 547 GACTTCTCTCATATCTCTCAAAAAGTTCTACATTTGGCCCCGGCCAGATCCAGGTGGA 606
Qy 41 PheIleValPheSerThrArgGlyThrThrLeuMetIleValLeuProGlyIleArgPheThrTyrMetHis 60
Db 607 ATAGTCCAGATGAGAAAGATGCCGTCATGATTCACCTT---AATGACTACAGGTCT 663
Qy 61 IleArgIleGlnIleuGlnIleuGlnIleValLeuProGlyIleArgPheThrTyrMetHis 80
Db 664 GTAAAGATGTGTGGAGAGCCGCCAGCCACATTTGAGAGAGAGGAGGAGACAGACCCGC 723
Qy 81 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGly 97
Db 724 ACCGCAATTTGGCATTGAATTTGACGCTCGAGGCTTTCCAGAAAGGTGAGAAAGAGG 783
Qy 98 TyrArgThrAlaSerValIleIleIleAlaLeuThrArgPheGlyIleuHisIleGluAsp----- 115
Db 784 GCCAAG-----AAAGTGATGATTTGTCTATCCGACGGGAAATCCACAGACGCCACAG 837
Qy 115 ----- 115
Db 838 CTGGAGAGGTGATCCGGCAGAGCGAGAGACAGTACAGTACGCTGTGGCGCTT 897
Qy 116 LeuPhePheTyrSerGluArgIleuAlaAsnArgSerArgAspLeuGlyAlaIleValTyr 135
Db 898 TTGGGCTACTACAAACCGCAGGGGATCATCCAGAGACTTTCTAAATGAATCAATAC 957
Qy 136 CyeValGlyValIleAsp-----PheAsnGluThrGlnIleuAlaArgIleAla 151
Db 958 ATGCCACGACCCCTGACAGACACACTTCTTCAACGTCAACAGTACAGTACGCGCCCTG--- 1014
Qy 152 AspSerIleAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGly 169
Db 1015 -----AAGGACATTTGTTGATGCCCTTGGGACAGATCTTCACTTGAAAGGC 1062

RESULT 7

US-10-601-368-19
; Sequence 19, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lota, Jose M.
; FILE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; TITLE REFERENCE: 07334-27501
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 4858
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (28)...(3591)
; US-10-601-368-19

Alignment Scores:

Pred. No.: 0.00581
Score: 108.00
Percent Similarity: 38.38%
Best Local Similarity: 24.24%
Query Match: 11.45%
DB: 6

Length: 4858
Matches: 48
Conservative: 28
Mismatch: 84
Indels: 38

US-09-970-076-2_COPY_42_222 (1-181) x US-10-601-368-19 (1-4858)

Qy 3 AspLeuTyrPheIleLeuAspIleSerGlySerValLeuHisIleThrPheAsnGluIleTyr 22
Db 517 GACATCGTCATTTGTTAGATGCTCCAGACAGCATC---TACCCCTGGGTGGAGCTCAA 573
Qy 23 TyrPheValIgluInLeuAlaHisIleValPhe---IleSerPro---GlnLeuArgMetSer 40
Db 574 GACTTCTCTCATATCTCTCAAAAAGTTCTACATTTGGCCCCGGCCAGATCCAGGTGGA 633
Qy 41 PheIleValPheSerThrArgGlyThrThrLeuMetIleValLeuProGlyIleArgPheThrTyrMetHis 60
Db 634 ATAGTCCAGATGAGAAAGATGCCGTCATGATTCACCTT---AATGACTACAGGTCT 690
Qy 61 IleArgIleGlnIleuGlnIleuGlnIleValLeuProGlyIleArgPheThrTyrMetHis 80
Db 691 GTAAAGATGTGTGGAGAGCCGCCAGCCACATTTGAGAGAGAGGAGGAGACAGACCCGC 750
Qy 81 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGly 97
Db 751 ACCGCAATTTGGCATTGAATTTGACGCTCGAGGCTTTCCAGAAAGGTGAGAAAGAGG 810
Qy 98 TyrArgThrAlaSerValIleIleIleAlaLeuThrArgPheGlyIleuHisIleGluAsp----- 115
Db 811 GCCAAG-----AAAGTGATGATTTGTCTATCCGACGGGAAATCCACAGACGCCACAG 864
Qy 115 ----- 115
Db 865 CTGGAGAGGTGATCCGGCAGAGCGAGAGACAGTACAGTACGCTGTGGCGCTT 924
Qy 116 LeuPhePheTyrSerGluArgIleuAlaAsnArgSerArgAspLeuGlyAlaIleValTyr 135
Db 925 TTGGGCTACTACAAACCGCAGGGGATCATCCAGAGACTTTCTAAATGAATCAATAC 984
Qy 136 CyeValGlyValIleAsp-----PheAsnGluThrGlnIleuAlaArgIleAla 151
Db 985 ATGCCACGACCCCTGACAGACACACTTCTTCAACGTCAACAGTACAGTACGCGCCCTG--- 1041
Qy 152 AspSerIleAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGly 169
Db 1042 -----AAGGACATTTGTTGATGCCCTTGGGACAGATCTTCACTTGAAAGGC 1089

RESULT 8

US-10-750-185-56394
; Sequence 56394, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; FILE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; TITLE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56394
; LENGTH: 1325
; TYPE: DNA
; ORGANISM: Bovine
; US-10-750-185-56394

Alignment Scores:

Pred. No.: 0.00117
Score: 107.00
Percent Similarity: 46.35%
Best Local Similarity: 23.44%
Query Match: 11.35%
DB: 26

Length: 1325
Matches: 45
Conservative: 44
Mismatch: 77
Indels: 26

US-09-970-076-2_COPY_42_222 (1-181) x US-10-601-368-19 (1-4858)

DB: 6 Gaps: 10
US-09-970-076-2_COPY_42_222 (1-181) x US-10-750-185-56394 (1-1325)
QY 3 AapleuTyRPhelIleuAaplySerGlySerVal-----LeuHisStrpAnGluIle 21
DB 483 GACGTGATCTTATTCATTCAGACATCCAGCGGTCAACACCCAGCATACGCAAGAGTC 542
QY 22 TyTyrPhe---ValGluGlnLeuAlaIlePhePheIleSerProGlnLeu---ArgMet 39
DB 543 AAGAGATTCATTTGGACATCTTCAGATCTTTGGACATTTGGCCCTGACGTCACCCGTG 602
QY 40 SerPheIleValPheSerThrArgGlyThrThrLeu-----MetLysLeu 54
DB 603 GGTGTGCTCAGATAT-----GGCAGCAGCGGTCAAGACAGATTCTCCCTCAAGACC 653
QY 55 ThrGluAapArgGluGlnIleArgGlnGlyLeuGluGlnLeuGlnLysValIleProGly 74
DB 654 TTCAGAGGAAGTCCGAGGTGAGCGGTCAAGAGATGCGGCACTGTCCACGCGGC 713
QY 75 GlyAapThrTyRMeHisGluGlyPheGluArgAlaSerGluGlnIleTyTyrGluAan 94
DB 714 ACCATGCGGGGCTGGCCATCCAGTAC-----GCCCTGAACATCGCTTCGGAA 764
QY 95 ArgGlnGlyTyRArg-----ThrAlaSerValIleIleAlaLeuThrAap 109
DB 765 GCAGAGGGGCGCGCCCTGAGGAGAGATGTGCTCGGTCAATGATCGTACGTGAT 824
QY 110 GlyGluLeuHisGluAapLeuPhePheTyRSerGluArgGluAlaAanArgSerArgAap 129
DB 825 GGGAGGCGCCAGACCTCGGTG-----GCCAGGTGCGCCGCAAGGCCCGGAGC 872
QY 130 LeuGlyAlaIleValTyRcyValGlyVal-----LysAapPheAanGluThrGlnLeu 147
DB 873 ACAGGCACTCTGATCTTTCGATCGTGTGGCGCCAGGTGACATTCAACAGCTGAAGGCC 932
QY 148 AlaArgIleAlaAapSerLysAapHisValPheProValAanAapGlyPheGlnAlaLeu 167
DB 933 ATGGAGGAGGAGCGCCAGAGACACATGCTTCTGTGGCCCAAC---TTCAGCCAGATT 989
QY 168 GlnGlyIleIleHisSerIleLeuLysSerGly 179
DB 990 GAGACGCTGACCTCAGTGTTCAGAGAAAGTTGTGC 1025
RESULT 9
US-10-821-234-182/c
; Sequence 182, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Steache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_SEQ_genes Version 1.0
; SEQ ID NO 182
; LENGTH: 2501
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-182
Alignment Scores:
Pred. No.: 0.00471 Length: 2501
Score: 105.50 Matches: 48
Percent Similarity: 43.40% Conservative: 44
Best Local Similarity: 22.64% Mismatches: 75
Query Match: 11.19% Indels: 45

DB: 6 Gaps: 10
US-09-970-076-2_COPY_42_222 (1-181) x US-10-821-234-182 (1-2501)
QY 3 AapleuTyRPhelIleuAaplySerGlySerVal-----LeuHisHis 17
DB 1550 AACATCTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1491
QY 18 TrpAanGluIleTyTyrPheValGluGlnLeuAlaIleLysPheIleSerProGlnLeu 37
DB 1490 AAAAGTCTTGTGATCACTTAATGAAAGTGGAGAGTAAAGTGAAGCA----- 1437
QY 38 ArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGlu--- 56
DB 1436 AGATATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1377
QY 57 -----AapArgGluGlnIleArgGlnGlyLeuGluGlnLeu-----Gln 69
DB 1376 GACAGCATTAAGCAGATCGGTCAAGAGCTCAATGAAATCAATTAATGAAAGCAC 1317
QY 70 LysValIleuProGlyGlyAapThrTyRMeHisGluGlyPheGluArgAlaSerGluGln 89
DB 1316 AAGTTGAAGTCAGGAGCTAACAC-----AAGAGGCCCTCCAGGCA 1275
QY 90 IleTyTyrGluAanArg-----GlnGlyTyR---ArgThrAla 101
DB 1274 GTGTACAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1215
QY 102 SerValIleIleAlaLeuThrAapGly----- 110
DB 1214 CATGTATATATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1155
QY 111 -----GluLeuHisGluAapLeuPhePheTyRSerGluArgGluAlaAanArgSerArg 128
DB 1154 ATTGAGAGATCCGGGACTTGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 1095
QY 129 AapLeuGlyAlaIleValTyRcyValGly-----ValLysAapPheAanGluThrGln 146
DB 1094 TATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1035
QY 147 LeuAlaArgIleAlaAapSerLysAapHisValPheProValAanAapGlyPheGlnAla 166
DB 1034 TTGGCTTCAAGAAAGACATGAGCAACATGTGTTCAAAAGTCAAGAT---ATGAAAC 978
QY 167 LeuGlnGlyIleIleHisSerIleLeuLysSerGly 178
DB 977 CTGGAAGATGTTTCTACCAATGATGATGATGATGATGATGATGATGATGATGATGAT 942
RESULT 10
US-10-601-368-2
; Sequence 2, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3564
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3564)
US-10-601-368-2

Alignment Scores:
Pred. No.: 0.0125 Length: 3564
Score: 104.00 Matches: 48
Percent Similarity: 38.38% Conservative: 28
Best Local Similarity: 24.24% Mismatches: 84
Query Match: 11.03% Indels: 38
DB: 6 Gaps: 9

US-09-970-076-2_COPY_42_222 (1-181) x US-10-601-368-2 (1-3564)

QY 3 AspLeuTyrPheIleValLeuAAspLysSerGlySerValLeuH18TrpAengIuIeTyr 22
DB 490 GACATGCTCATTTGCTCGATGAGTGGCTCCAGACGATC---TACCCCTGGGGAGGTTCCAG 546
QY 23 TyrPheValGluGlnLeuAlaHisIlePhe---IleSerPro---GlnLeuAArgMetSer 40
DB 547 CACTTCTCATCAACACCTCGAAGAAAGTTTACATGGCCAGGCGAGATCCAGTTTGA 606
QY 41 PheIleValPheSerThrArgGlyThrThreuMetLysLeuThrGluAArgGluGln 60
DB 607 GTTGTGAGTATGCGCAAGAGTGGTGATGATTCACCTC---AAGCACTACAGGCT 663
QY 61 IleArgGlnGlyLeuGlnGluLeuValLeuProGlyIleAspThrTyrMetHis 80
DB 664 GTAAAGATGTGTGAGAGTGGCCAGCCAGCATTTAGACAGAGAGAGAGACAGACCCGG 723
QY 81 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyrGluAAspArgGlnGly 97
DB 724 ACGGCATTGTCATTTGATTTGACAGCTCAGAGGCTTTCCAGAAAGGTGGAGAAAGGA 783
QY 98 TyrArgThrAlaSerValIleIleIleAlaLeuThrAspGlyGluLeuHisGluAAsp 115
DB 784 GCCAAG-----AAGGTGATGATTTGATCATCAGATGGGAGTCCACAGCCAGAC 837
QY 115 ----- 115
DB 838 CTGAGAGAGGTGATCCAGCAAGAGAAAGACAGACGTAACAAGATATGGCGTGGCCCTC 897
QY 116 LeuPhePheTyrSerGluArgGluAlaAspArgSerArgAspLeuGlyAlaIleValTyr 135
DB 898 CTGGGCTACTACAAACCGAGGGGATCATTCAGAAACCTTTCTTAATGAATCAATAC 957
QY 136 CysValGlyValIleAsp-----PheAsnGluThrGlnLeuAlaArgIleAla 151
DB 958 ATGCCAGATGACCTGATGACAGACACTTCTTCAATGTCATGATGAGGCTGCTTG--- 1014
QY 152 AspSerLysAspHisValPheProValAspAspGlyPheGlnAlaLeuGlnGly 169
DB 1015 -----AAGGACATTGTGATGCTGCTGGGGAGACAGATCTTCAAGCTGGAAGGC 1062

RESULT 11
US-11-000-463-574
; Sequence 574, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhilwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dimaenac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08

PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 574
; LENGTH: 3967
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-000-463-574

Alignment Scores:
Pred. No.: 0.0147 Length: 3967
Score: 104.00 Matches: 48
Percent Similarity: 38.38% Conservative: 28
Best Local Similarity: 24.24% Mismatches: 84
Query Match: 11.03% Indels: 38
DB: 7 Gaps: 9

US-09-970-076-2_COPY_42_222 (1-181) x US-11-000-463-574 (1-3967)

QY 3 AspLeuTyrPheIleValLeuAAspLysSerGlySerValLeuH18TrpAengIuIeTyr 22
DB 539 GACATGCTCATTTGCTCGATGAGTGGCTCCAGACGATC---TACCCCTGGGGAGGTTCCAG 595
QY 23 TyrPheValGluGlnLeuAlaHisIlePhe---IleSerPro---GlnLeuAArgMetSer 40
DB 596 CACTTCTCATCAACACCTCGAAGAAAGTTTACATTTAGCCAGGCGAGATCCAGTTTGA 655
QY 41 PheIleValPheSerThrArgGlyThrThreuMetLysLeuThrGluAArgGluGln 60
DB 656 GTTGTGAGTATGCGCAAGAGTGGTGATGATTCACCTC---AAGCACTACAGGCT 712
QY 61 IleArgGlnGlyLeuGlnGluLeuValLeuProGlyIleAspThrTyrMetHis 80
DB 713 GTAAAGATGTGTGAGAGTGGCCAGCCAGCATTTAGACAGAGAGAGAGACAGACCCGG 772
QY 81 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyrGluAAspArgGlnGly 97
DB 773 ACGGCATTGTCATTTGATTTGACAGCTCAGAGGCTTTCCAGAAAGGTGGAGAAAGGA 832
QY 98 TyrArgThrAlaSerValIleIleIleAlaLeuThrAspGlyGluLeuHisGluAAsp 115
DB 833 GCCAAG-----AAGGTGATGATTTGATCATCAGATGGGAGTCCACAGACAGCCAGAC 886
QY 115 ----- 115
DB 887 CTGAGAGAGGTGATCCAGCAAGCGAAAGACAGACGTAACAAGATATGGCGTGGCCCTC 946
QY 116 LeuPhePheTyrSerGluArgGluAlaAspArgSerArgAspLeuGlyAlaIleValTyr 135
DB 947 CTGGGCTACTACAAACCGAGGGGATCATTCAGAAACCTTTCTTAATGAATCAATAC 1006
QY 136 CysValGlyValIleAsp-----PheAsnGluThrGlnLeuAlaArgIleAla 151
DB 1007 ATGCCAGATGACCTGATGACAGACACTTCTTCAATGTCATGATGAGGCTGCTTG--- 1063
QY 152 AspSerLysAspHisValPheProValAspAspGlyPheGlnAlaLeuGlnGly 169
DB 1064 -----AAGGACATTGTGATGCTGCTGGGGAGACAGATCTTCAAGCTGGAAGGC 1111

RESULT 12
US-11-000-463-102
; Sequence 102, Application US/11000463


```
Dh 850 ACCGCAATTGGCATGTGAATTTCAGCGCTTCAGAGGCTTTCAGAAAGGTGGAGAAAGGA 909
Qy 98 TyArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAsp----- 115
Dh 910 GCCAAG-----AAGTGATGATTGTTCATCAGATGGAGTCCCGACGACAGCCAGAC 963
Qy 115 ----- 115
Dh 964 CTGGAGAGGTGATTCAGCAAGAGAAAGACAGCACTAACAAGATATGCGGTGGCCGTC 1023
Qy 116 LeuPhePheTySerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyr 135
Dh 1024 CTGGGCTACTACCAACCGCGGGGATCATCCAGAACTTTCTCAATGAATCAATCATAC 1083
Qy 136 CyValaGlyValIleAsp-----PheAsnGluThrGlnLeuAlaArgIleAla 151
Dh 1084 ATGCCCAAGTACCCCTGATGACAAAGCAACTCTTCAATCTCACTGATGAGCTGCGCTTG-- 1140
Qy 152 AspSerLysAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGly 169
Dh 1141 -----AAGCACTATTGTGATGCCCTGGGGAGACAGATCTTCAGCCCTGAAGGC 1188

RESULT 14
US-10-995-561-464
; Sequence 464, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 464
; LENGTH: 3175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-464

Alignment Scores:
Pred. No.: 0.0123 Length: 3175
Score: 103.50 Matches: 49
Percent Similarity: 40.00% Conservative: 37
Best Local Similarity: 22.79% Mismatches: 84
Query Match: 10.98% Indels: 45
DB: Gaps: 9

US-09-970-076-2_COPY_42_222 (1-181) x US-10-995-561-464 (1-3175)
Qy 4 LeuTyPheIleLeuAspLysSerGlySerVal----- 14
Dh 243 GTGTACTCTGCTGTCGACACTCGAAGAGGTCAACATGACATGCCCGCCAGCATCTG 302
Qy 15 LeuHisIleTyrAsnGlu-----IleTyrTyrPheValGlnGluLeuAlaHisLysPheIle 33
Dh 303 CTCTCCACATGAAGAGTTCGTGCGCGACGTTTCATCAGCGCTGCGAAGAGAGTTCTAC 362
Qy 34 SerProGlnLeuArgMetSerPhe-----IleValPheSerThrArgGlyThr 49
Dh 363 CTGAGCAGAGGTGGCGCTGAGCTGGCGCTTAGCGCGGCTGCACTTCTGACCGAGTGGAG 422
Qy 50 ThrLeuMetLysLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGlnGluLeuGln 69
Dh 423 GTGTTCAGCCCAACCGGCGAGCAACCGGCGCTCTTCATCAAGAACTGCGAGGGCATCAGC 482
Qy 70 LysValLeuProGlyLysAspThrTyrMetHisGluGlyPheGluArgAlaSerGluGln 89
Dh 483 TCCTTCGCGCGCGG-----ACCTTCACCGACTGCGCGCTGCGCAACATGACGAGGACAG 536
Qy 90 IleTyTyrGluMetArgGlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAsp 109
```

```
Dh 537 ATCCGGCAGGACCGCAGCAAGGCG-----ACCGTCACCTTCCCGCGGTCTATCACCGAC 590
Qy 110 GlyGluLeuHisGluLysPhePheTySerGluArgGluAlaAsnArgSerArgAsp 129
Dh 591 GCGCAGGTACACCGCGAGCCCTTGGCGGGGATCATCAGCTGAGCGCGAGCGGCGCGAG 650
Qy 130 LeuGlyAlaIleValTyrCyVal-----GlyValLys 140
Dh 651 GAGGCAATCCGCGCTTTCGCGCTGGCGCCCAACCAAGACTTGAAGAGCAGGCGCTGGCG 710
Qy 141 AspPheAsnGluThr-----GlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 158
Dh 711 GACATCGCCAGCAGCGCGCGAGCTCTACCGC-----AACGACTACGCGCAC 758
Qy 159 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu----- 175
Dh 759 ATGCTGCTGATCTCCACCGAGATCTACAGACCATCAACCGATCATCAAGATCATG 818
Qy 176 -----LysLysSerCysIleGlu 181
Dh 819 AAACAGAAAGCTTACGAGAGAGTCTACAGGTAGCTGCTGGAA 863

RESULT 15
US-10-995-561-465
; Sequence 465, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 3464
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-465

Alignment Scores:
Pred. No.: 0.014 Length: 3464
Score: 103.50 Matches: 49
Percent Similarity: 40.00% Conservative: 37
Best Local Similarity: 22.79% Mismatches: 84
Query Match: 10.98% Indels: 45
DB: Gaps: 9

US-09-970-076-2_COPY_42_222 (1-181) x US-10-995-561-465 (1-3464)
Qy 4 LeuTyPheIleLeuAspLysSerGlySerVal----- 14
Dh 243 GTGTACTCTGCTGTCGACACTCGAAGAGGTCAACATGACATGCCCGCCAGCATCTG 302
Qy 15 LeuHisIleTyrAsnGlu-----IleTyrTyrPheValGlnGluLeuAlaHisLysPheIle 33
Dh 303 CTCTCCACATGAAGAGTTCGTGCGCGACGTTTCATCAGCGCTGCGAAGAGAGTTCTAC 362
Qy 34 SerProGlnLeuArgMetSerPhe-----IleValPheSerThrArgGlyThr 49
Dh 363 CTGAGCAGAGGTGGCGCTGAGCTGGCGCTTAGCGCGGCTGCACTTCTGACCGAGTGGAG 422
Qy 50 ThrLeuMetLysLeuThrGluAspArgGluGlnIleArgGlnGlyLeuGlnGluLeuGln 69
Dh 423 GTGTTCAGCCCAACCGGCGAGCAACCGGCGCTCTTCATCAAGAACTGCGAGGGCATCAGC 482
Qy 70 LysValLeuProGlyLysAspThrTyrMetHisGluGlyPheGluArgAlaSerGluGln 89
Dh 483 TCCTTCGCGCGCGG-----ACCTTCACCGACTGCGCGCTGCGCAACATGACGAGGACAG 536
```

```
QY      90  IletYrTyrGluAsnArgGlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAsp 109
      |||  ::|  ::|  |||  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||
Db      537  ATCCGGCAGGACCGCGCAGCAAGGCG-----ACCGTCGACTTCGCGGTGGTCATCACCGAC 590
QY      110  GlyGluLeuHisGluAsnLeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAsp 129
      |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      591  GGCACAGTCACCGCGCAGCCCGCTGCGGGGCATCAAGCTGCAGCGCGCGCGCGAG 650
QY      130  LeuGlyAlaIleValTyrCysVal-----GlyValLys 140
      |||  |||  ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      651  GAGGGCATTCGGGCTCTTCGCGCGTGGCCCCCAACCAAGAACTGAAGAGCAGGGCTGCGG 710
QY      141  AspPheAsnGluThr-----GlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 158
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      711  GACATCGCCGCGACGCGCGCAGAGCTCTACCGC-----AACGACTAGCGCACCC 758
QY      159  ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu----- 175
      ::|  ::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      759  ATGCTGCCTGACTCCACCGAGATCRAACGAGACACCATCAACCGCATCATCAAGTCATG 818
QY      176  -----LysLysSerCysIleGlu 181
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      819  AAACACGAGAGCTTACGAGAGTCTTACAGAGTGAAGTGTGCTGGAA 863
```

Search completed: December 19, 2005, 02:30:57
Job time : 162.057 secs


```
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-889-37

Query Match      15.4%; Score 138.5; DB 1; Length 1151;
Best Local Similarity 28.3%; Pred. No. 7.5e-07;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;

QY 1 DLYFLIDKSGSV-LHMHNEIYFVEQLAHKFI SPQLMSFIVFSTGTTLMKLT----- 54
DB 142 DIAFLIDGSGSINQRFQAKMDPVKALMGEPASTSTLSLMQYSNLIKHTFTTERKNIL 201
QY 55 DREQIRQGLEELQKVLPGSDTYMHGFERASEQIYENRQGYRTA-SVIALTDGELHED 113
DB 202 DPQSLVDPIVQLQ-----GLTYTATGIRVMEELFHSKNGSRKSAKKILLVITDGQKYRD 256
QY 114 LFYFSE--REANSRDLGAIYVCVGYKD-FNE-TQLARI-----ADSKHVPFVNDGFOA 164
DB 257 PLEYSDVIPADAKA---GIIRYALGVDAFOEPTALKELNTIGSAPPODHVFQVGN-FAA 312
QY 165 LQGI 168
DB 313 LRSL 316

RESULT 3
US-08-485-618-37
Sequence 37, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunitc
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
```

```
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-37

Query Match      15.4%; Score 138.5; DB 1; Length 1151;
Best Local Similarity 28.3%; Pred. No. 7.5e-07;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;

QY 1 DLYFLIDKSGSV-LHMHNEIYFVEQLAHKFI SPQLMSFIVFSTGTTLMKLT----- 54
DB 142 DIAFLIDGSGSINQRFQAKMDPVKALMGEPASTSTLSLMQYSNLIKHTFTTERKNIL 201
QY 55 DREQIRQGLEELQKVLPGSDTYMHGFERASEQIYENRQGYRTA-SVIALTDGELHED 113
DB 202 DPQSLVDPIVQLQ-----GLTYTATGIRVMEELFHSKNGSRKSAKKILLVITDGQKYRD 256
QY 114 LFYFSE--REANSRDLGAIYVCVGYKD-FNE-TQLARI-----ADSKHVPFVNDGFOA 164
DB 257 PLEYSDVIPADAKA---GIIRYALGVDAFOEPTALKELNTIGSAPPODHVFQVGN-FAA 312
QY 165 LQGI 168
DB 313 LRSL 316

RESULT 4
US-08-362-652-37
Sequence 37, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunitc
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
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/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32391
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1151 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-362-652-37
```

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Query Match 15.4%; Score 138.5; DB 1; Length 1151;
Best Local Similarity 28.3%; Pred. No. 7.5e-07;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;
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QY 1 DLYFILDKSGSV-LHHMNEIYFVEQLAHKFIQPLRMSTIVSTRCTTLMKLT----- 54
DB 142 DIAFLIDSGSINORDPAQMKDFKALMGFASTSTLFSIMQYSNLIKHTFTFEFNIL 201
QY 55 DRQIRQGLBELQKVLPGCDTYMHEGFERASBOIYYENRGYRTA-SVIALTDEGELHED 113
DB 202 DPGSLVDPIVQLQ-----GLTYTATGIRTYMELFHSKNSRKSAAKILLVITDGOQYRD 256
QY 114 LFFYSE--REANRSRDGAIVYCVGYKD-FNE-TOLARI-----ADSKDHVPYNDGFOA 164
DB 257 PLEYSDVTPADRA---GIIRVAIGVDARFQEPFLAKELNTIGSAPPDHVFVKGN-FAA 312
QY 165 LQGI 168
DB 313 LRSI 316
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RESULT 5
US-08-605-672-37
/ Sequence 37, Application US/08605672
/ Patent No. 5817515
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/605,672
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1151 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-605-672-37
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```
Query Match 15.4%; Score 138.5; DB 1; Length 1151;
Best Local Similarity 28.3%; Pred. No. 7.5e-07;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;
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```
QY 1 DLYFILDKSGSV-LHHMNEIYFVEQLAHKFIQPLRMSTIVSTRCTTLMKLT----- 54
DB 142 DIAFLIDSGSINORDPAQMKDFKALMGFASTSTLFSIMQYSNLIKHTFTFEFNIL 201
QY 55 DRQIRQGLBELQKVLPGCDTYMHEGFERASBOIYYENRGYRTA-SVIALTDEGELHED 113
DB 202 DPGSLVDPIVQLQ-----GLTYTATGIRTYMELFHSKNSRKSAAKILLVITDGOQYRD 256
QY 114 LFFYSE--REANRSRDGAIVYCVGYKD-FNE-TOLARI-----ADSKDHVPYNDGFOA 164
DB 257 PLEYSDVTPADRA---GIIRVAIGVDARFQEPFLAKELNTIGSAPPDHVFVKGN-FAA 312
QY 165 LQGI 168
DB 313 LRSI 316
```

```
RESULT 6
US-08-482-293A-37
/ Sequence 37, Application US/08482293A
/ Patent No. 5831029
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vieren, Monica
/ TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 103
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/482,293A
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ APPLICATION NUMBER: US 08/286,889
```

```

FILING DATE: 5-AUG-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-37

Query Match
Best Local Similarity 15.4%; Score 138.5; DB 1; Length 1151;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;

1 DLYFIIDKSGSV-LHHNNEIYFVEQLAHKFI SPQLRMSFIVFSTRGTTLMKLT-----54
142 DIAFLIDSGSINORDPAQKDFV KALMGFEFASTSTLFSLMQYSNLIKHTFTTEFNKIL 201
QY 55 DREQIRQGLEELQKVLPGSDTYMHGEFERASEQIYYENRGYRTA-SVIALTDGELHED 113
DB 202 DPQSLVDPIVQLQ-----GLTYATGIRTVMEELFHSKNGSRKSAKKILLVITDGGKYRD 256
QY 114 LFFYSE--REANSRDLGAIYVCVGVKD-PNE-TOLARI-----ADSKDHVPFVNDGFOA 164
DB 257 PLEYSDVIPAADKA---GIIRYAIGVGDAFOEPFALKELNTIGSAPPQDHVFVGN-FAA 312
QY 165 LQGI 168
DB 313 LRSI 316

RESULT 7
US-08-943-363-37
Sequence 37, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
```

```

APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-37

Query Match
Best Local Similarity 15.4%; Score 138.5; DB 1; Length 1151;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;

1 DLYFIIDKSGSV-LHHNNEIYFVEQLAHKFI SPQLRMSFIVFSTRGTTLMKLT-----54
142 DIAFLIDSGSINORDPAQKDFV KALMGFEFASTSTLFSLMQYSNLIKHTFTTEFNKIL 201
QY 55 DREQIRQGLEELQKVLPGSDTYMHGEFERASEQIYYENRGYRTA-SVIALTDGELHED 113
DB 202 DPQSLVDPIVQLQ-----GLTYATGIRTVMEELFHSKNGSRKSAKKILLVITDGGKYRD 256
QY 114 LFFYSE--REANSRDLGAIYVCVGVKD-PNE-TOLARI-----ADSKDHVPFVNDGFOA 164
DB 257 PLEYSDVIPAADKA---GIIRYAIGVGDAFOEPFALKELNTIGSAPPQDHVFVGN-FAA 312
QY 165 LQGI 168
DB 313 LRSI 316

RESULT 8
US-09-193-043-37
Sequence 37, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 37
LENGTH: 1151
TYPE: PRT
ORGANISM: Rattus rattus
US-09-193-043-37

Query Match
Best Local Similarity 15.4%; Score 138.5; DB 2; Length 1151;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;

1 DLYFIIDKSGSV-LHHNNEIYFVEQLAHKFI SPQLRMSFIVFSTRGTTLMKLT-----54
142 DIAFLIDSGSINORDPAQKDFV KALMGFEFASTSTLFSLMQYSNLIKHTFTTEFNKIL 201
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Oy      55 DREGIRGGLLELOKVLPGGDVTYMHGFEERASPOIYENRQGYRTA-SVIALTDGELHED 113
Db      202 DPGSLVDPRVLOQ-----GLTYTANGIRTWMEELFSSKNGSRKSAAKILLVITDGGKTRD 256
Oy      114 LFFYEE--REANRSRDLGAIIVYCVGVKD-FNE-TOLARI-----ADSKDHVEPVNDGPOA 164
Db      257 PLEYSDVLPADAKA---GIIRYAIGVGDAFOEPTALKEINTIGSAPPDHVFKNV-FDA 312
Oy      165 LOGI 168
Db      313 LRSI 316

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RESULT 9
US-09-688-307A-37
Sequence 37. Application US/09688307A
Patent No. 6432404
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 6432404el Human Beta-2
FILE REFERENCE: 27866/36646
CURRENT APPLICATION NUMBER: US/09/688,307A
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 08/605,672
PRIOR FILING DATE: 1996-02-22
PRIOR APPLICATION NUMBER: 08/173,497
PRIOR FILING DATE: 1993-12-23
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR FILING DATE: 1994-08-05
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR FILING DATE: 1994-12-21
PRIOR APPLICATION NUMBER: 08/943,363
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
LENGTH: 1151
TYPE: PRT
ORGANISM: Rattus rattus
FEATURE:
NAME/KEY: misc_feature
LOCATION: 361
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 464
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 486
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 506
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 1117
OTHER INFORMATION: Xaa = any or unknown amino acid
NAME/KEY: misc_feature
LOCATION: 1118
OTHER INFORMATION: Xaa = any or unknown amino acid
US-09-688-307A-37

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[illegible]

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Db      202  DPGSLVDPITVLQ-----GLFTYTAGIRTWEELEPHSKNGSKRSKAKILLVITIDGQKYRD 256
OY      114  LFFPSE--REANRKRDLGAIYVCVGVK-D-FNE-TOLARI-----ADSKHVFPPVNDGFOA 164
Db      257  PLEPSDVIPADKA---GIRYAIYGVDAFOEPALTKELINTIGSAPPOHVEKVN-FAA 312
OY      165  LOGI 168
Db      313  LRST 316

```

```

RESULT 10
US-09-350-259-37
; Sequence 37, Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6620915e1 Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/153,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatencIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 1151
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-350-259-37

```

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Query Match          15.4%; Score 138.5; DB 2; Length 1151;
Best Local Similarity 28.3%; Pred. No. 7.5e-07;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;

QY      1 DLYTLKSGSV-LHMNNEYYPYEQLAHKFISQQLMSFVSTRTGTLTKLTE----- 54
Db      142 DIALLDGGSSINORDPAOMKDFKALMGEPASTSTLSLMQYSNLLKTHFTFEPKNIL 201
QY      55 DREQIROGLEELQKVLPGCDTYMHEGFERASEQIYENRQGYRA-SVIALTDGELHED 113
Db      202 DPGSLVDPIYQLQ-----GLTYTATGIRTWMBELFHSKNSRKSAKKILLVITDGQKRRD 256
QY      114 LFPFSE--REANSRDLGALVYCYGVKD-FNE-TQLARI-----ADSKDHVFPNDGFOA 164
Db      257 PLEPSDVIIPADKX--GIIRYALGVDAFOEPTALKELTGSGAPQDHFVKGN-FAA 312
QY      165 LQGI 168
Db      313 LRSI 316

RESULT 11
US-08-485-618-55
Sequence 55, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 5728533bel Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

```

```

; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,618
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32797
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1161 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-618-55

Query Match      15.4%; Score 138.5; DB 1; Length 1161;
Best Local Similarity 28.3%; Pred. No. 7.6e-07;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;

QY 1 DLYFIDKSGSV-LHMHNEIYFVEQLAHKFIISQURMSFIVSTRGTTLMKLT----- 54
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 152 DIFFLIDSGSINQRPFAQMKDFVKALMGEPASTSTLFSLMQVSNLTKHTFTTEFNIL 211
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 55 DREQIRQGLELQKVLPGSDTYMHGEPERASEQIYENROGYRTA-SVIALTDGELHED 113
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 212 DPQSLVDPIYQLQ-----GLTYTATGIRTYMELFHSKNGSRKSAKKILLIVTDGQKYRD 266
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 114 LFYFSE--REANRSRLGAIYVCVYKD-FNE-TQLARI-----ADSKHVFVNNGFOA 164
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 267 PLEYSVDVIPADKA--GIIRYAIQVGDAFOEPTALKELNTIGSAPPQDHVFKVGN-FAA 322
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 165 LQGI 168
   |:::|
DB 323 LRSI 326

RESULT 12
US-08-362-652-55
; Sequence 55, Application US/08362652
; Patent No. 5766850
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
```

```

; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,652
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1161 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-362-652-55

Query Match      15.4%; Score 138.5; DB 1; Length 1161;
Best Local Similarity 28.3%; Pred. No. 7.6e-07;
Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;
```

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QY 1 DLYFIDKSGSV-LHMHNEIYFVEQLAHKFIISQURMSFIVSTRGTTLMKLT----- 54
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 152 DIFFLIDSGSINQRPFAQMKDFVKALMGEPASTSTLFSLMQVSNLTKHTFTTEFNIL 211
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 55 DREQIRQGLELQKVLPGSDTYMHGEPERASEQIYENROGYRTA-SVIALTDGELHED 113
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 212 DPQSLVDPIYQLQ-----GLTYTATGIRTYMELFHSKNGSRKSAKKILLIVTDGQKYRD 266
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 114 LFYFSE--REANRSRLGAIYVCVYKD-FNE-TQLARI-----ADSKHVFVNNGFOA 164
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 267 PLEYSVDVIPADKA--GIIRYAIQVGDAFOEPTALKELNTIGSAPPQDHVFKVGN-FAA 322
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 165 LQGI 168
   |:::|
DB 323 LRSI 326

RESULT 13
US-08-605-672-55
; Sequence 55, Application US/08605672
; Patent No. 5817515
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-55

Query Match 15.4%; Score 138.5; DB 1; Length 1161;
Best Local Similarity 28.3%; Pred. No. 7.6e-07;

Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;

QY 1 DLVFIIDKSGSV-LHMHNEIYFVEQLAHKFIISPOLMSFIVSTRTGTLTKLTE----- 54
DB 152 DIAFLIDSGSINQRDPAQKMDFKALMGFASTLFSIMQYSLIKHTFTFTEFNIL 211
QY 55 DREQIQGLELEOKVLPFGDTYHGEFERASEQIYVENRGYTA-SVIALTDGELHED 113
DB 212 DPQSLVDPIVQLQ-----GLTYATGIRTYMEELFHSKNGSRKSAKKILVITDGQKRD 266
QY 114 LFFYSE--REANSRDGAIVYCVGVD-FNE-TOLARI-----ADSKHVPVNDGFOA 164
DB 267 PLEYSDVIPAADKA---GIIRYAIYGDAFQEPFALKELNTIGSAPPQDHVFGVN-FAA 322
QY 165 LQGI 168
DB 323 LRSI 326

RESULT 14
US-08-482-293A-55
Sequence 55, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-55

Query Match 15.4%; Score 138.5; DB 1; Length 1161;
Best Local Similarity 28.3%; Pred. No. 7.6e-07;

Matches 52; Conservative 36; Mismatches 71; Indels 25; Gaps 10;

QY 1 DLVFIIDKSGSV-LHMHNEIYFVEQLAHKFIISPOLMSFIVSTRTGTLTKLTE----- 54
DB 152 DIAFLIDSGSINQRDPAQKMDFKALMGFASTLFSIMQYSLIKHTFTFTEFNIL 211
QY 55 DREQIQGLELEOKVLPFGDTYHGEFERASEQIYVENRGYTA-SVIALTDGELHED 113
DB 212 DPQSLVDPIVQLQ-----GLTYATGIRTYMEELFHSKNGSRKSAKKILVITDGQKRD 266
QY 114 LFFYSE--REANSRDGAIVYCVGVD-FNE-TOLARI-----ADSKHVPVNDGFOA 164
DB 267 PLEYSDVIPAADKA---GIIRYAIYGDAFQEPFALKELNTIGSAPPQDHVFGVN-FAA 322
QY 165 LQGI 168
DB 323 LRSI 326

RESULT 15
US-08-943-363-55
Sequence 55, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:


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; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PaSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-26

Query Match      100.0%; Score 899; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 1,1e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISQRLMSFIVFSTRTGTTLMKLTEDREQIR 60
    |||
DB 44 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISQRLMSFIVFSTRTGTTLMKLTEDREQIR 103
    |||

QY 61 QGLEELQKVLPGGDTYMHGFEFASBQIYYENRQGYRTASVIALTDGELHEDLFFYSER 120
    |||
DB 104 QGLEELQKVLPGGDTYMHGFEFASBQIYYENRQGYRTASVIALTDGELHEDLFFYSER 163
    |||

QY 121 EANRSRDGLAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIHSIL 173
    |||
DB 164 EANRSRDGLAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIHSIL 216
    |||

RESULT 3
US-09-796-753-12
; Sequence 12, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
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; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 12
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-12

Query Match      100.0%; Score 899; DB 3; Length 333;
Best Local Similarity 100.0%; Pred. No. 1,1e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISQRLMSFIVFSTRTGTTLMKLTEDREQIR 60
    |||
DB 44 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISQRLMSFIVFSTRTGTTLMKLTEDREQIR 103
    |||

QY 61 QGLEELQKVLPGGDTYMHGFEFASBQIYYENRQGYRTASVIALTDGELHEDLFFYSER 120
    |||
DB 104 QGLEELQKVLPGGDTYMHGFEFASBQIYYENRQGYRTASVIALTDGELHEDLFFYSER 163
    |||

QY 121 EANRSRDGLAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIHSIL 173
    |||
DB 164 EANRSRDGLAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIHSIL 216
    |||

RESULT 4
US-10-038-307-2
; Sequence 2, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PaSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-2

Query Match      100.0%; Score 899; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 1,1e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISQRLMSFIVFSTRTGTTLMKLTEDREQIR 60
    |||
DB 44 DLYFIIDKSGSVLHHNNEIYFVEQLAHKFIISQRLMSFIVFSTRTGTTLMKLTEDREQIR 103
    |||

QY 61 QGLEELQKVLPGGDTYMHGFEFASBQIYYENRQGYRTASVIALTDGELHEDLFFYSER 120
    |||
DB 104 QGLEELQKVLPGGDTYMHGFEFASBQIYYENRQGYRTASVIALTDGELHEDLFFYSER 163
    |||

QY 121 EANRSRDGLAIYVCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIHSIL 173
    |||
```



```
Db      164 EANRSDLGAIYVCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSIL 216
|||||
RESULT 5
US-10-201-292-2
; Sequence 2, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match      100.0%; Score 899; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 1,1e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DLYFIIDKSGSVLHNMNEIYFVEQLAHKFI SPOLRMSFIVFSTRGTTLMKLTEDRQIR 60
|||||
Db      44 DLYFIIDKSGSVLHNMNEIYFVEQLAHKFI SPOLRMSFIVFSTRGTTLMKLTEDRQIR 103
|||||
Qy      61 QGLEELQKVLPGGDTYHHEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYSER 120
|||||
Db      104 QGLEELQKVLPGGDTYHHEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYSER 163
|||||
Qy      121 EANRSDLGAIYVCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSIL 173
|||||
Db      164 EANRSDLGAIYVCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSIL 216
|||||

RESULT 6
US-11-047-278-8
; Sequence 8, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Antitoxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match      100.0%; Score 899; DB 6; Length 333;
Best Local Similarity 100.0%; Pred. No. 1,1e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DLYFIIDKSGSVLHNMNEIYFVEQLAHKFI SPOLRMSFIVFSTRGTTLMKLTEDRQIR 60
|||||
```

```
Db      44 DLYFIIDKSGSVLHNMNEIYFVEQLAHKFI SPOLRMSFIVFSTRGTTLMKLTEDRQIR 103
|||||
Qy      61 QGLEELQKVLPGGDTYHHEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYSER 120
|||||
Db      104 QGLEELQKVLPGGDTYHHEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYSER 163
|||||
Qy      121 EANRSDLGAIYVCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSIL 173
|||||
Db      164 EANRSDLGAIYVCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSIL 216
|||||

RESULT 7
US-10-038-307-22
; Sequence 22, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match      100.0%; Score 899; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 1,2e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DLYFIIDKSGSVLHNMNEIYFVEQLAHKFI SPOLRMSFIVFSTRGTTLMKLTEDRQIR 60
|||||
Db      53 DLYFIIDKSGSVLHNMNEIYFVEQLAHKFI SPOLRMSFIVFSTRGTTLMKLTEDRQIR 112
|||||
Qy      61 QGLEELQKVLPGGDTYHHEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYSER 120
|||||
Db      113 QGLEELQKVLPGGDTYHHEGFERASEQIYYENRGYRTASVIALTDGELHEDLFFYSER 172
|||||
Qy      121 EANRSDLGAIYVCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSIL 173
|||||
Db      173 EANRSDLGAIYVCVGVKDFNETOLARIADSKDHVPVNDGFQALQGIHSIL 225
|||||

RESULT 8
US-10-201-292-22
; Sequence 22, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match      100.0%; Score 899; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 1,2e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	DVEFLIDKSSVLAHNNNEIYFVEQALAHFISPOLRMSFIVSTGTLMLQJTDRCQIR	60
Db	53	DLFIILDKSSVLAHNNNEIYFVEQALAHFISPOLRMSFIVSTGTLMLQJTDRCQIR	112
Qy	61	QGEELOKVLPGGDTYVHEGFEPASBOIYYENRQGYRTSAVIALTDGELHEDLFPYSER	120
Db	113	QGEELOKVLPGGDTYVHEGFEPASBOIYYENRQGYRTSAVIALTDGELHEDLFPYSER	172
Qy	121	EANRSRLGAIIVYCVGKVDNFENFQRLIRIDSXDHFVPVNDGQALQGIITHSIL	173
Db	173	EANRSRLGAIIVYCVGKVDNFENFQRLIRIDSXDHFVPVNDGQALQGIITHSIL	225

```

RESULT 9
US-10-038-307-24
: Sequence 24, Application US/10038307
: Publication No. US20030134786A1
: GENERAL INFORMATION:
: APPLICANT: James B. ROTTMAN
: APPLICANT: Theresa L. O'KEEFE
: APPLICANT: Engin OZKAYNAK
: APPLICANT: Judith J. HEALEY
: TITLE OF INVENTION: Tango 197
: FILE REFERENCE: 7853-253-999
: CURRENT APPLICATION NUMBER: US/10/038.307
: CURRENT FILING DATE: 2002-06-28
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 24
: LENGTH: 345
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-038-307-24

```

Query Match	100.0%;	Score 899;	DB 4;	Length 345;
Best Local Similarity	100.0%;	Pred. No. 1.2e-86;		
Matches 173;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY DLVFLIDKSGSVLHHNNEIYYFVEOLAHKISPOLNRSFVFSRGTGLTKLLEDEBQIR 60
Db DIFYFLIDKSGSVLHHNNEIYYFVEOLAHKISPOLNRSFVFSRGTGLTKLLEDEBQIR 103
QY 61 OGLEELQKLVPGGDTVMHSGFERASEQIYYENRGYRTASVIALTFGELEHEDLFFYSER 120
Db 104 OGLEELQKLVPGGDTVMHSGFERASEQIYYENRGYRTASVIALTDGELEHEDLFFYSER 163
QY 121 EANRSKDLAIYVCVGKDFNETQLARIADSKOHVFPVNDGFOALOGIIHSIL 173
Db 164 EANRSKDLAIYVCVGKDFNETQLARIADSKOHVFPVNDGFOALOGIIHSIL 216

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RESULT 10
US-10-201-292-24
Sequence 24, Application US/10201292
Publication NO. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-24

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Query Match	100.0%;	Score 899;	DB 4;	Length 345;
Best Local Similarity	100.0%;	Pred. No. 1.2e+86;		
Matches 173; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	DLVFIIDKSGSVLHHNNELYYVEVDLAKFTISPOLHMSFIYFSRGTTLKLKLTEDRQIR	60
Db	DLVFIIDKSGSVLHHNNELYYVEVDLAKFTISPOLHMSFIYFSRGTTLKLKLTEDRQIR	103
QY	QGLLELQKTLPGGDTYMHGEFERRASEQIYYENRQSGYRTASVIALTLTGELHEDLFPYSER	120
Db	QGLLELQKTLPGGDTYMHGEFERRASEQIYYENRQSGYRTASVIALTLTGELHEDLFPYSER	163
QY	EANRSHDLGAIYCVGVKDFNETQIARLADSKDHVPVNDGFOALQGIHHSIL	173
Db	EANRSHDLGAIYCVGVKDFNETQIARLADSKDHVPVNDGFOALQGIHHSIL	216

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RESULT 11
US-11-047-278-2
; Sequence 2, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OR INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047, 278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970, 076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 368
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-047-278-2

```

Query Match	100.0%;	Score 899;	DB 6;	Length 368;
Best Local Similarity	100.0%;	Pred. No. 1.3e-86;		
Matches 173;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	DLVFILDKSGSVLHHNNEIYYVEEDLAKFKTSPQLRMSFIVFSRGTLLMLQJEDRQOIR	60
Db	44	DLVFILDKSGSVLHHNNEIYYVEEDLAKFKTSPQLRMSFIVFSRGTLLMLQJEDRQOIR	103
QY		OGLEELQKYLPGSDTYMHGFEPRASQIYYENRQOYFRASYITIALTGGELHEDLFFPSER	120
Db	104	OGLEELQKYLPGSDTYMHGFEPRASQIYYENRQOYFRASYITIALTGGELHEDLFFPSER	165
QY		EANRSRDGLAIYCVGKDFNETQIARLADSQDHYFVNDGFPALOGIHSIL	173
Db	164	EANRSRDGLAIYCVGKDFNETQIARLADSQDHYFVNDGFPALOGIHSIL	216

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RESULT 12
US-09-833-245-621
; Sequence 621, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/4225, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
;

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PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 621
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
US-09-833-245-621

Query Match 100.0%; Score 899; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.5e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYFIIDKSGSVLHNNIEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 60
DB 44 DLYFIIDKSGSVLHNNIEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 103
QY 61 QGLEBLQKVLPGGDTYMHGFEFERSAQIYYENRQGYRTASVIALTDGELHEDLFFYSER 120
DB 104 QGLEBLQKVLPGGDTYMHGFEFERSAQIYYENRQGYRTASVIALTDGELHEDLFFYSER 163
QY 121 EANRSRDLAGIIVYCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIIHSIL 173
DB 164 EANRSRDLAGIIVYCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIIHSIL 216

RESULT 13
US-10-201-292-28
Sequence 28, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT FILING DATE: 2003-02-14
CURRENT APPLICATION NUMBER: US/10/201,292
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 460
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-28

Query Match 100.0%; Score 899; DB 4; Length 460;
Best Local Similarity 100.0%; Pred. No. 1.8e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYFIIDKSGSVLHNNIEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 60
DB 44 DLYFIIDKSGSVLHNNIEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 103
QY 61 QGLEBLQKVLPGGDTYMHGFEFERSAQIYYENRQGYRTASVIALTDGELHEDLFFYSER 120
DB 104 QGLEBLQKVLPGGDTYMHGFEFERSAQIYYENRQGYRTASVIALTDGELHEDLFFYSER 163
QY 121 EANRSRDLAGIIVYCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIIHSIL 173
DB 164 EANRSRDLAGIIVYCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIIHSIL 216

RESULT 14
US-10-201-292-30
Sequence 30, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 460
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-30

Query Match 100.0%; Score 899; DB 4; Length 460;
Best Local Similarity 100.0%; Pred. No. 1.8e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYFIIDKSGSVLHNNIEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 60
DB 44 DLYFIIDKSGSVLHNNIEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 103
QY 61 QGLEBLQKVLPGGDTYMHGFEFERSAQIYYENRQGYRTASVIALTDGELHEDLFFYSER 120
DB 104 QGLEBLQKVLPGGDTYMHGFEFERSAQIYYENRQGYRTASVIALTDGELHEDLFFYSER 163
QY 121 EANRSRDLAGIIVYCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIIHSIL 173
DB 164 EANRSRDLAGIIVYCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIIHSIL 216

RESULT 15
US-10-201-292-32
Sequence 32, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT FILING DATE: 2003-02-14
CURRENT APPLICATION NUMBER: US/10/201,292
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-32

Query Match 100.0%; Score 899; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.9e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLYFIIDKSGSVLHNNIEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 60
DB 44 DLYFIIDKSGSVLHNNIEIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDRQIR 103
QY 61 QGLEBLQKVLPGGDTYMHGFEFERSAQIYYENRQGYRTASVIALTDGELHEDLFFYSER 120
DB 104 QGLEBLQKVLPGGDTYMHGFEFERSAQIYYENRQGYRTASVIALTDGELHEDLFFYSER 163
QY 121 EANRSRDLAGIIVYCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIIHSIL 173
DB 164 EANRSRDLAGIIVYCVGVKDFNETQLARIADSKDHVPVNDGFQALOGIIHSIL 216

Search completed: December 14, 2005, 11:59:01
Job time : 53.2862 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 11:18:48 ; Search time 2.54242 Seconds
(without alignments)
458.218 Million cell updates/sec

Title: US-09-970-076-2_COPY_44_216

Perfect score: 899
Sequence: 1 DLVFLDKSGSVLHNNNEIY.....HVFVNDGFOALGQIHSIL 173

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 51441 seqs, 6734002 residues

Total number of hits satisfying chosen parameters: 51441

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:

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2: /cgn2_6/ptodaca/1/pubpaa/US06_NEW_PUB pep:*
3: /cgn2_6/ptodaca/1/pubpaa/US07_NEW_PUB pep:*
4: /cgn2_6/ptodaca/1/pubpaa/US08_NEW_PUB pep:*
5: /cgn2_6/ptodaca/1/pubpaa/PCT_NEW_PUB pep:*
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7: /cgn2_6/ptodaca/1/pubpaa/US11_NEW_PUB pep:*
8: /cgn2_6/ptodaca/1/pubpaa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	899	100.0	564	7 US-11-186-284-199	Sequence 199, App
2	128.5	14.3	1152	7 US-11-080-026-4	Sequence 26, App
3	118.5	13.2	3063	7 US-11-186-284-26	Sequence 24, App
4	108	12.0	1141	6 US-10-601-368-24	Sequence 22, App
5	108	12.0	1166	6 US-10-601-368-22	Sequence 21, App
6	108	12.0	1188	6 US-10-601-368-21	Sequence 6, App
7	104	11.6	1141	6 US-10-601-368-6	Sequence 4, App
8	104	11.6	1166	6 US-10-601-368-4	Sequence 3, App
9	104	11.6	1188	6 US-10-601-368-3	Sequence 318, App
10	104	11.6	1188	7 US-11-000-463-338	Sequence 810, App
11	104	11.6	1188	7 US-11-000-463-810	Sequence 25, App
12	103.5	11.3	739	7 US-10-057-047-2	Sequence 2, App
13	101.5	11.3	764	7 US-11-057-047-1	Sequence 1, App
14	101.5	11.3	764	7 US-10-821-234-1034	Sequence 1034, App
15	101.5	11.3	798	6 US-10-821-234-1034	Sequence 294, App
16	100.5	11.2	915	6 US-10-131-826A-294	Sequence 39, App
17	100.5	11.2	956	6 US-11-113-424-39	Sequence 7, App
18	99.5	11.1	182	6 US-10-601-368-7	Sequence 6, App
19	96.5	10.7	761	7 US-10-057-047-6	Sequence 983, App
20	93.5	10.4	828	6 US-10-995-561-883	Sequence 981, App
21	93.5	10.4	918	6 US-10-995-561-881	Sequence 982, App
22	93.5	10.4	1019	6 US-10-995-561-982	Sequence 1, App
23	91.5	10.2	1179	7 US-11-097-125-1	Sequence 921, App
24	91.5	10.2	1196	6 US-10-995-561-921	Sequence 18, App
25	90	10.0	1167	6 US-10-601-368-18	

26	86.5	9.6	1167	7 US-11-097-125-2	Sequence 2, App
27	82	9.1	678	7 US-11-102-240-34	Sequence 34, App
28	81.5	9.1	353	7 US-11-137-465-44	Sequence 44, App
29	81.5	9.1	448	7 US-11-137-465-45	Sequence 45, App
30	74	8.2	384	6 US-10-510-386-158	Sequence 158, App
31	73.5	8.2	509	6 US-10-793-626-2880	Sequence 2880, App
32	72	8.0	264	6 US-10-793-626-388	Sequence 388, App
33	72	8.0	766	6 US-10-467-6628-103	Sequence 103, App
34	70	7.8	292	6 US-10-467-626-2636	Sequence 2636, App
35	70	7.8	468	6 US-10-467-657-5696	Sequence 5696, App
36	69.5	7.7	489	6 US-10-467-657-7846	Sequence 7846, App
37	69	7.7	242	6 US-10-467-657-7306	Sequence 7306, App
38	68.5	7.6	1734	7 US-11-192-967-6	Sequence 6, App
39	68.5	7.6	1734	7 US-11-193-715-6	Sequence 6, App
40	68	7.6	348	6 US-10-674-767-4	Sequence 4, App
41	66	7.3	403	6 US-10-467-657-7066	Sequence 7066, App
42	66	7.3	919	7 US-11-102-240-70	Sequence 70, App
43	65.5	7.3	1299	6 US-10-821-234-1145	Sequence 1145, App
44	65	7.2	167	6 US-10-467-657-7272	Sequence 7272, App
45	64.5	7.2	629	6 US-10-467-657-250	Sequence 250, App

ALIGNMENTS

RESULT 1
US-11-186-284-199
; Sequence 199, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Subhangt
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Tonhedeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MEMO1-029P2RM
; CURRENT APPLICATION NUMBER: US/11/186,284
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-199

Query Match 100.0%; Score 899; DB 7; Length 564;
Best Local Similarity 100.0%; Pred. No. 2.6e-81;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLVFLDKSGSVLHNNNEIYFVEQLAKHFIISPOLMSPFVSTRTGTLTKLTFEDRQIR 60
DB 44 DLVFLDKSGSVLHNNNEIYFVEQLAKHFIISPOLMSPFVSTRTGTLTKLTFEDRQIR 103
QY 61 QGIEELQKVLPGDDTYTHRESEFASBOIYYENQGRITASVIALTDGELHEDLFFYSER 120
DB 104 QGIEELQKVLPGDDTYTHRESEFASBOIYYENQGRITASVIALTDGELHEDLFFYSER 163
QY 121 EARRSRDLGAIYCVGKVDNENETQLARIADSKDHVFVNDGFOALGQIHSIL 173

Db 164 EANRSRDGAIVYCVGVDFNETQLARIADSKDHVPVNDGFOALOGIHSIL 216

```
RESULT 2
US-11-080-026-4
/ Sequence 4, Application US/11080026
/ Publication No. US20050260192A1
/ GENERAL INFORMATION:
/ APPLICANT: Springer, Timothy A.
/ APPLICANT: Shimooka, Motomu
/ APPLICANT: Lu, Chafen
/ TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
/ FILE REFERENCE: CFBF-P02-021
/ CURRENT APPLICATION NUMBER: US/11/080,026
/ CURRENT FILING DATE: 2005-03-15
/ PRIOR APPLICATION NUMBER: 09/945,265
/ PRIOR FILING DATE: 2001-08-31
/ PRIOR APPLICATION NUMBER: US 60/229,700
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 1152
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-080-026-4
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Query Match 14.3%; Score 128.5; DB 7; Length 1152;
Best Local Similarity 26.7%; Pred. No. 5.6e-05;
Matches 51; Conservative 38; Mismatches 63; Indels 39; Gaps 11;

QY 1 DIVFIIDKSGSVL-HHNNETIYFVEQLAHKFISQLRMSFTIVSTRTGLTKLTD----- 55
DB 150 DIAFLIDSGSIIIPHDRKKEFVST-----VMEQLKSKITLPS-----LMQYSEFRRIH 199
QY 56 -----REQIROLGELQKVLPGDVTYHGEFPERASEQIYYENRQGYRTA-SVILALT 106
DB 200 FTREKPNNNPRLSLVPIQLL--GRTHATATGRKTVRELFINITNARCAKRLIVIT 257
QY 107 DGEIHEDLFFYYS--REANRSRDGAIVYCVGVDFNETQLAR-----IADS--KDHVP 157
DB 258 DGEKFGDPLGVEDVTPADRE---GVIRYVIGVDADPRSEKSKQELNTVIASKPRDHVQ 314
QY 158 VNDGFOALOGI 168
DB 315 VNN-FEALKTI 324
```

```
RESULT 3
US-11-186-284-26
/ Sequence 26, Application US/11186284
/ Publication No. US20050266493A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: Berger, Allison
/ APPLICANT: Guillemette, Tracy L.
/ APPLICANT: Kamatkar, Shubhangi
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Monahan, John E.
/ APPLICANT: Thibodeau, Stephen N.
/ APPLICANT: Burgart, Lawrence J.
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
/ TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ FILE REFERENCE: MEMO1-029P2RMM
/ CURRENT APPLICATION NUMBER: US/11/186,284
/ CURRENT FILING DATE: 2005-07-21
/ PRIOR APPLICATION NUMBER: US/10/301,822
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 60/339,971
/ PRIOR FILING DATE: 2001-12-10
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/ PRIOR APPLICATION NUMBER: US 60/361,978
/ PRIOR FILING DATE: 2002-03-05
/ PRIOR APPLICATION NUMBER: US 60/381,988
/ PRIOR FILING DATE: 2002-05-20
/ NUMBER OF SEQ ID NOS: 228
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 26
/ LENGTH: 3063
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-11-186-284-26
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Query Match 13.2%; Score 118.5; DB 7; Length 3063;
Best Local Similarity 30.0%; Pred. No. 0.0019;
Matches 54; Conservative 35; Mismatches 68; Indels 23; Gaps 12;

QY 1 DIVFIIDKSGSVL-HHNNETIYFVEQLAHKF-ISP-QLRMSFTIVST---RRTGLTKLTE 54
DB 440 DIVFLVDGSYSIGIANFVRAFLVLVKSFEISPNRVOISLVQSRDPHTFTLKKFTK 499
QY 55 DREQIROLGELQKVLPGDVTYHGEFPERASEQIYYENRQGYRT--ASVILALTGDEL 110
DB 500 VEDII-----EAINTPPYRGSTTNGKAMTYREKIFVPSK-GSRSNVPKMWILITDCK- 552
QY 111 HEDLFFYSERREANRSRDGAIVYCVGVDFNETQLARIAD--SKDHVPVNDGFOALOGI 168
DB 553 SSDAF---RDPAIKLRNSDVEIFAVGVKDAVSELEAIASPPAEHTVETVED-FDAFORI 608
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```
RESULT 4
US-10-601-368-24
/ Sequence 24, Application US/10601368
/ Publication No. US20050260702A1
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ APPLICANT: Lora, Jose M.
/ TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
/ FILE REFERENCE: 0734-275001
/ CURRENT APPLICATION NUMBER: US/10/601,368
/ CURRENT FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: US/09/561,263A
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/322,790
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 24
/ LENGTH: 1141
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-10-601-368-24
```

```
Query Match 12.0%; Score 108; DB 6; Length 1141;
Best Local Similarity 24.2%; Pred. No. 0.0058;
Matches 48; Conservative 28; Mismatches 84; Indels 38; Gaps 9;

QY 1 DIVFIIDKSGSVL-HHNNETIYFVEQLAHKF-ISP-QLRMSFTIVSTRTGLTKLTDREQ 58
DB 164 DIVIIVDGSNST-YPMVEVQHILINLTKFTYIGPGIOVGIVGYGDAAHEPHL-NDYNS 221
QY 59 IROGLEELQKVLPGDVTYHGEF--RASEQIYYENRQGYRTASVILALTGDELHD-- 113
DB 222 VKQVVEASHIEBQGTETRTAFGLIEFARSEAFQKGRGAK--KVMIVITDGSHESDPD 279
QY 114 -----LFFYSREANRSRDGAIVYCVGVND-----FNETQLARI 149
DB 280 LKRVIRQSEKDNVTRVAVALGYNNRGINPETFLMEIRYIASDPDKHFPNVTDEAL- 338
QY 150 DSKDHVPVNDGFOALOG 167
DB 339 --KDIYDALGDRIRFSLEG 354
```


[illegible]

Db 303 DSSNADWYTKQLEINVEDHKLKSGTNT-----KKALQAVYSMMSPDDVPEEGMNRTR 356
QY 100 SVTIALTDG-----ELHEDLFFYSERERANRBDIGAIYCYG--VKDFNETQ 144
Db 357 HVIILMTDGLHNMGGDPITVIDEIRDLIYGKDRKNRPEDYLDVYVGVGLVNOVNINA 416
QY 145 LARIADSKDHVPFVNDGFOALQGIHSIL 173
Db 417 LASKKDNQHFVKVD-MENLEDVIFYOMI 444

RESULT 14
US-11-057-047-1
Sequence 1, Application US/11057047
Publication No. US20050260198A1
GENERAL INFORMATION:
APPLICANT: Holers, Vernon
APPLICANT: Thurman, Joshua
APPLICANT: Taube, Christian
APPLICANT: Gelfand, Erwin
APPLICANT: Gilkeson, Gary
TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
FILE REFERENCE: 2848-66
CURRENT FILING DATE: 2005-02-10
PRIOR FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: 60/543,594
PRIOR FILING DATE: 2004-12-14
PRIOR APPLICATION NUMBER: 60/536,239
PRIOR FILING DATE: 2004-12-14
PRIOR APPLICATION NUMBER: US04/015040
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LENGTH: 764
TYPE: PRT
ORGANISM: Homo sapiens
US-11-057-047-1

Query Match 11.3%; Score 101.5; DB 7; Length 764;
Best Local Similarity 22.5%; Pred. No. 0.015;
Matches 47; Conservative 43; Mismatches 74; Indels 45; Gaps 10;

QY 1 DLYFLDKSGSV-----LHHMNEIYFVEQLAHKFISPOLRMSFVFSRGTTLMLKTE- 54
Db 270 NIYLVLDGSDSISASNFQAKKCLVNIKVASYGVP--RYGLVTYATYPKIWKVSESA 327
QY 55 ---DREQIRQGLEEL---QKVLPGGDTYMHGFEFASSEQIYYENR-----QGY-RTA 99
Db 328 DSSNADWYTKQLEINVEDHKLKSGTNT-----KKALQAVYSMMSPDDVPEEGMNRTR 381
QY 100 SVTIALTDG-----ELHEDLFFYSERERANRBDIGAIYCYG--VKDFNETQ 144
Db 382 HVIILMTDGLHNMGGDPITVIDEIRDLIYGKDRKNRPEDYLDVYVGVGLVNOVNINA 441
QY 145 LARIADSKDHVPFVNDGFOALQGIHSIL 173
Db 442 LASKKDNQHFVKVD-MENLEDVIFYOMI 469

RESULT 15
US-10-821-234-1034
Sequence 1034, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmant, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234

/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: PC_SEQ_genes Version 1.0
/ SEQ ID NO 1034
/ LENGTH: 798
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-1034

Query Match 11.3%; Score 101.5; DB 6; Length 798;
Best Local Similarity 22.5%; Pred. No. 0.016;
Matches 47; Conservative 43; Mismatches 74; Indels 45; Gaps 10;

QY 1 DLYFLDKSGSV-----LHHMNEIYFVEQLAHKFISPOLRMSFVFSRGTTLMLKTE- 54
Db 304 NIYLVLDGSDSISASNFQAKKCLVNIKVASYGVP--RYGLVTYATYPKIWKVSESA 361
QY 55 ---DREQIRQGLEEL---QKVLPGGDTYMHGFEFASSEQIYYENR-----QGY-RTA 99
Db 362 DSSNADWYTKQLEINVEDHKLKSGTNT-----KKALQAVYSMMSPDDVPEEGMNRTR 415
QY 100 SVTIALTDG-----ELHEDLFFYSERERANRBDIGAIYCYG--VKDFNETQ 144
Db 416 HVIILMTDGLHNMGGDPITVIDEIRDLIYGKDRKNRPEDYLDVYVGVGLVNOVNINA 475
QY 145 LARIADSKDHVPFVNDGFOALQGIHSIL 173
Db 476 LASKKDNQHFVKVD-MENLEDVIFYOMI 503

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Job time : 2.54242 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: December 18, 2005, 07:35:12 : Search time 554.247 Seconds
(without alignments)
2581.163 Million cell updates/sec

Title: US-09-970-076-2_COPY_44_216

Perfect score: 899

Sequence: 1 DLYFIDKSGSVLHHNNEY.....HVFVNDGFOALGIIHSIL 173

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-MODE=frame_p2n.model -DEV=xlh
-Q=/cg2_1/USPTO.epool/US09970076/runac.14122005_111852_21035/app_query.fasta.1.2410
-DB=Published Applications NA_Main -QPM=faetap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOP=0 -LOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blonsum62
-TRANS=human40.csl -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076 -CGN_1_1_2715 -ORNA_14122005_111852_21035
-NCPU=6 -ICPU=3 -NO_MMAP -LARGESUBSTRY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA_Main.*

1: /cg2_6/ptodaca/1/pubpna/US07_PUBCOMB.seq:*
2: /cg2_6/ptodaca/1/pubpna/US08_PUBCOMB.seq:*
3: /cg2_6/ptodaca/1/pubpna/US09_PUBCOMB.seq:*
4: /cg2_6/ptodaca/1/pubpna/US09_PUBCOMB.seq:*
5: /cg2_6/ptodaca/1/pubpna/US10_PUBCOMB.seq:*
6: /cg2_6/ptodaca/1/pubpna/US10_PUBCOMB.seq:*
7: /cg2_6/ptodaca/1/pubpna/US10_PUBCOMB.seq:*
8: /cg2_6/ptodaca/1/pubpna/US10_PUBCOMB.seq:*
9: /cg2_6/ptodaca/1/pubpna/US10_PUBCOMB.seq:*
10: /cg2_6/ptodaca/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	899	100.0	1008	US-10-038-307-25	Sequence 25, Appl
2	899	100.0	1008	US-10-201-292-25	Sequence 25, Appl
3	899	100.0	1047	US-10-038-307-21	Sequence 21, Appl
4	899	100.0	1047	US-10-201-292-21	Sequence 21, Appl
5	899	100.0	1056	US-10-038-307-23	Sequence 23, Appl
6	899	100.0	1056	US-10-201-292-23	Sequence 23, Appl
7	899	100.0	1401	US-10-201-292-27	Sequence 27, Appl
8	899	100.0	1401	US-10-201-292-29	Sequence 29, Appl

9	899	100.0	1414	US-11-047-278-1	Sequence 1, Appl
10	899	100.0	1436	US-11-047-278-9	Sequence 9, Appl
11	899	100.0	1454	US-10-133-937-58	Sequence 58, Appl
12	899	100.0	1454	US-10-159-863-58	Sequence 58, Appl
13	899	100.0	1464	US-10-201-292-31	Sequence 31, Appl
14	899	100.0	1534	US-10-201-292-33	Sequence 33, Appl
15	899	100.0	1608	US-10-037-970-8	Sequence 8, Appl
16	899	100.0	1609	US-10-117-122-8	Sequence 8, Appl
17	899	100.0	1609	US-10-122-851-8	Sequence 8, Appl
18	899	100.0	1623	US-10-038-307-11	Sequence 11, Appl
19	899	100.0	1623	US-10-201-292-11	Sequence 11, Appl
20	899	100.0	1633	US-10-047-542-98	Sequence 98, Appl
21	899	100.0	1650	US-10-038-307-13	Sequence 13, Appl
22	899	100.0	1650	US-10-038-307-13	Sequence 13, Appl
23	899	100.0	1650	US-10-038-307-15	Sequence 15, Appl
24	899	100.0	1650	US-10-201-292-9	Sequence 9, Appl
25	899	100.0	1650	US-10-201-292-13	Sequence 13, Appl
26	899	100.0	1650	US-10-201-292-15	Sequence 15, Appl
27	899	100.0	1674	US-10-038-307-17	Sequence 17, Appl
28	899	100.0	1674	US-10-201-292-17	Sequence 17, Appl
29	899	100.0	1713	US-10-038-307-19	Sequence 19, Appl
30	899	100.0	1713	US-10-201-292-19	Sequence 19, Appl
31	899	100.0	1718	US-10-357-930-30300	Sequence 30300, A
32	899	100.0	2112	US-11-047-278-7	Sequence 7, Appl
33	899	100.0	2272	US-09-796-753-11	Sequence 11, Appl
34	899	100.0	2272	US-10-038-307-1	Sequence 1, Appl
35	899	100.0	2272	US-10-201-292-1	Sequence 1, Appl
36	899	100.0	2353	US-10-198-846-9957	Sequence 9957, Ap
37	899	100.0	5540	US-09-918-715-176	Sequence 176, App
38	899	100.0	5540	US-09-918-715-231	Sequence 231, App
39	899	100.0	5540	US-10-301-822-198	Sequence 198, App
40	899	100.0	5540	US-10-474-794-176	Sequence 176, App
41	899	100.0	5540	US-10-474-794-231	Sequence 231, App
42	899	100.0	5540	US-10-979-159-176	Sequence 176, App
43	899	100.0	5540	US-10-979-159-231	Sequence 231, App
44	899	100.0	5540	US-11-047-278-5	Sequence 5, Appl
45	899	100.0	5540	US-11-047-278-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-10-038-307-25 Application US/10038307
Sequence 25, Appl
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 1008
TYPE: DNA
ORGANISM: Homo sapiens
US-10-038-307-25

Alignment Scores:

Pred. No.: 3.58e-111
Score: 899.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6
Matches: 1008
Conservative: 173
Mismatches: 0
Indels: 0
Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-10-038-307-25 (1-1008)

QY 1 AsplenTyRhetleuAplySerGlySerValLeuHisHisrTpangIuIetyr 20

Db 142 GACCGTCACTTATTTGGACAACATCGAAGGTGCTGCACCATCGAATGAACTTAT 201

Qy 21 TyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMetSerPheIle 40

Db 202 TACTTTGTGGACACAGTGGCTCCACAAATTCATCAGGCCACAGTTGAGANTGTCCTTATT 261

Qy 41 ValPheSerThrArgGlyThrThrIleuMetLysLeuThrGluAspArgGlnIleArg 60

Db 262 GTTTTCTCCACCCGAGGAACAACCTTAAAGAACTGACAGAAAGACAGAGAAACCAATCCGT 321

Qy 61 GlnGlyLeuGlnGlnLeuGlnIleLysValIleuProGlnGlyAspPheThrIleMetHisGlnGly 80

Db 322 CAAGGCTTGAAGAAACTCCAGAAAGTTGTGGCCAGAGAGAGACACTTACATCATGAAAGGA 381

Qy 81 PheGluArgAlaSerGlnGlnIleIleTyrTyrGluAsnArgGlnGlyTyrArgThrAlaSer 100

Db 382 TTGTAAGGCGCCAGTGAAGCATTTATTTATGAAAACAGACAAAGGTACAGACAGCCAGC 441

Qy 101 ValIleIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGluArg 120

Db 442 GTCATCATATGCTTTGACTGATGGAAGAACTCCAAAGAAAGATCTCTTTTCTCATTTAGAGAGG 501

Qy 121 GluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAspPhe 140

Db 502 GAGGCTTAATAGGCTTCGAGATCTTGGTGCAAATGCTTACTGCTGTGGTGGAAAGATTTC 561

Qy 141 AsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAsp 160

Db 562 AATGAGACACACAGCTGGCCCGGATTTGGCGACAGTAAGGATCATGTGTTTCCCGTAAGTAC 621

Qy 161 GlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu 173

Db 622 GGCTTTGACGCTCTGCAGGACATCATCCATCAATTTTG 660

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RESULT 2
US-10-201-292-25
; Sequence 25, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-25

Alignment Scores:
Pred. No.:      3,58e-111      Length:      1008
Score:          899.00         Matches:      173
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    100.00%        Indels:      0
DB:             6              Gaps:        0

US-09-970-076-2 COPY 44 216 (1-173) x US-10-201-292-25 (1-1008)

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US-09-970-076-2_COPY_44_216 (1-173) x US-10-201-292-25 (1-1008)

QY 1 AapleuTyPheIleLeuAaplySeSeGlySeValLeuHshIstPaenGlnIleTy 20

Db 142 GACCTGACTTCATTGGACAAATCAGAAAGTGTCGTGCACCACTGAAAGAAATCAT 201

QY 21 TyPheValGlnIleuAlshIlyPheIleSePProGlnIleuAArgMeSePheIle 40

Db 202 TACTTTGTGAAACAGTTGGCTCAAAATTCATCGCCACAGTTGAGAAATGTCCTTAAT 261

Qy	41	VaIphseSerThrArgGlyThrThrIleuMetLysLeuThrGluAaPaArgGluInIleArg	60
Db	262	GYTTTCTCCACCCGGAGAACCACTTAATGAAACGACAGAAACAGAAACAATCCGT	322
Qy	61	GIaNGlyLeuGIuGIaLeuGIuILyValLeuProGIyGIyAaEPThrTYrMetHISGLuGIy	80
Db	322	CAAGGCGTGAAGAACTCCAGAAATTTCTGCCAGGAGAGACACTTACATCATGAAAGGA	381
Qy	81	PheGIuARgALaSerGIuGIuInIleTYrTYrGIuAaNaArgInGIyTYrArgThAlaSer	100
Db	382	TTTGAAAGGCGCCAGTGACAGATTATTATGAAAACAGACAAGGTGCAGAGACAGCCAGC	441
Qy	101	VaIIleIleIaLeuThrArgPcLyGIuLeuHISGIuAaPLeuPheThrTYrSerGIuArg	120
Db	442	GTGATATTGCTTTGATCGATGAAACCTCCATGAAATCTCTTTTCTATTTCAGAAAGG	501
Qy	121	GIuAlaAaMaArgSerArgPLeuGIyAlaIleValTYrCyVaIaGIyValIyAaAPhe	140
Db	502	GAAAGCTAAATAGCTCTCGAATCTTGTGTGCATTTGTTACTGTGTGGGTGAAGATTTC	561
Qy	141	AaNGIuThrGIuLeuAlaArgIleAlaAPSerLyAaAPHisValPheProValAaNaAP	160
Db	562	AATGAAGACACAGCTGGCCGGATTCCGGCAGTAAGATCATGTGTTCCTCCGTAAATGAC	621
Qy	161	GIyPheGIuAlaLeuGIuInIyIleIleHisSerIleLeu	173
Db	622	GAGCTTTCAGGCTCTGCAGACATCATCACTAAATTTTG	660

```

RESULT 3
US-10-038-307-21
; Sequence 21, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-21

```

Alignment Scores:	
Pred. No.:	3,79e-111
Score:	899.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
nr:	6
	Gaps: 0
	Indels: 0
	Mismatches: 0
	Conservative: 0
	Matches: 173
	Length: 1047

US-09-970-076-2, COPY_44_216 (1-173) x US-10-038-307-21 (1-1047)

Qy 1 AepLeuTyrPheIleuAspLysSerGlySerValIleuHiIstTyrpAngIuIleTyr 20

Db 169 GACCTGTACTTCATTTTGACAAATCAGGAAGTGCTCTCACCACTGGAAATGAATCTAT 228

Qy 21 TyrpHeValGIuGIleuAlaHisLysPheIleSerProGIleuArpMetSerPheIle 40

Db 229 TACTTTGGGAACAGTGGCTCACAAATTCATCAGCCACAGTTGGAATGTCTTTATT 288

Qy 41 ValPheSerThrArgGlyThrThrIleuMetLysIleuThrGIuAspArgGIuIleArg 60

Db 289 GTTTTCTCCACCCGAGGAACAACCTTAATGAACACTGACAGAAACAGAAACAATTCGT 348

Qy 61 GIuGIleuGIuGIuIleuGIuIleValIleuProGIuGIuAspThrTyrMetHisGIuGIu 80

Db	349	CAAGCGCTTAAGAACTCCAGAAAGTTCTCCAGAGAGACACTTAATCATCATGAAGA	408
Qy	81	PheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArgThrAlaSer	100
Db	409	TTTGAAAGGGCCAGTGAAGCAGATTTATTATGAAAAACAGCAAGGGTATCAGGACAGCAGC	468
Qy	101	ValIleIleIleLeuThrArgGlyGluMetHisGluAspLeuPhePheTyrSerGluArg	120
Db	469	GTCATCATGCTTTGACTGATGGAGAAACCTCATTGAAGATCTCTTTTATTATTCAGAGG	528
Qy	121	GluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValIleAspPhe	140
Db	529	GAGGCTAATAGGCTCTGAGATCTTGGTGCATTTGTTTACTGTTGGTGGTGAAGAATTTC	588
Qy	141	AsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPheProValAsnAsp	160
Db	589	AATGAGACACAGCTGGCCCGAGATTGGCGGACAGATTAAGGATCATGTGTTTCCCGTAATGAC	648
Qy	161	GlyPheGlnAlaLeuGlnGlnGlyIleIleHisSerIleLeu	173
Db	649	GGGCTTCAGGCTCTGGACAGCATCATCCATCAATTTTGG	687

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RESULT 4
US-10-201-292-21
; Sequence 21, Application US/10201292
; Publication No. US20030144199A1
GENERAL INFORMATION:
APPLICANT: James E. ROTHMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 1047
TYPE: DNA
ORGANISM: Homo sapiens
US-10-201-292-21

```

Alignment Scores:	
Pred. No.:	3.79e-111
Score:	899.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	6
	Gaps: 0
	Indels: 0
	Mismatches: 0
	Conservative: 0
	Matches: 173
	Length: 1047

US-09-970-076-2_COPY_44_216 (1-173) X US-10-201-292-21 (1-1047)

Qy	AspLeuTyrPheIleuLeuArgLysSerGlySerValIleuNH ₂ HN ₂ STPAAngIiIleTyr	20
Db	169 GACCTGACTCTCACTTTTGGACAAATCAGAAATGCTGCTGCACACCTGAAAGAAATCTAT	228
Qy	21 TyrPheValGluGluLeuAlaHnIuYrPheIleSerProGluLeuAlaMetSerPheIle	40
Db	229 TACTTTGTGGAAAGATTGGCTCCAAATTCATCAGCCACAGTTGAGAAATGCTCTTAT	288
Qy	41 ValPheSerThrArgGlyIleThrIleMetIuValLeuThrGluAlaArgGluGlnIleArg	60
Db	289 GTTTTCTCCACCCGAGAGAACACTTAAAGAACTGACAGAAACAGAGAAACAAATCCGT	348
Qy	61 GlnGlyLeuGluIuLeuGlnIuYrValLeuProGlyGlyAspThrTyrMetHnGluGly	80
Db	349 CAAGGCTAGAGAACTCCGAAAGTTCTGCCAGAGAGAGACATTACATCATGAAAGA	408
Qy	81 PheGluArgAlaSerGluGlnIleTyrTyrGluAlaArgGlnGlyTyrArgThrAlaSer	100
Db	409 TTTGAAAGGGCCAGTAGAGAGATTATTATTGAAACAACAAGGAGTACAGACAGCCAGC	468

Oy	10	VallIeIleIleAeuThrAspGlyGluLeuHISgluAAspLeuPhePheTyrSeGIArg	120
Db	469	GTCAATCTTCCTTTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTATTCCAGAGG	528
Oy	121	GIuAlaAsnAspSerArgAspLeuGlyAlaIleValTyrCySValGlyValIlyAspPhe	140
Db	529	GAGGCTAATAGGCTCTGAGATCTTGGTGCAATGTTTACTGAGTGGTGTAAGAATTTC	588
Oy	141	AsnGIuThrGlnLeuAlaArgIleAlaAspSerIlyAspHisValPheProValAsnAsp	160
Db	589	AAAGAGCAACAAGTGGCCGGAATTCGGCAAGTAAGATCAATGTTCCCGGGAATGAC	648
Oy	161	GIyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeu	173
Db	649	GAGCTTCAGGCTCTGCAGACATCAATCCACTCAATTTTG	687

```

RESULT 5
US-10-038-307-23
; Sequence 23, Application US/10038307
; Publication No. US20030134766A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKANAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 1056
TYPE: DNA
ORGANISM: Homo sapiens
US-10-038-307-23

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Alignment Scores:	
Pred. No.:	3,84e-11
Score:	899.0
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	6
Gaps:	0
Length:	1056
Matches:	173
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-970-076-2_COPY_44_216 (1-173) X US-10-038-307-23 (1-1056)

Qy	AspLeuTYrPheIleuLeuAspIysSerGlySerValIleuH1SH1STTPASGIIleTYr	20
Db	142 GACCTGACTCACTTTTGACAAATACAGAGATGTGCTGCACCACTGGATGAATATAT	201
Qy	21 TyrPheValGIuGIuLeuAlaHisIstPheIleSePerGIIuLeuAAGmeSerPheIle	40
Db	202 TACTTTGTGGACAGTGTGGCTCACAAATTCAATCAGCCACAGTTGAGAAATGCTTTATT	261
Qy	41 ValPheSerThrArgGlyIYrThrThreuMetIysLeuThrgIuAspArgGIuIIleArg	60
Db	262 GTTTTCTCCACCCGAGAGAACCACTTATTAAGAACTGACAGAAACAGAGAACCAATCCGT	321
Qy	61 GInGlyIleuGIuGIuLeuGIuIlyValIeuProGIyGIyAspThrTYrMeHISGIuGly	80
Db	322 CAAGGCGCTTGAAGAAGACTCCAGAAAGTTCTGCGCAGAGAGAGACACTTCAATGAGTAAGGA	381
Qy	81 PheGIuArgAlaSerGIuGIuIIleTYrTYrGIuAsnArgGInGIyTYrArgThrAlaSer	100
Db	382 TTTGAAAAGGSCCAAGTACGACGATTTATTAATGAAAAACAGCAAGGGTACAGGACGCCAGC	441
Qy	101 ValIleIleAlaLeuThrAspGIyGIuIleuHISGIuAspIeuPhePheTYrSerGIuArg	120
Db	442 GTGATCATTCGCTTTGACTGATGAGAAACTCCATGAAGATCTCTTTTCTATTACAGAGG	501
Qy	121 GluAlaAsnArgSerArgAspIeuGIuValIleValTYrCySValGIyValIyAspPhe	140

```
|||||
Db      502 GAGGCTAATAGCTCGAATCTTGGTGCATTTACTGTGTGTGGTGAAGATTC 561
Qy      141 AaagltthGlnleuAaagllleAaapserLyAaaphiAaIaPheProVaIaAaap 160
Db      562 AATGAACAACAAGTGGCCCGGATTCGGAACAGTAAGATCAATGTGTTCCCGTAATGAC 621
Qy      161 GtPheGlnAlaLeuGlnGlyIleIleHISerIleLeu 173
Db      622 GGCTTTCAGGCTCTGCAGGATCATTCACCTCAATTTTG 660

RESULT 6
US-10-201-292-23
; Sequence 23, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-23
```

```
Alignment Scores:
Pred. No.:      3,84e-111      Length:      1056
Score:          899.00        Matches:      173
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             6            Gaps:          0
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US-09-970-076-2_COPY_44_216 (1-173) x US-10-201-292-23 (1-1056)

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Qy      1 AaPLeuTyRpheIleleuAaPlySerGlySerVaIleuHISITPaengluIleTyR 20
Db      142 GACCTGTAATCTCAATTTGGCAAAATCAGAAAGTGTGTGCACACCTGAATGAATCTAT 201
Qy      21 TyRpheVaIaGlnleuAaHISyRpheIleSerProGlnleuAaGMeSerPheIle 40
Db      202 TACTTGTGGAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAATGTCCTTATT 261
Qy      41 ValPheSerThyRArgIyThrThIleuMetLyIleuThrGlnAaPArgGlnIleArg 60
Db      262 GTTTTCTCAACCCAGGAACAACCTTAATGAATGACAGAAAGCAAGAAACCAATCCGT 321
Qy      61 GlnGlyLeuGlnleuGlnleuValIleuProGlyGlyAaPThyRmeChISGlnGly 80
Db      322 CAAGGCTTAAGAACTCCAGAAAGTCTGCGAGGAGAAACCTTACATGAAAGAA 381
Qy      81 PheGlnAaRgaIaSerGlnGlnIleTyRtyGlnAaAaRgGlnGlytyAaGThraIaSer 100
Db      382 TTGAAAGGCGCAGTGAAGAGATTTATTAAGAAACAGAAAGGGTACAGAGACGCCAGC 441
Qy      101 ValIleIleAlaLeuThyRArgIyGlnleuHISGlnAaPleuPheTyRserGlnArg 120
Db      442 GTCAATCAATGCTTTGATGAGAGAACTCCATGAAGATCTCTTTTCTAATTCAGAGAG 501
Qy      121 GlnAaAaAaRgSerAaPleuGlyAlaIleValTyRCyAaIaGlyValIyAaPhe 140
Db      502 GAGGCTAATAGGCTCGAATCTTGGTGCATTTACTGTGTGTGGTGAAGATTC 561
Qy      141 AaagltthGlnleuAaagllleAaapserLyAaaphiAaIaPheProVaIaAaap 160
Db      562 AATGAACAACAAGTGGCCCGGATTCGGAACAGTAAGATCAATGTGTTCCCGTAATGAC 621
```

```
Qy      161 GtPheGlnAlaLeuGlnGlyIleIleHISerIleLeu 173
Db      622 GGCTTTCAGGCTCTGCAGGATCATTCACCTCAATTTTG 660
```

```
RESULT 7
US-10-201-292-27
; Sequence 27, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-27
```

```
Alignment Scores:
Pred. No.:      5.9e-111      Length:      1401
Score:          899.00        Matches:      173
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             6            Gaps:          0
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US-09-970-076-2_COPY_44_216 (1-173) x US-10-201-292-27 (1-1401)

```
Qy      1 AaPLeuTyRpheIleleuAaPlySerGlySerVaIleuHISITPaengluIleTyR 20
Db      142 GACCTGTAATCTCAATTTGGCAAAATCAGAAAGTGTGTGCACACCTGAATGAATCTAT 201
Qy      41 ValPheSerThyRArgIyThrThIleuMetLyIleuThrGlnAaPArgGlnIleArg 60
Db      262 GTTTTCTCAACCCAGGAACAACCTTAATGAATGACAGAAAGCAAGAAACCAATCCGT 321
Qy      61 GlnGlyLeuGlnleuGlnleuValIleuProGlyGlyAaPThyRmeChISGlnGly 80
Db      322 CAAGGCTTAAGAACTCCAGAAAGTTCGCGAGGAGAAACCTTACATGAAAGAA 381
Qy      81 PheGlnAaRgaIaSerGlnGlnIleTyRtyGlnAaAaRgGlnGlytyAaGThraIaSer 100
Db      382 TTGAAAGGCGCAGTGAAGAGATTTATTAAGAAACAGAAAGGGTACAGAGACGCCAGC 441
Qy      101 ValIleIleAlaLeuThyRArgIyGlnleuHISGlnAaPleuPheTyRserGlnArg 120
Db      442 GTCAATCAATGCTTTGATGAGAGAACTCCATGAAGATCTCTTTTCTAATTCAGAGAG 501
Qy      121 GlnAaAaAaRgSerAaPleuGlyAlaIleValTyRCyAaIaGlyValIyAaPhe 140
Db      502 GAGGCTAATAGGCTCGAATCTTGGTGCATTTACTGTGTGTGGTGAAGATTC 561
Qy      141 AaagltthGlnleuAaagllleAaapserLyAaaphiAaIaPheProVaIaAaap 160
Db      562 AATGAACAACAAGTGGCCCGGATTCGGAACAGTAAGATCAATGTGTTCCCGTAATGAC 621
Qy      161 GtPheGlnAlaLeuGlnGlyIleIleHISerIleLeu 173
Db      622 GGCTTTCAGGCTCTGCAGGATCATTCACCTCAATTTTG 660

RESULT 8
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```
US-10-201-292-29
; Sequence 29, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-29

Alignment Scores:
Pred. No.: 5.99e-111      Length: 1401
Score: 899.00           Matches: 173
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%         Indels: 0
DB: 6                     Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-10-201-292-29 (1-1401)
QY 1 AspleuTyrrPheilleuAaplySerGlySerValIleuHishIstrPaengluIleTyr 20
DB 142 GACCTGACTTCATTTTGGACAATTCAGAAAGTGTGTGCAACCACTGGAAATGAATCTAT 201
QY 21 TyrPheValGluGluLeuAahIshIlyPheIleSerProGluLeuArgMetSerPheIle 40
DB 202 TACTTGTGGACAGTGGTGTCAAAATTCATCAGCCACAGTTGAGAAATGTCCTTATT 261
QY 41 ValPheSerThrArgGlyThrThrLeuMetIleuThrGluuAparGluGluIleArg 60
DB 262 GTTTTCTCCACCCGAGGAAACCACTTAATGAAATGACAGAAAGCAAGAAACAATCCGT 321
QY 61 GluGlyLeuGluGluLeuGluValIleuProGlyValAspThrTyrMetHisGluGly 80
DB 322 CAAGGCTTAAGAAACTCCAGAAAGTTCTGCCAGAGAGAGACACTTACATGATGAAGA 381
QY 81 PheGluArgAlaSerGluGluIleTyrTyrGluuAparGluGlyTyrArgThrAlaSer 100
DB 382 TTGAAAGGCGCAGTAGAGATTTATTATGAAACAGACAGAGGTACAGAGCCAGC 441
QY 101 ValIleIleAlaLeuThrArgGlyGluLeuHishIleuAparIleuPheThrTyrSerGluArg 120
DB 442 GTCATCATTCCTTTGATGATGAGAACTCCATGAAAGATCTCTTTTCTATTTCAGAGG 501
QY 121 GluAlaAsnArgSerArgAparIleuValIleValTyrCysValGlyValIlyAspPhe 140
DB 502 GAAGCTAATAGCTTCAGAGATCTTGGTGCATATGTTTACTGTGTGTGTAAGAAATTC 561
QY 141 AsnGluThrGluLeuAlaArgIleAlaAspSerIlyAspHisValPheProValAsnAsp 160
DB 562 AATGAGACACAGCTGGCCGGATTTGGGACAGTAAAGATCATGTGTTCCCGTAATGAC 621
QY 161 GlyPheGluAlaLeuGluGlyIleIleHisSerIleLeu 173
DB 622 GGCTTTCAGGCTCTGCAAGGATCATCATCAATTTTG 660

RESULT 9
US-11-047-278-1
; Sequence 1, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
```

```
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)..(1207)
US-11-047-278-1

Alignment Scores:
Pred. No.: 5.99e-111      Length: 1414
Score: 899.00           Matches: 173
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%         Indels: 0
DB: 10                     Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-11-047-278-1 (1-1414)
QY 1 AspleuTyrrPheilleuAaplySerGlySerValIleuHishIstrPaengluIleTyr 20
DB 233 GACCTGACTTCATTTTGGACAATTCAGAAAGTGTGTGCAACCACTGGAAATGAATCTAT 232
QY 21 TyrPheValGluGluLeuAahIshIlyPheIleSerProGluLeuArgMetSerPheIle 40
DB 293 TACTTGTGGACAGTGGTGTCAAAATTCATCAGCCACAGTTGAGAAATGTCCTTATT 352
QY 41 ValPheSerThrArgGlyThrThrLeuMetIleuThrGluuAparGluGluIleArg 60
DB 353 GTTTTCTCCACCCGAGGAAACCACTTAATGAAATGACAGAAAGCAAGAAACAATCCGT 412
QY 61 GluGlyLeuGluGluLeuGluValIleuProGlyValAspThrTyrMetHisGluGly 80
DB 413 CAAGGCTTAAGAAACTCCAGAAAGTTCTGCCAGAGAGAGACACTTACATGATGAAGA 472
QY 81 PheGluArgAlaSerGluGluIleTyrTyrGluuAparGluGlyTyrArgThrAlaSer 100
DB 473 TTGAAAGGCGCAGTAGAGATTTATTATGAAACAGACAGAGGTACAGAGCCAGC 532
QY 101 ValIleIleAlaLeuThrArgGlyGluLeuHishIleuAparIleuPheThrTyrSerGluArg 120
DB 533 GTCATCATTCCTTTGATGATGAGAACTCCATGAAAGATCTCTTTTCTATTTCAGAGG 592
QY 121 GluAlaAsnArgSerArgAparIleuValIleValTyrCysValGlyValIlyAspPhe 140
DB 593 GAAGCTAATAGCTTCAGAGATCTTGGTGCATATGTTTACTGTGTGTGTAAGAAATTC 652
QY 141 AsnGluThrGluLeuAlaArgIleAlaAspSerIlyAspHisValPheProValAsnAsp 160
DB 653 AATGAGACACAGCTGGCCGGATTTGGGACAGTAAAGATCATGTGTTCCCGTAATGAC 712
QY 161 GlyPheGluAlaLeuGluGlyIleIleHisSerIleLeu 173
DB 713 GGCTTTCAGGCTCTGCAAGGATCATCATCAATTTTG 751

RESULT 10
US-11-047-278-9
; Sequence 9, Application US/11047278
; Publication No. US20050196407A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
```

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; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/11/047,278
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: US/09/970,076
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (380)..(1033)
US-11-047-278-9

Alignment Scores:
Pred. No.: 6,136-111 Length: 1436
Score: 899.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-11-047-278-9 (1-1436)

QY 1 AspleuTYRPhelIleuAaplySerGISeValIeuHISHTPaNSGluIleTYr 20
DB 272 GACCTGTAATTCAATTTGGCAAAATCAGAAAGTGTGTGACCACTGGAAATGAAATCTAT 331
QY 21 TYRPhelValIGluInleuAaHISlySPheIIeserProGInleuArgMetSerPheIIe 40
DB 332 TACTTTGTGAAACAGTTGGCTCACAATTCATCCAGCCCAAGTTGAGAAATGCTCTTATT 391
QY 41 ValPheSerThrArgIlyThrThrLeuMetIlySeuThrGIuAapArgGIuInIleArg 60
DB 392 GTTTTTCACACCCGAGAAACAACTTAATGAACTGACAGAGACAGAGAAACAATCCGT 451
QY 61 GInGIyLeuGIuGIuLeuGIuInlyValIeuProGIyGIyAapThrTYrMetHISGIuGIy 80
DB 452 CAAGGCTAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGCAATGAAAGGA 511
QY PheGIuArgAlaSerGIuInIleTYrTYrGIuAaArgGIuInIlyTYrArgThraIaSer 100
DB 512 TTTTAAAGGCCAGTGAAGCATTTTATTTGAAACAGACAAAGGTTACAGAGACGCTAGC 571
QY 101 ValIleIleAlaIeuThraSPGIyGIuInleuHISGIuAapLeuPheTYrSerGIuArg 120
DB 572 GTATCATTTGCTTGACGTAGTGAAGAACTCCATGAAGATCTTTTCTATTCCAGAGAG 631
QY 121 GIuAlaAaArgSerArgAapLeuGIyAlaIleValTYrCySValIGIyValIyAaSPhe 140
DB 632 GAGGCTAAATAGGTCTCGAGATCTTGCTGTCATTTTAATCTGTGTGGTGGAAAGATTC 691
QY 141 AaNGluThrGIuInleuAaArgIleAlaAaSPSerIyAaSPHISValIPheProValAaAaSP 160
DB 692 AATGAGACACAGCTGGCCCGGATTCGGACAGTAAGATCATGTGTTCCTCCGTAAATGAC 751
QY 161 GIyPheGInAlaLeuGIuInIyIleIleHISerIleu 173
DB 752 GGCTTTCAAGCTCTGCAAGGATCATTCATCAATTTTG 790

RESULT 11
US-10-133-937-58
; Sequence 58, Application US/10133937
; Publication No. US20030207278A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
```

```
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; FILE REFERENCE: OTHER BIOLOGICAL STATES
; CURRENT APPLICATION NUMBER: US/10/133,937
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 58
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-937-58

Alignment Scores:
Pred. No.: 6,246-111 Length: 1454
Score: 899.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-10-133-937-58 (1-1454)

QY 1 AspleuTYRPhelIleuAaplySerGISeValIeuHISHTPaNSGluIleTYr 20
DB 273 GACCTGTAATTCAATTTGGCAAAATCAGAAAGTGTGTGACCACTGGAAATGAAATCTAT 332
QY 21 TYRPhelValIGluInleuAaHISlySPheIIeserProGInleuArgMetSerPheIIe 40
DB 333 TACTTTGTGAAACAGTTGGCTCACAATTCATCCAGCCCAAGTTGAGAAATGCTCTTATT 392
QY 41 ValPheSerThrArgIlyThrThrLeuMetIlySeuThrGIuAapArgGIuInIleArg 60
DB 393 GTTTTTCACACCCGAGAAACAACTTAATGAACTGACAGAGACAGAGAAACAATCCGT 452
QY 61 GInGIyLeuGIuGIuLeuGIuInlyValIeuProGIyGIyAapThrTYrMetHISGIuGIy 80
DB 453 CAAGGCTAGAAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATGCAATGAAAGGA 512
QY PheGIuArgAlaSerGIuInIleTYrTYrGIuAaArgGIuInIlyTYrArgThraIaSer 100
DB 513 TTTGAAAGGCCAGTGAAGCATTTTATTTGAAACAGACAAAGGTTACAGAGACGCTAGC 572
QY 101 ValIleIleAlaIeuThraSPGIyGIuInleuHISGIuAapLeuPheTYrSerGIuArg 120
DB 573 GTATCATTTGCTTGACGTAGTGAAGAACTCCATGAAGATCTTTTCTATTCCAGAGAG 632
QY 121 GIuAlaAaArgSerArgAapLeuGIyAlaIleValTYrCySValIGIyValIyAaSPhe 140
DB 633 GAGGCTAAATAGGTCTCGAGATCTTGCTGTCATTTTAACTGTGTGGTGGAAAGATTC 692
QY 141 AaNGluThrGIuInleuAaArgIleAlaAaSPSerIyAaSPHISValIPheProValAaAaSP 160
DB 693 AATGAGACACAGCTGGCCCGGATTCGGACAGTAAGATCATGTGTTCCTCCGTAAATGAC 752
QY 161 GIyPheGInAlaLeuGIuInIyIleIleHISerIleu 173
DB 753 GGCTTTCAAGCTCTGCAAGGATCATTCATCAATTTTG 791

RESULT 12
US-10-159-563-58
; Sequence 58, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
```



```
/ TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
/ FILE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
/ FILE REFERENCE: 11613.56US11
/ CURRENT APPLICATION NUMBER: US/10/159,563
/ CURRENT FILING DATE: 2002-12-09
/ PRIOR APPLICATION NUMBER: US 10/133,937
/ PRIOR FILING DATE: 2002-04-25
/ NUMBER OF SEQ ID NOS: 444
/ SOFTWARE: PatentIn Version 3.1
/ SEQ ID NO 58
/ LENGTH: 1454
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-159-563-58

Alignment Scores:
Pred. No.: 6,24e-111 Length: 1454
Score: 899.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-10-159-563-58 (1-1454)
QY 1 AspleuTyRphejleuAaplySerglySerValleuHshstRPaengluileTyR 20
DB 273 GACCTGTACTTCAATTTGGACAAATTCAGAAAGTGCTGCAACCACTGAATGAATTTAT 332
QY 21 TyrPheValgluInleuAlahlslyPheIleSerProglInleuArgMetSerPheIle 40
DB 333 TACTTTGTGGAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAAGATGCTTTATT 392
QY 41 ValPheSerThrArgglyThrThleuMetIlyleuThrgluAapArggluInIleArg 60
DB 393 GTTTTCTCCACCCGAGAACAACTTAATGAACTGACAGAGACAGAAACAAATCCGT 452
QY 61 GluGlYleuGlYleuGlYleuValleuProglYglYAspThrTYrMetHsgluGlY 80
DB 453 CAAGGCTTACAGAACTCCAGAAAGTTCTCCAGAGAGACACTTACATGACATGAAGA 512
QY 81 PheGlYArgAlaSerGluInIleTyRtyGluAsnArgGlnGlyTYrArgThraAlaSer 100
DB 513 TTTGAAAGGCCCACTGACGAGATTATTATGAAGAAACAGAAAGGTTACAGAGACGCC 572
QY 101 ValIleIleAlaLeuThraPglyGluLeuHsgluAapleuPhePheTYrSerGluArg 120
DB 573 GTCATCATTCCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTCTATTGAGAGAG 632
QY 121 GluAlaAsnArgSerArgAapleuGlyAlaIleValTYrCySValGlyValIyAspPhe 140
DB 633 GAGGCTAATAGGCTTCAGATCTTGGTGCATATTGTTACTGTGTGTGAGAAAGATTTC 692
QY 141 AsnGlYthrgInleuAlaArgIleAlaAspSerIyAspHsValPheProValAsnAsp 160
DB 693 AATGAGACACAGCTGGCCCGATTTGCCGACAGTAAAGATCATGTGTTCCCGTAATGAC 752
QY 161 GlyPheGlnAlaLeuGlnGlyIleIleHsSerIleleu 173
DB 753 GGCCTTCAGGCTCTGCAAGGATCATCATCAATTTTG 791

RESULT 13
US-10-201-292-31
/ Sequence 31, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
```

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/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 31
/ LENGTH: 1464
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-201-292-31

Alignment Scores:
Pred. No.: 6,31e-111 Length: 1464
Score: 899.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-10-201-292-31 (1-1464)
QY 1 AspleuTyRphejleuAaplySerglySerValleuHshstRPaengluileTyR 20
DB 142 GACCTGTACTTCAATTTGGACAAATTCAGAAAGTGCTGCAACCACTGAATGAATTTAT 201
QY 21 TyrPheValgluInleuAlahlslyPheIleSerProglInleuArgMetSerPheIle 40
DB 202 TACTTTGTGGAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAAGATGCTTTATT 261
QY 41 ValPheSerThrArgglyThrThleuMetIlyleuThrgluAapArggluInIleArg 60
DB 262 GTTTTCTCCACCCGAGAACAACTTAATGAACTGACAGAGACACTTACATGACATGAAGA 321
QY 61 GluGlYleuGlYleuGlYleuValleuProglYglYAspThrTYrMetHsgluGlY 80
DB 322 CAAGGCTTACAGAACTCCAGAAAGTTCTCCAGAGAGACACTTACATGACATGAAGA 381
QY 81 PheGlYArgAlaSerGluInIleTyRtyGluAsnArgGlnGlyTYrArgThraAlaSer 100
DB 382 TTTGAAAGGCCCACTGACGAGATTATTATGAAGAAACAGAAAGGTTACAGAGACGCC 441
QY 101 ValIleIleAlaLeuThraPglyGluLeuHsgluAapleuPhePheTYrSerGluArg 120
DB 442 GTCATCATTCCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTCTATTGAGAGAG 501
QY 121 GluAlaAsnArgSerArgAapleuGlyAlaIleValTYrCySValGlyValIyAspPhe 140
DB 502 GAGGCTAATAGGCTTCAGATCTTGGTGCATATTGTTACTGTGTGTGAGAAAGATTTC 561
QY 141 AsnGlYthrgInleuAlaArgIleAlaAspSerIyAspHsValPheProValAsnAsp 160
DB 562 AATGAGACACAGCTGGCCCGATTTGCCGACAGTAAAGATCATGTGTTCCCGTAATGAC 621
QY 161 GlyPheGlnAlaLeuGlnGlyIleIleHsSerIleleu 173
DB 622 GGCCTTCAGGCTCTGCAAGGATCATCATCAATTTTG 660

RESULT 14
US-10-201-292-33
/ Sequence 33, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 33
/ LENGTH: 1534
/ TYPE: DNA
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ORGANISM: Homo sapiens
US-10-201-292-33

Alignment Scores:

Pred. No.:	6.77e-111	Length:	1534
Score:	899.00	Matches:	173
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-970-076-2_copy_44_216 (1-173) x US-10-201-292-33 (1-1534)

```
QY 1 AspleuTyPheIleuAapLySerGlySerValIleuHsiSTrPaangIuIeTy 20
DB 142 GACCTGACTTCATTGGAACAATCGAAGTGTGTCACCACTGGAATGAATCTAT 201
QY 21 TyrPheValGluGluLeuAaHsiLyPheIleSerProGluLeuArgMetSerPheIle 40
DB 202 TACTTGTGGAACAAGTGGCTCAAAATTCATCAGCCCAAGTTGAAGATGCTTTATT 261
QY 41 ValPheSerThrArgGlyThrThrLeuMetLyLeuThrGluAapArgGluGluIleArg 60
DB 262 GTTTCTCCACCCGAGGAAACAACCTTAATGAACAGACAGAAACAATCCGT 321
QY 61 GlnGlyLeuGluGluLeuGluIleValIleuProGlyGlyAspThrTyrmethIsgIuGly 80
DB 322 CAAGGCTTAGAAGAACTCCGAAAGTTCTCCAGAGAGAACACTTACATGCAATGAAGA 381
QY 81 PheGluArgAlaSerGluGluIleTyTyTyGluAaArgGlnGlyTyraArgThrAlaSer 100
DB 382 TTGAAAGGGCCAGTGAGAGATTTATATGAAGAAACAGACAGAGTACAGACAGCCAGC 441
QY 101 ValIleIleAlaLeuThrAapGlyGluLeuHsiGluAapLeuPhePheTySerGluArg 120
DB 442 GTCATCATTCCTTGAATGATGAGAACTCCATGAAGATCTCTTTTCTATTCCAGAGAG 501
QY 121 GluAlaAaArgSerArgAapLeuGlyAlaIleValTyCyValGlyValIleAaApphe 140
DB 502 GAGGCTTAATAGGCTTCGAAATCTTGTCATATGTTTACTGTGTGTGAAGATTTTC 561
QY 141 AaArgIuThrGluLeuAaArgIleAlaAaPserLyAaPheIleValPheProValAaAaP 160
DB 562 AATGAGACACAGCTGCCGCGATTCGCGACAGTAAAGATCATGTGTTCCCGTAATGAC 621
QY 161 GlyPheGlnAlaLeuGlnGlyIleIleHsiSerIleu 173
DB 622 GGCTTCAGGCTCTGCAAGGATCATCATCAATTTTG 660
```

RESULT 15

US-10-201-292-35
; Sequence 35, Application US/10201292
; Publication No. US20030141193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 1608
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-35

Alignment Scores:

Pred. No.:	7.28e-111	Length:	1608
Score:	899.00	Matches:	173

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-970-076-2_copy_44_216 (1-173) x US-10-201-292-35 (1-1608)

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QY 1 AspleuTyPheIleuAapLySerGlySerValIleuHsiSTrPaangIuIeTy 20
DB 142 GACCTGACTTCATTGGAACAATCGAAGTGTGTCACCACTGGAATGAATCTAT 201
QY 21 TyrPheValGluGluLeuAaHsiLyPheIleSerProGluLeuArgMetSerPheIle 40
DB 202 TACTTGTGGAACAAGTGGCTCAAAATTCATCAGCCCAAGTTGAAGATGCTTTATT 261
QY 41 ValPheSerThrArgGlyThrThrLeuMetLyLeuThrGluAapArgGluGluIleArg 60
DB 262 GTTTCTCCACCCGAGGAAACAACCTTAATGAACAGACAGAAACAATCCGT 321
QY 61 GlnGlyLeuGluGluLeuGluIleValIleuProGlyGlyAspThrTyrmethIsgIuGly 80
DB 322 CAAGGCTTAGAAGAACTCCGAAAGTTCTCCAGAGAGAACACTTACATGCAATGAAGA 381
QY 81 PheGluArgAlaSerGluGluIleTyTyTyGluAaArgGlnGlyTyraArgThrAlaSer 100
DB 382 TTGAAAGGGCCAGTGAGAGATTTATATGAAGAAACAGACAGAGTACAGACAGCCAGC 441
QY 101 ValIleIleAlaLeuThrAapGlyGluLeuHsiGluAapLeuPhePheTySerGluArg 120
DB 442 GTCATCATTCCTTGAATGATGAGAACTCCATGAAGATCTCTTTTCTATTCCAGAGAG 501
QY 121 GluAlaAaArgSerArgAapLeuGlyAlaIleValTyCyValGlyValIleAaApphe 140
DB 502 GAGGCTTAATAGGCTTCGAAATCTTGTCATATGTTTACTGTGTGTGAAGATTTTC 561
QY 141 AaArgIuThrGluLeuAaArgIleAlaAaPserLyAaPheIleValPheProValAaAaP 160
DB 562 AATGAGACACAGCTGCCGCGATTCGCGACAGTAAAGATCATGTGTTCCCGTAATGAC 621
QY 161 GlyPheGlnAlaLeuGlnGlyIleIleHsiSerIleu 173
DB 622 GGCTTCAGGCTCTGCAAGGATCATCATCAATTTTG 660
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Search completed: December 19, 2005, 02:10:29
Job time : 561.247 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2005, 07:41:36 ; Search time 139.602 Seconds
(Without alignments)
607.449 Million cell updates/sec

Title: US-09-970-076-2_COPY_44_216

Perfect score: 899

Sequence: 1 DLYFIDKSGSVLHMNEIF.....HFPVNDGFGALGIIHSIL 173

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q/cg2_1/USPTO.epool/US09970076/rnuc.14122005.11853_21065/app.query.fasta.1.2410
-DB=Published Applications NA New -QMT=fastap -SUFF=trpbp -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -MATRIX=blosum62
-TRANS=human0.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09970076 @CGN_1_1_675 @rnuc.14122005.11853_21065
-NCPUB=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA New.*

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2: /cg2_6/prodata/1/pubpna/US06_NEW_PUB.seq.*
3: /cg2_6/prodata/1/pubpna/US07_NEW_PUB.seq.*
4: /cg2_6/prodata/1/pubpna/US08_NEW_PUB.seq.*
5: /cg2_6/prodata/1/pubpna/PCT_NEW_PUB.seq.*
6: /cg2_6/prodata/1/pubpna/US10_NEW_PUB.seq.*
7: /cg2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
8: /cg2_6/prodata/1/pubpna/US11_NEW_PUB.seq2.*
9: /cg2_6/prodata/1/pubpna/US11_NEW_PUB.seq3.*
10: /cg2_6/prodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	899	100.0	5540	7 US-11-186-284-198	Sequence 198, App
2	128.5	14.3	4740	7 US-11-080-026-3	Sequence 3, Appl
3	118.5	13.2	11447	7 US-11-186-284-25	Sequence 25, Appl
4	115	12.8	2834	6 US-10-750-185-39040	Sequence 39040, A
5	108	12.0	3564	6 US-10-601-368-20	Sequence 20, Appl
6	108	12.0	4858	6 US-10-601-368-19	Sequence 19, Appl
7	104	11.6	3564	6 US-10-601-368-2	Sequence 2, Appl
8	104	11.6	3967	7 US-11-000-463-574	Sequence 574, App

9	104	11.6	3969	7 US-11-000-463-102	Sequence 102, App
10	104	11.6	5042	6 US-10-601-368-1	Sequence 1, Appl
11	101.5	11.3	2501	6 US-10-821-234-182	Sequence 182, App
12	100.5	11.2	3449	6 US-10-131-826A-293	Sequence 293, App
13	98.5	11.0	1325	6 US-10-750-185-56394	Sequence 56394, A
14	96.5	10.7	3175	6 US-10-995-561-464	Sequence 464, App
15	96.5	10.7	3464	6 US-10-995-561-465	Sequence 465, App
16	96.5	10.7	3468	6 US-10-995-561-466	Sequence 466, App
17	96.5	10.7	47572	6 US-10-995-561-13356	Sequence 13356, A
18	95	10.6	3884	6 US-10-601-368-17	Sequence 17, Appl
19	91.5	10.2	3868	6 US-10-995-561-404	Sequence 404, App
20	82	9.1	2773	7 US-11-102-240-33	Sequence 33, Appl
21	81.5	9.1	1062	7 US-11-137-465-11	Sequence 11, Appl
22	81.5	9.1	1347	7 US-11-137-465-12	Sequence 12, Appl
23	79.5	8.8	3366	6 US-10-467-657-6111	Sequence 6111, App
24	75	8.3	3435	6 US-10-793-626-3648	Sequence 3648, App
25	74	8.2	1688	6 US-10-510-186-157	Sequence 157, App
26	73.5	8.2	1530	6 US-10-793-626-2879	Sequence 2879, App
27	73.5	8.2	2996	6 US-10-793-626-3563	Sequence 3563, App
28	73.5	8.2	3092	6 US-10-793-626-3559	Sequence 3559, App
29	73.5	8.2	3900	6 US-10-793-626-4177	Sequence 4177, App
30	72	8.0	795	6 US-10-793-626-387	Sequence 387, App
31	72	8.0	2361	6 US-10-467-962B-102	Sequence 102, App
32	72	8.0	2657	6 US-10-793-626-4324	Sequence 4324, App
33	72	8.0	3281	6 US-10-793-626-4324	Sequence 4324, App
34	72	8.0	3633	6 US-10-793-626-4307	Sequence 4307, App
35	70	7.8	1305	6 US-10-467-657-5693	Sequence 5693, App
36	70	7.8	1305	6 US-10-467-657-5693	Sequence 5693, App
37	70	7.8	1404	6 US-10-467-657-5695	Sequence 5695, App
38	70	7.8	3290	6 US-10-793-626-3960	Sequence 3960, App
39	70	7.8	96988	7 US-11-117-187-196	Sequence 196, App
40	69.5	7.7	730	6 US-10-750-185-61019	Sequence 61019, A
41	69.5	7.7	1457	6 US-10-467-657-7845	Sequence 7845, App
42	69	7.7	726	6 US-10-467-657-7305	Sequence 7305, App
43	69	7.7	766	6 US-10-467-657-7299	Sequence 7299, App
44	68.5	7.6	3144	6 US-10-392-234A-17	Sequence 17, Appl
45	68.5	7.6	5592	7 US-11-192-967-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-11-186-284-198
Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: BURGART, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF COLON CANCER
FILE REFERENCE: MEMO-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
PRIORITY FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 198
LENGTH: 5540
TYPE: DNA

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/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (144)...(1838)
US-11-186-284-198

Alignment Scores:
Pred. No.: 1,71e-108 Length: 5540
Score: 899.00 Matches: 173
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-970-076-2_COPY_44_216 (1-173) x US-11-186-284-198 (1-5540)

QY 1 AapLeuTyRPhelIeLeuAapLySeRgLySeRValLeuHIsHtRPaNgLuIleTyR 20
DB 273 GACCTGTACTTCTTATTTGACAAATCAGAAAGTGTGTGCACACCTGGAATGAAATCTTAT 332
QY 21 TyRPhVaIgLuGInLeuAlAhIsLySPheISeRProGInLeuArGMeSeRPhelle 40
DB 333 TACTTTGTGGAACAAGTTGGCTCACAATTCATCAGCCACAGTTGAGAAATGCTTTATT 392
QY 41 ValPheSeRThArGgLyThRThLeuMeLyLeuThRgLuAaPArGgLuGInIleArG 60
DB 393 GTTTTCTCCACCCGAGGAACAACCTTAATGAACTGACAGAAACAGAAACAATCCGT 452
QY 61 GInGlyLeuGluGInLeuGInLyVaIleuPProGlyGlyAaSPHrTyRMeThIsGluGly 80
DB 453 CAAGGCTTAAAGAAATCCAGAAAGTTCTGCGAGAGAGACACTTAATCATGTGAAGGA 512
QY 81 PhGgLuAaRgAlaSeRgLuGInIleTyRThRgLuAaAaRgGInGlyTyRArGThRaIaSeR 100
DB 513 TTTGAAAGGCGCATGAGCATTTATTATGAAACAGACAGGATCAGACAGCCAGC 572
QY 101 ValIleIleAlaLeuThRaSPgLyGluLeuHIsGluAaPLeuPheRhySeRgLuArG 120
DB 573 GTCATCATCTTCTTGAATGATGAGAACTCATGAACATCTTTTCTATTCAGAGAGG 632
QY 121 GluAlaAaAaRgSeRArGaPLeuGlyAlaIleValTyRcySvaIgLyVaIlyAaSPHe 140
DB 633 GAGGCTAAATGAGTCTCAGATCTTGTCGCAATGTTAACTGTGTGTGAAAGATTC 692
QY 141 AaSPgThRgInLeuAlaRgIleAlaAaSPSeRlyAaSPHIsValPheProValaAaSP 160
DB 693 AATGACACACAGCTGCGCCGATTCGCGACATGAGATCATGTGTTCCCGATGAC 752
QY 161 GlyPheGInAlaLeuGInGlyIleIleHIsSeRtleu 173
DB 753 GGCCTTCAGGCTCTGCAAGGATCATCATCAATTTTG 791

RESULT 2
US-11-080-026-3
/ Sequence 3, Application US/11080026
/ Publication No. US20050260192A1
/ GENERAL INFORMATION:
/ APPLICANT: Springer, Timothy A.
/ APPLICANT: Shimooka, Motomu
/ TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
/ FILE REFERENCE: CBPF-P02-021
/ CURRENT APPLICATION NUMBER: US/11/080, 026
/ PRIOR FILING DATE: 2005-03-15
/ PRIOR APPLICATION NUMBER: 09/945,265
/ PRIOR FILING DATE: 2001-08-31
/ PRIOR APPLICATION NUMBER: US 60/229,700
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: fastseq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 4740
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/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-11-080-026-3

Alignment Scores:
Pred. No.: 8,26e-06 Length: 4740
Score: 128.50 Matches: 51
Percent Similarity: 46.60% Conservative: 38
Best Local Similarity: 26.70% Mismatches: 63
Query Match: 14.29% Indels: 39
DB: 7 Gaps: 11

US-09-970-076-2_COPY_44_216 (1-173) x US-11-080-026-3 (1-4740)

QY 1 AapLeuTyRPhelIeLeuAapLySeRgLySeRValLeu---HIsHtRPaNgLuIle 19
DB 520 GACATTCCTTCTTATTTGATGAGCTGTGTGATCAGATCCACATGACTTGGCGGAG 579
QY 20 TyRTyRPhVaIgLuGInLeuAlAhIsLySPheISeRProGInLeuArGMeSeRPh 39
DB 580 AAGGAGTTGTCTCACT-----GTGATGAGCAATTAATAAAGTCCAA 624
QY 40 IleValPheSeRThArGgLyThRThLeuMeLyLeuThRgLuAaP----- 55
DB 625 ACCTGTCTCT-----TTGATGCACTCTGAGAAATTCGGATTCAC 669
QY 56 -----ArgGluGInIleArGInGlyLeuGluGluGluGln 67
DB 670 TTACCTTCAAGAGATTCAGAAACAACCTTAACCAAGATCATCTGTGAAGCAATTAAG 729
QY 68 LyVaIleuPProGlyGlyAaSPHrTyRMeThIsGluGlyPhGgLuAaRgAlaSeRgLuGln 87
DB 730 CAGCTGCTT-----GGCGGACACACACGCGCAGCGGATCCGCAAGTGTGACAGAG 783
QY 88 IleTyRThRgLuAaAaRgInGlyTyRArGThRaIa---SeRValIleAlaLeuThR 106
DB 784 CTGTTTAACATCACCAACGAGCCGAAAGAAATGCTTTAAGATCTTCAATGTGATCAG 843
QY 107 AaSPgLyGluLeuHIsGluAaPLeuPheRhySeRgLu-----ArgGluAlaAaArG 124
DB 844 GATGAGAAATGTTGGCATCTTGGATATGAGATGATCATCCCTGAGGACAGACAG 903
QY 125 SeRArGaPLeuGlyAlaIleValTyRcySvaIgLyVaIlyAaSPHeaSPHIsVal 144
DB 904 GAG-----GAGTCACTGCTCAATCATGAGTGGGTGAGATCCCTTCGCACTGAG 954
QY 145 LeuAlaArG-----IleAlaAaSPe-----LyAaSPHIsValPhePro 157
DB 955 AATCCCGCAAGAGCTTAATACATCGATCCAGACCGCCCTGTGATCAGATGTTCCAG 1014
QY 158 ValaAaSPgLyPheGInAlaLeuGInGlyIle 168
DB 1015 GTGAATAC---TTTGAGGCTCTGAAGACATT 1044

RESULT 3
US-11-186-284-25
/ Sequence 25, Application US/11186284
/ Publication No. US20050266493A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: Berger, Allison
/ APPLICANT: Guillemette, Tracy L.
/ APPLICANT: Kamatkar, Shubhangi
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Monahan, John E.
/ APPLICANT: Thibodeau, Stephen N.
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
/ FILE REFERENCE: THERAPY FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ CURRENT FILING DATE: 2005-07-21
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; PRIOR APPLICATION NUMBER: US/10/301,832
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11447
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(9192)
; US-11-186-284-25
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Alignment Scores:
Pred. No.: 0.00645 Length: 11447
Score: 118.50 Matches: 54
Percent Similarity: 49.44% Conservative: 35
Best Local Similarity: 30.00% Mismatches: 68
Query Match: 13.18% Indels: 23
DB: Gaps: 12
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US-09-970-076-2_COPY_44_216 (1-173) x US-11-186-284-25 (1-11447)

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DB 1318 GATATTGTGTTTGGTGGTATGCTCTATAGCATGGAGTGGAACTTTGTTAAAGTT 1377
QY 20 TyTyTyRheValGluGlnLeuAlaHishLyPhe---lleSeRPro---GlnLeuArgMet 37
DB 1378 AGAGCCCTTTTGGAAAGTTCTTGTAAGAAAGTTTGAAATTTCCACCAATAGGGTCCAGATT 1437
QY 38 SerPheIleValPheSeRThr-----ArgGlyThrPheLeuMetLySeuThrGlu 54
DB 1438 AGCTTGTGCAATACACCGCGGATCTCTATAGCATGGTTCATGAAAATTTCCACCA 1497
QY 55 AspArgGluGlnIleArgGlnGlyLeuGlnGluLeuGlnLySeuValleuPro-----Gly 72
DB 1498 GTTGAAGATATTAATT-----GAAGCATTAACAACCTTCCTTACAGAGGA 1542
QY 73 GlyAspThrTyRheHishGluGlyPheGluArgAlaSeRgLuGlnIleTyTyTyGluAsn 92
DB 1543 GGATCTCAAAATACCTGGCAAGCATAGCTTATGTCCAGAGAAATATTTGTGCTACG 1602
QY 93 ArgGlnGlyTyTyTyRgThr-----AlaSeRValIleIleAlaLeuThrAspGlyGluLeu 110
DB 1603 AAG--GGATCAAGAACCAATGTCGCAAGGTCTATCTTATCAGAGTGGGAA-- 1656
QY 111 HieGluAspLeuPhePheTyRSeRgLuArgGluAlaAsnArgSeRArgAspLeuGlyAla 130
DB 1657 TCATTCAGATCTTTC-----AGAGATCCCTGCGCTAAACCTGAGGAATTCAGATGT 1707
QY 131 IleValTyCyValGlyValIlyAspPheAsnGluThrGlnLeuAlaArgIleAlaAsp 150
DB 1708 GAATCTTTCAGATGGTGGTGAAGATGCGCTTCGTCAGAAATTTGAAAGCTATTCCTCT 1767
QY 151 -----SerLyAspHishValPheProValAsnAspGlyPheGlnAlaLeuGlnGlyIle 168
DB 1768 CTTCTGCAAGAACCCATGTGTTCACAGTGAAGAT--TTGATGCTTTTTCAGAGGATA 1824
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RESULT 4
US-10-750-185-39040/c
; Sequence 39040, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
```

```
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Denise
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: NM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39040
; LENGTH: 2834
; TYPE: DNA
; ORGANISM: Bovine
; US-10-750-185-39040
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Alignment Scores:
Pred. No.: 0.00247 Length: 2834
Score: 115.00 Matches: 53
Percent Similarity: 50.00% Conservative: 38
Best Local Similarity: 29.12% Mismatches: 69
Query Match: 12.79% Indels: 24
DB: Gaps: 10
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US-09-970-076-2_COPY_44_216 (1-173) x US-10-750-185-39040 (1-2834)

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QY 1 AspleuTyRheileuApLySeRgLySeValleuHishTRPaengluile 18
DB 2115 GACATTATCTCTCTATATGACGGGCTCGGACAGTACC-----CACCAAGACGACTTCTC 2062
QY 19 ---lleTyTyRheValGluGlnLeuAlaHishLyPhe---lleSeRProGlnLeuArg 36
DB 2061 GCGATGAAGGTGTTCTATGATGAAGATGAAGATGTTCCACCTGGAACCGAC--AGA 2005
QY 37 MetSerPheIleValPheSeRThrArgGlyThrPheLeuMetLySeuThrGluAsp 56
DB 2004 GTCCAGTTGGAGTCTTCACTGATCTCGATGAAGTCAAGTCCAGTTACCTCAGCCAG 1945
QY 56 gGluGlnIleArgGlnGlyLeuGln-----GlnLeuGlnLySeuValleuProG 72
DB 1944 CACTCCAGTGTGCAAGGCTGAGGATAGCCGTTGACAGATCCAGACAG-----AAGGG 1891
QY 72 yGlyAspThrTyRheHishGluGlyPheGluArgAlaSeRgLuGlnIleTyTyTyGluAs 92
DB 1890 AGGGGACACCAAGATGGTGAAGGCGCTG--GGACACATGATCCAGGTCTTTCAGAGCTC 1834
QY 92 nArgGlnGlyTyTyTyRgThrAlaSeRValIleIleAlaLeuThrAspGlyGluLeuHishG 112
DB 1833 TGCTCGAGCA--CGTGCCTT--GGTATCTCATTTGTTGCTACCTGACGCGCAATCTATGCA 1776
QY 112 uAspLeuPhePheTyRSeRgLuArgGluAlaAsnArgSeRArgAspLeuGlyAlaIleVa 132
DB 1775 CCGGCG-----GCTGATGCTGACAGAGGCGGAGGCGGCAATGATCAACAT 1728
QY 132 lTyTyCyValGlyValIlyAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLy 152
DB 1727 TTATGAGATTTGGAGTCAAGATCTCTAATATTGCTGAGCTTCAAGAGATTTGCTAA-- 1673
QY 152 sAspHishValPheProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHishSerI 172
DB 1672 -GACAGAGTGTTTTGTGATGAT--TTTGAATCTTGAAGACCATCCACAAAGAGT 1617
QY 172 eLeu 173
DB 1616 GGTAA 1613
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RESULT 5
US-10-601-368-20
; Sequence 20, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
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APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
CURRENT APPLICATION NUMBER: US/10/601,368
PRIOR FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 3564
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(3564)
US-10-601-368-20

Alignment Scores:
Pred. No.: 0.00296 Length: 3564
Score: 108.00 Matches: 48
Percent Similarity: 38.38% Conservative: 28
Best Local Similarity: 24.24% Mismatch: 84
Query Match: 12.01% Indels: 38
DB: Gaps: 9

US-09-970-076-2_COPY_44_216 (1-1173) x US-10-601-368-20 (1-3564)

QY 1 AspleuTyRheIleuLeuAplySerGIySerValIleuH18H18TPA8nGIuIleTyR 20
Db 490 GACATCTCATCTGATCTTCTAGATGGCTCCACACAGCATC--TACCCCTGGGTGAAGTCCAA 546
QY 21 TyRPhelAluIuIuIeumIaH1sluysPhe---IleSerPro---GIleuAixMetSer 38
Db 547 CACTTCTCATCAATATCTCAAAAAGTTCTACATTTGGCCCGGCGCAAGATCAGAGTGGGA 606
QY 39 PheIleValPheSerThiArgGIyThiRThIleuMetIyLeuThiGIuAspAArgGIuIn 58
Db 607 ATATGTCAGATATGAGAAAGATGCGGTCATGAGTTCACACTT---AATGACTACAGGCT 663
QY 59 IleaArgInIyIeuGIuIuIeunIyValIeuProGIyAspThiTyMetHis 78
Db 664 GTAAAGAATGATGGTGAAGCCGCGACGACCATTTGAGACAGAGAGGAGGACAGACCCGC 723
QY 79 GIuGIyPheGIu-----ArgAlaSerGIuGIuIleTyRThiGIuAsnAArgGIuIy 95
Db 724 ACGGCATTTGGCATTTGCAATTGCAAGCTCGAGGCTTTCCAGAAAGGTGGAAAGAAAGG 789
QY 96 TytaRgThraIaSerValIleIleAlaIleuThiAspGIyGIuIeunIsgIuAsp----- 113
Db 784 GCCAAG-----AAAGTATGATTTGATCATCAGGACGGGGAAATCCACAGACGCCCAAC 833
QY 113 ----- 1113
Db 838 CTGGAAGAAGTGATCCGGCAGAGCAGAAAGCAACGTGACAGATACGCTGTGGCCGTT 897
QY 114 LeuPhePheTySerGIuAArgGIuIaIeunAArgSerThiAspLeuGIyAlaIleValTyR 133
Db 898 TTGGGCTACTTCAACCCACGGGGGATCAATACAGAGACTTTTCTAAATGAATCAAAATAC 955
QY 134 CyuValGIyValIyAsp-----PheAsnGIuThGIuIeunAlaArgIleAla 145
Db 958 ATCCGCAAGCAGCCCTGAGACAGACACTTTTCAAGCTCACAGATGAGGCGGCGCTG--- 1015
QY 150 AspSerIyAspPheIleValIlePheProValAsnAspGIyPheGIuAlaIeuGIuIy 167
Db 1015 -----AAGGACATTTGATGATGCCCTTGGGGACAGGATCTTACAGCTTGAAGGC 1062

RESULT 6
US-10-601-368-19

```

```

Sequence 19, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lora, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
CURRENT APPLICATION NUMBER: US/10/601,366
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 4858
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (28) ... (3591)
US-10-601-368-19

Alignment Scores:
Pred. No.: 0.00465 Length: 4858
Score: 108.00 Matches: 48
Percent Similarity: 38.38% Conservative: 28
Best Local Similarity: 24.24% Mismatches: 84
Query Match: 12.01% Indels: 38
DB: Gaps: 9

US-09-970-076-2_COPY_44_216 (1-173) x US-10-601-368-19 (1-4858)
QY 1 AspleuYrPheleleAeApLySeSerValLeuHishITrPaengIleTyr 20
   |||::: ::|||::: |||::: ::|||:::
DB 517 GACATCGCATGTGCTTATGATGGCTCCACAACGATC---TACCCTGGGTGGAGTCCAA 573
   21 TyrPheValGluInLeuAlaHishLyPhe---IleSerPro---GlnLeuArgMetSer 38
   ::|||::: ::|||::: |||::: |||:::
DB 574 CACTTCCCATCAATATCTCTCAAAAAGTTCTACATTTGGCCCCCGCCAGATCCAGTGGGA 633
   39 PheIleValPheSerThrArgGlyThrThiLeuMetLyLeuThrGluAerArgGluIn 58
   ::|||::: ::|||::: |||::: |||:::
DB 634 ATAGTCCAGTGTGGAGAAGATGCGCGTCACATGATTCACCTT---AATGACTACAGTCT 690
   59 IleArgGlnGlyLeuGluGluLeuGlnIleValLeuProGlyGlyAspThrTyrMetHis 78
   ::|||::: ::|||::: |||::: |||:::
DB 651 GTAAAGATGTGTGGAGAACCCGCCACGACACTTGACGACAGAGAGGAGACAGAACCCGC 750
   79 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyrGluAerArgGlnGly 95
   |||::: |||::: |||::: |||:::
DB 751 ACGGCAATTGGCATTTGATTTGCACGCGTCCGAGCGCTTCCAGAAAGGTGGAAAGAGCG 810
   96 TyrArgThrAlaSerValIleIleAlaLeuThrArgGlyGluLeuHishGluAsp----- 113
   ::|||::: |||::: |||::: |||:::
DB 811 GCCAAG-----AAGATGATATTGTCTACAGAGCGGGAATCCACGACAGCCCGAC 864
   113 ----- 113
DB 865 CTGGAGAAAGTGTATCCGCGCAGAGGAGAAAGCAAACTGACCAATACGTGTGCGCGT 924
   114 LeuPhePheTyrSerGluArgGluAlaAerArgSerArgAerLeuGlyAlaIleValTyr 133
   |||::: |||::: |||::: |||:::
DB 925 TTGGGCTACTACAAACCGCAGGGGGATCAATCCAGAGACTTTTCTTAATGATAAATAC 984
   134 CysValIGlyValLyAsp-----PheAerGluThrGlnLeuAlaArgIleAla 149
   |||::: |||::: |||::: |||:::
DB 985 ATGCCCAACGACCTTCGACGACAGACACTTCTTCAACGTCAACAGATGAGCGGCCCTG--- 1041
   150 AepSerLyAspPheValPheProValAerAerGlyPheGlnAlaLeuGlnGly 167
   |||::: |||::: |||::: |||:::
DB 1042 -----AAGCATCTTGTGATGCGCTTGGGAGCAGAGATCTTCAGCTTGGAGGC 1089

```

```
RESULT 7
US-10-601-368-2
; Sequence 2, Application US/10601368
; Publication No. US20050260702a1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Jose M.
; TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
; FILE REFERENCE: 07334-275001
; CURRENT APPLICATION NUMBER: US/10/601,368
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US/09/561,263A
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/322,790
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3564
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3564)
US-10-601-368-2
```

```
Alignment Scores:
Pred. No.: 0.0101 Length: 3564
Score: 104.00 Matches: 48
Percent Similarity: 38.38% Conservative: 28
Best Local Similarity: 24.24% Mismatches: 84
Query Match: 11.57% Indels: 38
Gaps: 9
```

US-09-970-076-2_COPY_44_216 (1-173) x US-10-601-368-2 (1-3564)

```
QY 1 AspleuTyrrheleleuaplysSerGlySerValLeuHisThrPaengluiletyr 20
Db 490 GACATCGTCATGTCCTGGATGCTCCACAGCATC--TACCCCTGGGTGAAGTTGAG 546
QY 21 TyrPheValGluGlnLeuAlaHisIlePhePhe--IleSerPro--GlnLeuArgMetSer 38
Db 547 CACTTCCTCATCAATCCTCGAATAAGTTTAACTATGCCAGGCGGACATCCAGTTGGA 606
QY 39 PheIleValPheSerThrArgGlyThrThleuMetIleuThrGluAspArgGluGln 58
Db 607 GTTGTGAGATGAGCGAAGATGTGTCATGATTCACCTC--AACGACTACAGGTCT 663
QY 59 IleArgGlnIleuGluGlnLeuGlnIleuValLeuProGlyGlyAspThrTyrrMetHis 78
Db 664 GTAAAGATGTGTGGAGAGCTGCCACCATTTGACGACAGAGAGAGAGAACAGACCCGG 723
QY 79 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrrGluAsnArgGlnGly 95
Db 724 ACGGCAATTTGGCATGTAATTTGACAGCGCTCAGAGGCTTCCAGAAAGGTGAGAAAGGA 783
QY 96 TyrArgThrAlaSerValIleIleAlaLeuThrArgGlyGluLeuHisIleuAsp----- 113
Db 784 GCCAAG-----AAGGTGATGATTTGATCACAATGGGGAGTCCACGACGCCAGAC 837
QY 113 ----- 113
Db 838 CTGAGAAAGTGATCCACGAAAGCGAAAGAGACAAGTAAACAGATATGCCGGCCGCTC 897
QY 114 LeuPhePheTyrrSerGluArgGluAlaAsnArgSerArgAspLeuGluAlaIleValTyrr 133
Db 898 CTGGGCACTACACACCGAGGGGATCAATCCAGAACTTTCTTAATGAATCAATATAC 957
QY 134 CysValGlyValIleAsp-----PheAsnGluThrGlnLeuAlaArgIleAla 149
Db 958 ATCCGCAAGTACCTGTATGACAGACACTTTCTTCAATGATGATGAGGCTGCTG--- 1014
```

```
QY 150 AspSerIysAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGly 167
Db 1015 -----AAGGACATTTGATGTCCTGGGGGACAGAAATCTTCACTCGAAAGGC 1062
```

```
RESULT 8
US-11-000-463-574
; Sequence 574, Application US/11000463
; Publication No. US20050266423a1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 574
; LENGTH: 3967
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-000-463-574
```

```
Alignment Scores:
Pred. No.: 0.0118 Length: 3967
Score: 104.00 Matches: 48
Percent Similarity: 38.38% Conservative: 28
Best Local Similarity: 24.24% Mismatches: 84
Query Match: 11.57% Indels: 38
Gaps: 9
```

US-09-970-076-2_COPY_44_216 (1-173) x US-11-000-463-574 (1-3967)

```
QY 1 AspleuTyrrheleleuaplysSerGlySerValLeuHisThrPaengluiletyr 20
Db 539 GACATCGTCATGTCCTGGATGCTCCACAGCATC--TACCCCTGGGTGAAGTTGAG 595
QY 21 TyrPheValGluGlnLeuAlaHisIlePhePhe--IleSerPro--GlnLeuArgMetSer 38
Db 596 CACTTCCTCATCAATCCTCGAATAAGTTTAACTATGCCAGGCGGACATCCAGTTGGA 655
QY 39 PheIleValPheSerThrArgGlyThrThleuMetIleuThrGluAspArgGluGln 58
Db 656 GTTGTGAGATGAGCGAAGATGTGTCATGATTCACCTC--AACGACTACAGGTCT 712
QY 59 IleArgGlnIleuGluGlnLeuGlnIleuValLeuProGlyGlyAspThrTyrrMetHis 78
Db 713 GTAAAGATGTGTGGAGAGCTGCCACCATTTGACGACAGAGAGAGAGAACAGACCCGG 772
QY 79 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrrGluAsnArgGlnGly 95
```

```
Db 773 ACGGCACTTTGGCATTTGATTTGACGCTCAGACGCTTTCCAGAAAGGTGGAGAAAGGA 832
Qy 96 TTTATGThralaservalllellealeuthrAspGlyGluLeuHISgluubp----- 113
Db 833 GCCAAG-----AAGGTGATGATTTGATTCACAGATGGGAGTCCACGACGACCCAGAC 886
Qy 113 ----- 113
Db 887 CTGGAGAGGTGATCCAGCAAGCGAAAGACACGTAACAAGATATGCGTGGCCGTC 946
Qy 114 LeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyr 133
Db 947 CTGGGCTACTACAAACGCGAGGGGAGTCAATCCAGAAACTTTCTTAATGAATCAAAATAC 1006
Qy 134 CysValGlyValIlyAsp-----PheAsnGluThrGlnLeuAlaArgIleAla 149
Db 1007 ATGCCAGATGACCCCTGATGACAAAGCACTTCTTCAATGTCACTGATGAGGCTGCTTG--- 1063
Qy 150 AspSerLysAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGly 167
Db 1064 -----AAGGACATTTGTGATGCCCTGGGGGACAGAAATCTTCACTTGGAAGGC 1111

RESULT 9
US-11-000-463-102
Sequence 102, Application US/11000463
Publication No. US20050266423A1
GENERAL INFORMATION:
APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Aaundi, Vinod
APPLICANT: Chen, Rui-hong
APPLICANT: Qian, Xiaohong B.
APPLICANT: Wang, Zhiwei
APPLICANT: Wehrman, Tom
APPLICANT: Zhang, Jie
APPLICANT: Zhou, Ping
APPLICANT: Cao, Yi-cheng
APPLICANT: Dimanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785CIP4CN
CURRENT APPLICATION NUMBER: US/11/000,463
CURRENT FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: 10/291,265
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 102
LENGTH: 3969
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (52)..(3618)
US-11-000-463-102

Alignment Scores:
Pred. No.: 0.0118 Length: 3969
Score: 104.00 Matches: 48
Percent Similarity: 38.38% Conservative: 28
Best Local Similarity: 24.24% Mismatches: 84
```

```
Query Match: 11.57% Indels: 38
DB: 7 Gaps: 9
US-09-970-076-2_COPY_44_216 (1-173) x US-11-000-463-102 (1-3969)
Qy 1 AppLeuTyrPheIleLeuAspLysSerGlySerValLeuHISgluubpIleTyr 20
Db 541 GACATGTCATGATGCTGGATGGCTGATCCAAACAGCATC---TACCCTGGGTGAGGTTCAG 597
Qy 21 TyrPheValGluGlnLeuAlaHisLysPhe---IleSerPro---GlnLeuArgMetSer 38
Db 598 CACTTCTCTATCAACATCTTGAAAAGTTTTCATTGCGCCGAGGCGAGATCCAGTTGGA 657
Qy 39 PheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGluGln 58
Db 658 GTTGTGCAGTATGGGGAAGATGTGTGATGATGATTCACCTC---AAGCATCAAGGTCT 714
Qy 59 IleArgGlnGlyLeuGluGlnLeuGlnLysValLeuProGlyGlyAspThrTyrMetHis 78
Db 715 GTAAAAAGATGTGTGGAAGCTGCCAGCCACATTTGAGCAGAGAGGAGGAACAGACCCGG 774
Qy 79 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGly 95
Db 775 ACGGCACTTTGGCATTTGATTTGACGCTCAGAGGCTTTCCAGAAAGGTGGAGAAAGGA 834
Qy 96 TTTATGThralaservalllellealeuthrAspGlyGluLeuHISgluubp----- 113
Db 835 GCCAAG-----AAGGTGATGATTTGATTCACAGATGGGAGTCCACGACGACCCAGAC 888
Qy 113 ----- 113
Db 889 CTGGAGAGGTGATCCAGCAAGCGAAAGACAAAGTAACAAGATATGCGTGGCCGTC 948
Qy 114 LeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyr 133
Db 949 CTGGGCTACTACAAACGCGAGGGGAGTCAATCCAGAAACTTTCTTAATGAATCAAAATAC 1008
Qy 134 CysValGlyValIlyAsp-----PheAsnGluThrGlnLeuAlaArgIleAla 149
Db 1009 ATGCCAGATGACCCCTGATGACAAAGCACTTCTTCAATGTCACTGATGAGGCTGCTTG--- 1065
Qy 150 AspSerLysAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGly 167
Db 1066 -----AAGGACATTTGTGATGCCCTGGGGGACAGAAATCTTCACTTGGAAGGC 1113

RESULT 10
US-10-601-368-1
Sequence 1, Application US/10601368
Publication No. US20050260702A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Lora, Jose M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
CURRENT APPLICATION NUMBER: US/10/601,368
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 5042
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (127)...(3690)
US-10-601-368-1

Alignment Scores:
Pred. No.: 0.0168 Length: 5042
```


Score: 104.00 Matches: 48
Percent Similarity: 38.38% Conservative: 28
Best Local Similarity: 24.24% Mismatches: 84
Query Match: 11.57% Indels: 38
DB: 6 Gaps: 9

US-09-970-076-2_COPY_44_216 (1-173) x US-10-601-368-1 (1-5042)

```
OY 1 AspleuYrhrheleuAerlySerGlySerValLeuHnHstPranGluIleTyr 20
DB 616 GACATCTCTATTCCTGAGTGGCTCCAAACGCAATC--TACCTCGGTGGAGGTTGAG 672
OY 21 TyrPheValGluGlnLeuAlaHnIleYrPhe--IleSerPro--GlnLeuArgMetSer 38
DB 673 CACTTCCTCATCAACATCCCGAAAAGTTTACCTTTGGCCAGGCGAGATCCAGCTTGA 732
OY 39 PheIleValPheSerThrArgGlyThrThreuMetLysLeuThrGluAerArgGluGln 58
DB 733 GTTGTGACAGTATGCGAAGATGTGTCATGATGTTCACTTC--AACGACTACAGGCT 789
OY 59 IleArgGlnGlyLeuGluGlnLeuGlnIleValLeuProGlyIleAerThrTyrMetHis 78
DB 790 GTAAGAATGTGTGGAAAGCTGCCAGCCACATTGAGAGAGAGGAGAACAGAGACCCGG 849
OY 79 GluGlyPheGlu-----ArgAlaSerGluGlnIleTyrTyrGluAerArgGlnGly 95
DB 850 ACGGCATTTGGCATGTAATTTGCACGCTCAGAGGCTTCCAGAAAGGTGGAAAGAACGA 909
OY 96 TyrArgThrAlaSerValIleIleAlaLeuThrAerGlyGluLeuHnIleGluAerPhe 113
DB 910 GCCAAG-----AAGTGATGATGTTCATCAGATGGAGTCCACAGACGCCAGAC 963
OY 113 ----- 113
DB 964 CTGAGAGAGGTATCCAGAAAGCAAGACAAACATTCAGGCTGGCCGCTC 1023
OY 114 LeuPhePheTyrSerGluArgGluAlaAerArgSerArgAerGluAlaIleValTyr 133
DB 1024 CTGGGCTACTTCAACACCGGAGGAGTATCCAGAACTTTCTTAATGAATCAATAC 1083
OY 134 CysValGlyValLysAer-----PheAerGluThrGlnLeuAlaArgIleAla 149
DB 1084 ATCGCCAGTACCCTGATGACAGCACTTCTCAATGTCACTGATGAGGCTGCTTG-- 1140
OY 150 AspSerLysAerPheIleValPheProValAerAerGlyPheGlnAlaLeuGlnGly 167
DB 1141 -----AAGGACATTTGTGATGCTGGGAGCAGAACTTTCAGCCTGAAAGGC 1188
```

RESULT 11

US-10-821-234-182/C
Sequence 182, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Steache-Crain, Birgit
APPLICANT: Andermani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: PC_SEQ_genes Version 1.0
SEQ ID NO 182
LENGTH: 2501
TYPE: DNA
ORGANISM: Homo sapiens
US-10-821-234-182
Alignment Scores: 0.013 Length: 2501

Score: 101.50 Matches: 47
Percent Similarity: 43.06% Conservative: 43
Best Local Similarity: 22.09% Mismatches: 74
Query Match: 11.29% Indels: 45
DB: 6 Gaps: 10

US-09-970-076-2_COPY_44_216 (1-173) x US-10-821-234-182 (1-2501)

```
OY 1 AspleuYrhrheleuAerlySerGlySerVal-----LeuHnHnHs 15
DB 1550 AACATCTACTGTGGTGAATGATGATGACAGACGATGGGCGCCAGCACTTCAACAGAGCC 1491
OY 16 TrpAerGluIleTyrTyrPheValGluGlnLeuAlaHnIleYrPheIleSerProGlnLeu 35
DB 1490 AAAAGTGTATGCAACTTAATTGACAGAGTGGCAAGTTATGTGTGAAGCCA----- 1437
OY 36 ArgMetSerPheIleValPheSerThrArgGlyThrThreuMetLysLeuThrGluAerArg 54
DB 1436 AGATATGTCTAGTATGACATATGCAATACCCCAAAATTTGGGTCAAAAGTGTGAAGCA 1377
OY 55 -----AspArgGluGlnIleArgGlnGlyLeuGlnIleu-----Gln 67
DB 1376 GACAGACATATGACAGCTGGTGCACAGAACACCTCAATGAATCAATTATGAAGACCA 1317
OY 68 LysValLeuProGlyIleAerThrTyrMetHisGluGlyPheGluArgAlaSerGluGln 87
DB 1316 AAGTTGAAGTCAGAGCAATACACC-----AAGAAAGCTTCCAGCA 1275
OY 88 IleTyrTyrGluAerArg-----GlnGlyTyr--ArgThrAla 99
DB 1274 GTGTACAGCATGATGATGAGCTGGCCAGATGACCTCCTCTGAAGCTGAAACCCGACCCG 1215
OY 100 SerValIleIleIleAlaLeuThrAerGly----- 108
DB 1214 CATGTATCATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1155
OY 109 -----GluLeuHnIleGluAerPhePheTyrSerGluArgGluAlaAerArgSerArg 126
DB 1154 ATTGATGATGATCCCGGACTTGTATATCATTTGCGAAGATGCAAAACCAAGGAGAT 1095
OY 127 AspleuGlyAlaIleValTyrCysValGly-----ValLysAerPheAerGluThrGln 144
DB 1094 TATCTGAGATGTATATGATGTTGGGTGCGGCTTGTGTGAACCAAGTGAATCATATGCT 1035
OY 145 LeuAlaArgIleAlaAerSerLysAerPheIleValPheProValAerAerGlyPheGlnAla 164
DB 1034 TTGCTTCCAAAGAAAGCAATGACAAACATGTGTTCAAAGTCAAGAT--ATGGAAC 978
OY 165 LeuGlnGlyIleIleHnHnHnHnHnHnHnHnHnHnHnHnHnHnHnHnHnHnHnHnHnHn 173
DB 977 CTGAAAGATGTTTCTTACCAATGATC 951
```

RESULT 12

US-10-131-826A-293
Sequence 293, Application US/10131826A
Publication No. US20050245730A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeNovo, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William

Db 873 ACAGCATCTGATCTTTCATCGGTGGCCAGGTGAGCTTCAACAGCTGAGGCC 932
Qy 146 AlAarglleAlAaerSerLyAaerPhValPheProVal 158
Db 933 ATTGGAGGAGCCGCCAGAGACGACCTTCTCTGATG 971

RESULT 14
US-10-995-561-464
/ Sequence 464, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 464
/ LENGTH: 3175
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-464

Alignment Scores:
Pred. No.: 0.0855 Length: 3175
Score: 96.50 Matches: 45
Percent Similarity: 41.12% Conservative: 36
Best Local Similarity: 22.84% Mismatches: 83
Query Match: 10.73% Indels: 33
Gaps: 8

US-09-970-076-2_COPY_44_216 (1-173) x US-10-995-561-464 (1-3175)

Qy 2 LeuTYrPheIleuAaerLySerGlySerVal----- 12
Db 243 GTGTACTCTGCTGGACACTCGAGAGGCTGACCATGCAATGCCCGCCAGCATCTCG 302
Qy 13 LeuNIHietrAaerGlu---IleTYrTYrPheValGluGluLeuAlaNIHValPheIle 31
Db 303 CTCTCCACATGAGCAGTTCGTGCGCCAGTTCATGACGAGCTCGAGACGAGTCTTAC 362
Qy 32 SerProGluLeuAaerMetSerPhe-----IleValPheSerThrAaerGlyThr 47
Db 363 CTGACACAGGTGGCGTGAAGTGGCGCTAAGCGGCGCTGACTTCTTACACAGGTGAG 422
Qy 48 ThrLeuMetLyLeuThrGluAaerAaerGluGluIleAaerGluLeuGluLeuGlu 67
Db 423 GTGTTCAGCCACCGGCGAGCGGCGCTCTTCATCAAGAACTGCGAGGCGATCAGC 482
Qy 68 LysValAlaLeuProGlyGlyAaerThyTyrMetNIHValGluIlePheGluAaerGluGlu 87
Db 483 TCCTTCGCGCGCGGCG-----ACCTTCACCGACTGCGCGCTGCGCAACATGAGGAGCAG 536
Qy 88 IleTYrTYrGluAaerAaerGluGluTYrAaerThraIleSerValIleIleAlaLeuThraP 107
Db 537 ATCCGCGAGAGCCGCGAGCAGAGGCG-----ACGTCACATTCGCGCGTGTGATCAGCCAGC 590
Qy 108 GlyGluLeuNIHietrAaerLyLeuPhePheTYrSerGluAaerGluAlaAaerAaerAaer 127
Db 591 GCGCAGCTACCGGCGAGCGGCGGCGGATCAAGCTGAGGCGCGAGCGGCGCGGCG 650
Qy 128 LeuGlyAlaIleValTYrGlyVal-----GlyValLys 138
Db 651 GAGGCGATCCGCGCTTTCGCGCGTGGCGCCCAACAGAACTGAAGAGCAGGCGCTGCGG 710
Qy 139 AaerPheAaerGluThr-----GluLeuAlaAaerGluIleAlaAaerSerLyAaerPhValPhe 156
Db 711 GACATGCGCAGACGCGCGAGCAGCTTACCGC-----AACGACTAGCGGCACC 758
Qy 157 ProValAaerAaerLyPheGluAlaLeuGluGluIleIleNIHietrLeu 173

Db 759 ATGCTGCTGATCTTCACCGAGATTCACAGACCAACCATCAACCGCATCATC 809
Qy 759 ATGCTGCTGATCTTCACCGAGATTCACAGACCAACCATCAACCGCATCATC 809

RESULT 15
US-10-995-561-465
/ Sequence 465, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 465
/ LENGTH: 3464
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-465

Alignment Scores:
Pred. No.: 0.0971 Length: 3464
Score: 96.50 Matches: 45
Percent Similarity: 41.12% Conservative: 36
Best Local Similarity: 22.84% Mismatches: 83
Query Match: 10.73% Indels: 33
Gaps: 8

US-09-970-076-2_COPY_44_216 (1-173) x US-10-995-561-465 (1-3464)

Qy 2 LeuTYrPheIleuAaerLySerGlySerVal----- 12
Db 243 GTGTACTCTGCTGGACACTCGTGAAGGCTGACCATGCAATGCCCGCCAGCATCTCG 302
Qy 13 LeuNIHietrAaerGlu---IleTYrTYrPheValGluGluLeuAlaNIHValPheIle 31
Db 303 CTCTCCACATGAGCAGTTCGTGCGCCAGTTCATGACGAGCTCGAGACGAGTCTTAC 362
Qy 32 SerProGluLeuAaerMetSerPhe-----IleValPheSerThrAaerGlyThr 47
Db 363 CTGACACAGGTGGCGTGAAGTGGCGCTAAGCGGCGCTGACTTCTTACACAGGTGAG 422
Qy 48 ThrLeuMetLyLeuThrGluAaerAaerGluGluIleAaerGluLeuGluLeuGlu 67
Db 423 GTGTTCAGCCACCGGCGAGCGGCGCTCTTCATCAAGAACTGCGAGGCGATCAGC 482
Qy 68 LysValAlaLeuProGlyGlyAaerThyTyrMetNIHValGluIlePheGluAaerGluGlu 87
Db 483 TCCTTCGCGCGCGGCG-----ACCTTCACCGACTGCGCGCTGCGCAACATGAGGAGCAG 536
Qy 88 IleTYrTYrGluAaerAaerGluGluTYrAaerThraIleSerValIleIleAlaLeuThraP 107
Db 537 ATCCGCGAGAGCCGCGAGCAGAGGCG-----ACGTCACATTCGCGCGTGTGATCAGCCAGC 590
Qy 108 GlyGluLeuNIHietrAaerLyLeuPhePheTYrSerGluAaerGluAlaAaerAaerAaer 127
Db 591 GCGCAGCTACCGGCGAGCGGCGGCGGATCAAGCTGAGGCGCGAGCGGCGCGGCG 650
Qy 128 LeuGlyAlaIleValTYrGlyVal-----GlyValLys 138
Db 651 GAGGCGATCCGCGCTTTCGCGCGTGGCGCCCAACAGAACTGAAGAGCAGGCGCTGCGG 710
Qy 139 AaerPheAaerGluThr-----GluLeuAlaAaerGluIleAlaAaerSerLyAaerPhValPhe 156
Db 711 GACATGCGCAGACGCGCGAGCAGCTTACCGC-----AACGACTAGCGGCACC 758
Qy 157 ProValAaerAaerLyPheGluAlaLeuGluGluIleIleNIHietrLeu 173
Db 759 ATGCTGCTGATCTTCACCGAGATTCACAGACCAACCATCAACCGCATCATC 809

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JOD time : 155.602 secs
